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(54) Titre: STREPTOCOCCUS AGALACTIAE GENOME SEQUENCE, USE FOR DEVELOPING VACCINES, DIAGNOSTIC
TOOLS, AND FOR IDENTIFYING THERAPEUTIC TARGETS

A2 (54) Titre : SEQUENCE DU GENOME STREPTOCOCCUS AGALACTIAE, APPLICATION AU DEVELOPPEMENT DE VAC-
CINS, D'OUTILS DE DIAGNOSTIC, ET A L'IDENTIFICATION DE CIBLES THERAPEUTIQUES

(57) Abstract: The invention concerns the genome sequence and nucleotide sequences coding for *Streptococcus agalactiae* polypep-
tides, such as cellular envelope polypeptides, or secreted or specific polypeptides, or polypeptides involved in the metabolism and the
replication process, as well as vectors or cells comprising said sequences. The invention also concerns the use thereof for developing
vaccines, diagnostic tools, DNA chips and for identifying therapeutic targets.

(57) Abrégé : L'invention a pour objet la séquence génomique et des séquences nucléotidiques codant pour des polypeptides de
Streptococcus agalactiae, tels que des polypeptides d'enveloppe cellulaire, ou des polypeptides sécrétés ou spécifiques, ou impliqués
dans le métabolisme et dans le processus de réplication, ainsi que des vecteurs ou cellules incluant lesdites séquences. L'invention
porte également sur leur application au développement de vaccins, d'outils de diagnostic, de puces à ADN et à l'identification de
cibles thérapeutiques.

Séquence du génome *Streptococcus agalactiae*, application au développement de vaccins, d'outils de diagnostic, et à l'identification de cibles thérapeutiques.

L'invention a pour objet la séquence génomique et des séquences nucléotidiques
5 codant pour des polypeptides de *Streptococcus agalactiae*, tels que des polypeptides d'enveloppe cellulaire, ou des polypeptides sécrétés ou spécifiques, ou impliqués dans le métabolisme et dans le processus de réplication, ainsi que des vecteurs ou cellules incluant lesdites séquences. L'invention porte également sur leur application au développement de vaccins, d'outils de diagnostic, de puces à ADN et à l'identification
10 de cibles thérapeutiques.

Streptococcus agalactiae est un streptocoque β -hémolytique qui constitue la seule espèce appartenant au groupe B de Lancefield (SGB). Les infections néonatales à streptocoques du groupe B posent un important problème de santé publique qui ne se
15 limite pas aux pays en voie de développement. Leur incidence est de 2,5 pour 1 000 naissances, avec un taux de mortalité qui varie actuellement dans les pays industrialisés entre 4 et 10 % selon les études. Cette bactérie est responsable d'environ 20 % des méningites bactériennes recensées en France et des séquelles neurologiques sont alors observées dans 25 à 50 % des cas. Elle est également à l'origine de mort foetale *in utero*.
20 Le polyoside capsulaire est l'antigène de surface majeur des SGB. Cinq sérotypes (Ia, Ib, II, III et V) sont généralement détectés au cours des infections humaines, le sérotype III étant retrouvé dans 75 % des infections néonatales avec atteinte méningée. Au niveau cellulaire et moléculaire, les différentes étapes du processus infectieux dû à *S. agalactiae* sont encore peu connues. Il est vraisemblable que, dans le cas du syndrome
25 précoce (infections survenant dans les 24 premières heures), la bactérie inhalée pénètre dans les cellules de l'épithélium alvéolaire du nouveau-né et traverse cette barrière pour disséminer ultérieurement dans la circulation générale. La genèse du syndrome tardif précoce (infections survenant entre le 7^{ème} jour et le 3^{ème} mois) et des autres infections à SGB reste encore très mal comprise. Le seul facteur de virulence des SGB
30 dont le rôle a été clairement démontré est le polyoside capsulaire qui permet l'échappement au système immunitaire de l'hôte. La contribution exacte de certaines protéines de surface (antigène C, protéine Rib et C5a peptidase) à la virulence de cette bactérie est encore peu connue.

Une recherche réalisée sur le site EXPASY (<http://www.expasy.ch/>) indique qu'il existe 112 références de séquences protéiques dans les banques Swissprot et TREMBL. Ce nombre inclut des protéines codées par des plasmides de *S. agalactiae*. Ces séquences représentent donc une vision partielle d'un nombre limité d'aspect de la biologie de *S. agalactiae*. La biosynthèse de la capsule polysaccharidique est un des aspects les mieux connus de la virulence de cette bactérie. Par ailleurs, les gènes codant pour 6 protéines exposées à la surface sont également connus (3).

Afin d'appréhender de manière globale les déterminants génétiques impliqués dans ces processus ainsi que le métabolisme de *Streptococcus agalactiae*, le séquençage du génome de *Streptococcus agalactiae* a été réalisé. Le génome de la souche *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) qui a été responsable d'une septicémie mortelle a été choisi pour ce séquençage. Cette souche possède un sérotype capsulaire III, ne présente pas de résistance acquise aux antibiotiques, est génétiquement modifiable et est virulente dans un modèle d'infection murin. La connaissance complète du génome est une étape cruciale pour la caractérisation des gènes impliqués dans le développement du processus infectieux : adhésion et franchissement des structures épithéliales, échappement au système immunitaire et adaptation à des conditions de culture variées et souvent hostiles (pH, stress oxydatif et carences nutritionnelles), qui constituent des cibles potentielles pour de nouvelles stratégies thérapeutiques. La comparaison du génome de *S. agalactiae* avec ceux d'autres pathogènes à Gram positif (*Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Staphylococcus aureus*, *Listeria monocytogenes*, ...) doit permettre d'identifier de nouveaux gènes de virulence ainsi que de nouvelles cibles pour construire des souches de virulence atténuées et des vaccins. Les protéines de surfaces constituent des candidats pour une future préparation vaccinale. Dans les tableaux 2 et 6 ci-après sont répertoriés respectivement 25 et 30 nouveaux gènes, nouvellement identifiés, codant pour des protéines potentiellement liées au peptidoglycane et présentant le motif de liaison LPXTG.

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La séquence complète du génome de *Streptococcus agalactiae* (CIP 82.45 (ATCC 12403)) a été obtenue. Ce génome est constitué d'un chromosome long d'environ 2,2 Mb identifié ici sous forme de 138 contigs représentés par les séquences SEQ ID No. 1 à SEQ ID No. 136, SEQ ID No. 138 et SEQ ID No. 139, et d'un plasmide

long de 45 kbases présent dans la souche séquencée représenté par la séquence SEQ ID No. 137. La séquence complète du génome est représentée par la séquence SEQ ID No. 2345.

5 Une liste des phases codantes annotées identifiées par l'analyse des séquences de ces contigs est donnée au tableau 1.

Une liste des phases codantes pour des protéines de surface nouvellement identifiées est donnée au tableau 2 comme indiqué précédemment.

Une liste des phases codantes annotées identifiées par l'analyse de la séquence génomique complète SEQ ID No. 2345 est donnée au tableau 3.

10 Une liste des phases codantes pour des protéines de surface identifiées à partir de l'analyse de la séquence génomique complète SEQ ID No. 2345 est donnée au tableau 6 (protéines liées au peptidoglycane), tableau 8 (lipoprotéines). Tableau 9 (autres protéines de surface), Tableau 10 (protéines impliquées dans la biosynthèse des composés polysaccharidiques)

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La présente invention concerne les séquences nucléotidiques et polypeptidiques de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403).

20 Ainsi, c'est un objet de la présente invention que de caractériser la séquence du génome de *Streptococcus agalactiae*, CIP 82.45 (ATCC 12403) contenu dans la banque génomique préparée à partir du génome de cette souche et déposée à la CNCM le 28 décembre 2000 sous le numéro I-2610, ainsi que de tous les gènes et séquences régulatrices non codantes contenus dans ledit génome.

25 La présente invention concerne donc une séquence nucléotidique isolée et/ou purifiée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi les séquences SEQ ID No. 1 à SEQ ID No. 139 et la séquence SEQ ID No. 2345.

La présente invention concerne également une séquence nucléotidique isolée et/ou purifiée, issue de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi :

- 30 a) une séquence nucléotidique comportant au moins 75 %, 80 %, 85 %, 90 %, 95 % ou 98 % d'identité avec une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345 ;
- b) une séquence nucléotidique hybridant dans des conditions de forte stringence avec une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345,

- et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ;
- c) une séquence nucléotidique complémentaire d'une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, ou complémentaire d'une séquence
- 5 nucléotidique telle que définie en a), ou b), ou une séquence nucléotidique de l'ARN correspondant à l'une des séquences a) ou b) ;
- d) une séquence nucléotidique d'un fragment représentatif d'une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, ou d'un fragment
- 10 représentatif d'une séquence nucléotidique telle que définie en a), b) ou c) et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ;
- e) une séquence nucléotidique comprenant une séquence telle que définie en a), b), c) ou d) ; et
- f) une séquence nucléotidique telle que définie en a), b), c), d) ou e) modifiée, de
- 15 préférence comportant au plus 10 %, 5 %, 1 % ou 0, 5 % de nucléotides modifiés par rapport à la séquence de référence.

De façon plus particulière, la présente invention a également pour objet les séquences nucléotidiques isolées et/ou purifiées, caractérisées en ce qu'elles sont issues de SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, et en ce qu'elles codent pour

20 un polypeptide choisi parmi les polypeptides de séquence SEQ ID No. 140 à SEQ ID No. 2344, et SEQ ID No. 2346 à SEQ ID No. 4481.

La présente invention concerne aussi de façon plus générale les séquences nucléotidiques issues de SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, et codant pour un polypeptide de *Streptococcus agalactia*, telles qu'elles peuvent être

25 isolées à partir de SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345.

De plus, les séquences nucléotidiques isolées et/ caractérisées en ce qu'elles comprennent une séquence nucléotidique choisie parmi :

- a) une séquence nucléotidique codant pour un polypeptide choisi parmi les séquences SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No. 2346 à SEQ ID No. 4481 ;
- 30 b) une séquence nucléotidique comportant au moins 75 %, 80 %, 85 %, 90 %, 95 % ou 98 % d'identité avec une séquence nucléotidique codant pour un polypeptide choisi parmi les séquences SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No. 2346 à SEQ ID No. 4481 ;

- c) une séquence nucléotidique s'hybridant dans des conditions de forte stringence avec une séquence nucléotidique codant pour un polypeptide, choisi parmi les séquences SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No. 2346 à SEQ ID No. 4481, et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ;
- 5 d) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a), b), c) ou d) et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ; et
- 10 f) une séquence telle que définie en a), b), c), d) ou e) modifiée, de préférence comportant au plus 10 %, 5 %, 1 % ou 0,5 % de nucléotides modifiés par rapport à la séquence de référence,
- 15 sont également des objets de l'invention.

Selon une réalisation avantageuse, l'invention a pour objet les séquences nucléotidiques isolées et/ caractérisées en ce qu'elles comprennent une séquence nucléotidique choisie parmi :

- a) une séquence nucléotidique SEQ ID No. 4482 à SEQ ID No. 6617 ;
- 20 b) une séquence nucléotidique comportant au moins 75 %, 80 %, 85 %, 90 %, 95 % ou 98 % d'identité avec une séquence nucléotidique choisi parmi les séquences SEQ ID No. 2346 à SEQ ID No. 4481 ;
- c) une séquence nucléotidique s'hybridant dans des conditions de forte stringence avec une séquence nucléotidique choisi parmi les séquences SEQ ID No. 4482 à SEQ ID
- 25 No. 6617, et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ;
- d) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que
- 30 définie en a), b), c) ou d) et comprenant au moins 20 nucléotides, de préférence 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 500, 750, 1000 ou 1500 nucléotides ; et

f) une séquence telle que définie en a), b), c), d) ou e) modifiée, de préférence comportant au plus 10 %, 5 %, 1 % ou 0,5 % de nucléotides modifiés par rapport à la séquence de référence,

- 5 Par acide nucléique, séquence nucléique ou d'acide nucléique, polynucléotide, oligonucléotide, séquence de polynucléotide, séquence nucléotidique, termes qui seront employés indifféremment dans la présente description, on entend désigner un enchaînement précis de nucléotides, modifiés ou non, permettant de définir un fragment ou une région d'un acide nucléique, comportant ou non des nucléotides non naturels, et
- 10 pouvant correspondre aussi bien à un ADN double brin, un ADN simple brin qu'à des produits de transcription desdits ADNs. Ainsi, les séquences nucléiques selon l'invention englobent également les PNA (Peptid Nucleic Acid).

- 15 Il doit être compris que la présente invention ne concerne pas les séquences nucléotidiques dans leur environnement chromosomique naturel, c'est-à-dire à l'état naturel. Il s'agit de séquences qui ont été isolées et/ou purifiées, c'est-à-dire qu'elles ont été prélevées directement ou indirectement, par exemple par copie, leur environnement ayant été au moins partiellement modifié. On entend ainsi également désigner les acides nucléiques obtenus par synthèse chimique.

- 20 Par « pourcentage d'identité » entre deux séquences d'acides nucléiques ou d'acides aminés au sens de la présente invention, on entend désigner un pourcentage de nucléotides ou de résidus d'acides aminés identiques entre les deux séquences à comparer, obtenu après le meilleur alignement, ce pourcentage étant purement statistique et les différences entre les deux séquences étant réparties au hasard et sur toute leur longueur. On entend désigner par "meilleur alignement" ou "alignement
- 25 optimal", l'alignement pour lequel le pourcentage d'identité déterminé comme ci-après est le plus élevé. Les comparaisons de séquences entre deux séquences d'acides nucléiques ou d'acides aminés sont traditionnellement réalisées en comparant ces séquences après les avoir alignées de manière optimale, ladite comparaison étant réalisée par segment ou par « fenêtre de comparaison » pour identifier et comparer les
- 30 régions locales de similarité de séquence. L'alignement optimal des séquences pour la comparaison peut être réalisé, outre manuellement, au moyen de l'algorithme d'homologie locale de Smith et Waterman (1981, Ad. App. Math. 2:482), au moyen de l'algorithme d'homologie locale de Needleman et Wunsch (1970, J. Mol. Biol. 48:443), au moyen de la méthode de recherche de similarité de Pearson et Lipman (1988, Proc.

Natl. Acad. Sci. USA 85:2444), au moyen de logiciels informatiques utilisant ces algorithmes (GAP, BESTFIT, BLAST P, BLAST N, FASTA et TFASTA dans le Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI). Afin d'obtenir l'alignement optimal, on utilise de préférence le programme BLAST, avec la matrice BLOSUM 62. On peut également utiliser les matrices PAM ou PAM250.

Le pourcentage d'identité entre deux séquences d'acides nucléiques ou d'acides aminés est déterminé en comparant ces deux séquences alignées de manière optimale, la séquence d'acides nucléiques ou d'acides aminés à comparer pouvant comprendre des additions ou des délétions par rapport à la séquence de référence pour un alignement optimal entre ces deux séquences. Le pourcentage d'identité est calculé en déterminant le nombre de positions identiques pour lesquelles le nucléotide ou le résidu d'acide aminé est identique dans les deux séquences, en divisant ce nombre de positions identiques par le nombre total de positions comparées et en multipliant le résultat obtenu par 100 pour obtenir le pourcentage d'identité entre ces deux séquences.

Par séquences nucléiques présentant un pourcentage d'identité d'au moins 75 %, de préférence 80 %, 85 % ou 90 %, de façon plus préférée 95 % voire 98 %, après alignement optimal avec une séquence de référence, on entend désigner les séquences nucléiques présentant, par rapport à la séquence nucléique de référence, certaines modifications comme en particulier une délétion, une troncation, un allongement, une fusion chimérique et/ou une substitution, notamment ponctuelle, et dont la séquence nucléique présente au moins 75 %, de préférence 80 %, 85 %, 90 %, 95 % ou 98 %, d'identité après alignement optimal avec la séquence nucléique de référence. Il s'agit de préférence de séquences dont les séquences complémentaires sont susceptibles de s'hybrider spécifiquement avec les séquences de référence. De préférence, les conditions d'hybridation spécifiques ou de forte stringence seront telles qu'elles assurent au moins 75 %, de préférence 80 %, 85 %, 90 %, 95 % ou 98 % d'identité après alignement optimal entre l'une des deux séquences et sa séquence complémentaire.

Une hybridation dans des conditions de forte stringence signifie que les conditions de température et de force ionique sont choisies de telle manière qu'elles permettent le maintien de l'hybridation entre deux fragments d'ADN complémentaires. A titre illustratif, des conditions de forte stringence de l'étape d'hybridation aux fins de

définir les fragments polynucléotidiques décrits ci-dessus, sont avantageusement les suivantes.

- L'hybridation ADN-ADN ou ADN-ARN est réalisée en deux étapes : (1) préhybridation à 42°C pendant 3 heures en tampon phosphate (20 mM, pH 7,5) contenant 5 x SSC (1 x SSC correspond à une solution 0,15 M NaCl + 0,015 M citrate de sodium), 50 % de formamide, 7 % de sodium dodécyl sulfate (SDS), 10 x Denhardt's, 5 % de dextran sulfate et 1 % d'ADN de sperme de saumon ; (2) hybridation proprement dite pendant 20 heures à une température dépendant de la taille de la sonde (i.e. : 42°C, pour une sonde de taille > 100 nucléotides) suivie de 2 lavages de 20 minutes à 20°C en 2 x SSC + 2 % SDS, 1 lavage de 20 minutes à 20°C en 0,1 x SSC + 0,1 % SDS. Le dernier lavage est pratiqué en 0,1 x SSC + 0,1 % SDS pendant 30 minutes à 60°C pour une sonde de taille > 100 nucléotides. Les conditions d'hybridation de forte stringence décrites ci-dessus pour un polynucléotide de taille définie, peuvent être adaptées par l'homme du métier pour des oligonucléotides de taille plus grande ou plus petite, selon l'enseignement de Sambrook et al., (1989, Molecular cloning : a laboratory manual. 2nd Ed. Cold Spring Harbor).

- De plus, par fragment représentatif de séquences selon l'invention, on entend désigner tout fragment nucléotidique présentant au moins 15 nucléotides, de préférence au moins 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300, 400, 450, 500, 750, 1000 ou 1500 consécutifs de la séquence dont il est issu.

Par fragment représentatif, on entend en particulier une séquence nucléique codant pour un fragment biologiquement actif d'un polypeptide, tel que défini plus loin.

- Par fragment représentatif, on entend également les séquences intergéniques, et en particulier les séquences nucléotidiques portant les signaux de régulation (promoteurs, terminateurs, voire enhancers, ...).

- Parmi lesdits fragments représentatifs, on préfère ceux ayant des séquences nucléotidiques correspondant à des cadres ouverts de lecture, dénommés séquences ORFs (ORF pour « Open Reading Frame »), compris en général entre un codon d'initiation et un codon stop, ou entre deux codons stop, et codant pour des polypeptides, de préférence d'au moins 100 acides aminés, tel que par exemple, sans s'y limiter, les séquences ORFs qui seront décrites par la suite.

La numérotation des séquences nucléotidiques ORFs qui sera utilisée par la suite dans la présente description correspond à la numérotation des séquences d'acides

aminés des protéines codées par lesdites ORFs pour les peptides de séquence SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No.2346 à SEQ ID No.4481.

Les fragments représentatifs selon l'invention peuvent être obtenus par exemple par amplification spécifique telle que la PCR ou après digestion par des enzymes de restriction appropriés de séquences nucléotidiques selon l'invention, cette méthode étant
5 décrite en particulier dans l'ouvrage de Sambrook et al.. Lesdits fragments représentatifs peuvent également être obtenus par synthèse chimique lorsque leur taille n'est pas trop importante, selon des méthodes bien connues de l'homme du métier.

Parmi les séquences contenant des séquences de l'invention, ou des fragments
10 représentatifs, on entend également les séquences qui sont naturellement encadrées par des séquences qui présentent au moins 75 %, 80 %, 85 %, 90 %, 95 % ou 98 % d'identité avec les séquences selon l'invention.

Par séquence nucléotidique modifiée, on entend toute séquence nucléotidique obtenue par mutagenèse selon des techniques bien connues de l'homme du métier, et
15 comportant des modifications par rapport aux séquences normales, par exemple des mutations dans les séquences régulatrices et/ou promotrices de l'expression du polypeptide, notamment conduisant à une modification du taux d'expression ou de l'activité dudit polypeptide.

Par séquence nucléotidique modifiée, on entend également toute séquence
20 nucléotidique codant pour un polypeptide modifié tel que définit ci-après.

Concernant les séquences nucléiques ou ORF codant pour les peptides de séquence SEQ ID No. 2346 à SEQ ID No. 4481, ces séquences nucléiques ou ORF sont représentées respectivement par les séquences SEQ ID No. 4482 à SEQ ID No. 6617.

L'invention concerne avantagusement une séquence nucléotidique isolée de
25 *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi :

a) une séquence choisie parmi les séquences SEQ ID N° 6194,6236,5497,5791,5103,4705,5610,5234,4926,6331,6247,5842,5741,4921,5090, 5180,4706,4708,5677,6246,6411,5578,6446,6447,5607,6209,6215,5406,5658,4965, de préférence parmi les séquences SEQ ID N°4926,6331,5491,5234,6246,5842 ;

30 b) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence nucléotidique du a) ;

c) une séquence nucléotidique s'hybridant dans des conditions de forte stringence avec une séquence nucléotidique du a) ou b) et comprenant au moins 20 nucléotides ;

d) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a), b) ou c) ;

e) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a), b), c) ou d) et comprenant au moins 20 nucléotides ; et

5 f) une séquence telle que définie en a), b), c), d) ou e) modifiée et comportant au plus 10 % de nucléotides modifiés par rapport à la séquence de référence ;

et en ce qu'elle code pour une protéine de surface avec un motif d'ancrage LPXTG.

L'invention concerne également les polypeptides codés par ces séquences.

10 L'invention concerne également avantageusement une séquence nucléotidique isolée de *Streptococcus agalactiae* caractérisée en ce qu'elle est choisie parmi les séquences

SEQ

ID

N°6035,6137,6335,6377,6386,4495,4596,4636,4730,4816,4836,4906,4920,4925,5158, 5247, 5306,5417,5450,5486,5559,5591,5677,5732,5799,5800,5861,5923 ; et en ce

15 qu'elle code pour une lipoprotéine. L'invention concerne également les polypeptides codés par ces séquences.

L'invention concerne également avantageusement une séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi les séquences

SEQ

ID

20 N°4861,6214,6061,6517,6518,6519,4743,6343,6342,5326,4952,5619,5618,5617,5616, 5615,5614,5613,5611,5696,5971,5233,5602,5156,5574,5573,5654,5656,5526,5527,552 9,5534,5625,5626,6223,6229,6230,6231,6232,6233,5764,6095,5089,5466,5465 ; et en ce qu'elle code pour une protéine impliquée dans la biosynthèse de composés polysaccharidiques de paroi. L'invention concerne également les polypeptides codés par

25 ces séquences.

Les fragments représentatifs selon l'invention peuvent également être des sondes ou amorces, qui peuvent être utilisées dans des procédés de détection, d'identification, de dosage ou d'amplification de séquences nucléiques.

30 Une sonde ou amorce se définit, au sens de l'invention, comme étant un fragment d'acides nucléiques simple brin ou un fragment double brin dénaturé comprenant par exemple de 12 bases à quelques kb, notamment de 15 à quelques centaines de bases, de préférence de 15 à 50 ou 100 bases, et possédant une spécificité d'hybridation dans des conditions déterminées pour former un complexe d'hybridation avec un acide nucléique cible.

Les sondes et amorces selon l'invention peuvent être marquées directement ou indirectement par un composé radioactif ou non radioactif par des méthodes bien connues de l'homme du métier, afin d'obtenir un signal détectable et/ou quantifiable (brevet FR 78 10975 et bDNA de Chiron EP 225 807 et EP 510 085).

5 Les séquences non marquées de polynucléotides selon l'invention peuvent être utilisées directement comme sonde ou amorce.

Les séquences sont généralement marquées pour obtenir des séquences utilisables pour de nombreuses applications. Le marquage des amorces ou des sondes selon l'invention est réalisé par des éléments radioactifs ou par des molécules non
10 radioactives.

Parmi les isotopes radioactifs utilisés, on peut citer le ^{32}P , le ^{33}P , le ^{35}S , le ^3H ou le ^{125}I . Les entités non radioactives sont sélectionnées parmi les ligands tels la biotine, l'avidine, la streptavidine, la dioxigénine, les haptènes, les colorants, les agents luminescents tels que les agents radioluminescents, chémoluminescents,
15 bioluminescents, fluorescents, phosphorescents.

Les polynucléotides selon l'invention peuvent ainsi être utilisés comme amorce et/ou sonde dans des procédés mettant en oeuvre notamment la technique de PCR (amplification en chaîne par polymérase) (Rolfs et al., 1991, Berlin : Springer-Verlag). Cette technique nécessite le choix de paires d'amorces oligonucléotidiques encadrant le
20 fragment qui doit être amplifié. On peut, par exemple, se référer à la technique décrite dans le brevet américain U.S. N° 4,683,202. Les fragments amplifiés peuvent être identifiés, par exemple après une électrophorèse en gel d'agarose ou de polyacrylamide, ou après une technique chromatographique comme la filtration sur gel ou la chromatographie échangeuse d'ions, puis séquencés. La spécificité de l'amplification
25 peut être contrôlée en utilisant les séquences nucléotidiques de polynucléotides de l'invention comme matrice, des plasmides contenant ces séquences ou encore les produits d'amplification dérivés. Les fragments nucléotidiques amplifiés peuvent être utilisés comme réactifs dans des réactions d'hybridation afin de mettre en évidence la présence, dans un échantillon biologique, d'un acide nucléique cible de séquence
30 complémentaire à celle desdits fragments nucléotidiques amplifiés.

L'invention vise également les acides nucléiques susceptibles d'être obtenus par amplification à l'aide d'amorces selon l'invention.

D'autres techniques d'amplification de l'acide nucléique cible peuvent être avantageusement employées comme alternative à la PCR (PCR-like) à l'aide de couple

- d'amorces de séquences nucléotidiques selon l'invention. Par PCR-like on entend désigner toutes les méthodes mettant en œuvre des reproductions directes ou indirectes des séquences d'acides nucléiques, ou bien dans lesquelles les systèmes de marquage ont été amplifiés, ces techniques sont bien entendu connues. En général il s'agit de
- 5 l'amplification de l'ADN par une polymérase ; lorsque l'échantillon d'origine est un ARN il convient préalablement d'effectuer une transcription reverse. Il existe actuellement de très nombreux procédés permettant cette amplification, comme par exemple la technique SDA (Strand Displacement Amplification) ou technique d'amplification à déplacement de brin (Walker et al., 1992, *Nucleic Acids Res.*
- 10 20:1691), la technique TAS (Transcription-based Amplification System) décrite par Kwoh et al. (1989, *Proc. Natl. Acad. Sci., USA*, 86, 1173), la technique 3SR (Self-Sustained Sequence Replication) décrite par Guatelli et al. (1990, *Proc. Natl. Acad. Sci., USA* 87:1874), la technique NASBA (Nucleic Acid Sequence Based Amplification) décrite par Kievitis et al. (1991, *J. Virol. Methods*, 35, 273), la technique TMA
- 15 (Transcription Mediated Amplification), la technique LCR (Ligase Chain Reaction) décrite par Landegren et al. (1988, *Science* 241, 1077), la technique de RCR (Repair Chain Reaction) décrite par Segev (1992, Kessler C. Springer Verlag, Berlin, New-York, 197-205), la technique CPR (Cycling Probe Reaction) décrite par Duck et al. (1990, *Biotechniques*, 9, 142), la technique d'amplification à la Q-béta-réplase décrite
- 20 par Miele et al. (1983, *J. Mol. Biol.*, 171, 281). Certaines de ces techniques ont depuis été perfectionnées.

- Dans le cas où le polynucléotide cible à détecter est un ARNm, on utilise avantageusement, préalablement à la mise en œuvre d'une réaction d'amplification à l'aide des amorces selon l'invention ou à la mise en œuvre d'un procédé de détection à
- 25 l'aide des sondes de l'invention, une enzyme de type transcriptase inverse afin d'obtenir un ADNc à partir de l'ARNm contenu dans l'échantillon biologique. L'ADNc obtenu servira alors de cible pour les amorces ou les sondes mises en œuvre dans le procédé d'amplification ou de détection selon l'invention.

- La technique d'hybridation de sondes peut être réalisée de manières diverses
- 30 (Matthews et al., 1988, *Anal. Biochem.*, 169, 1-25). La méthode la plus générale consiste à immobiliser l'acide nucléique extrait des cellules de différents tissus ou de cellules en culture sur un support (tels que la nitrocellulose, le nylon, le polystyrène) et à incuber, dans des conditions bien définies, l'acide nucléique cible immobilisé avec la sonde. Après l'hybridation, l'excès de sonde est éliminé et les molécules hybrides

formées sont détectées par la méthode appropriée (mesure de la radioactivité, de la fluorescence ou de l'activité enzymatique liée à la sonde).

- Selon un autre mode de mise en œuvre des sondes nucléiques selon l'invention, ces dernières peuvent être utilisées comme sondes de capture. Dans ce cas, une sonde, dite « sonde de capture », est immobilisée sur un support et sert à capturer par hybridation spécifique l'acide nucléique cible obtenu à partir de l'échantillon biologique à tester et l'acide nucléique cible est ensuite détecté grâce à une seconde sonde, dite « sonde de détection », marquée par un élément facilement détectable.

- Parmi les fragments d'acides nucléiques intéressants, il faut ainsi citer en particulier les oligonucléotides anti-sens, c'est-à-dire dont la structure assure, par hybridation avec la séquence cible, une inhibition de l'expression du produit correspondant. Il faut également citer les oligonucléotides sens qui, par interaction avec des protéines impliquées dans la régulation de l'expression du produit correspondant, induiront soit une inhibition, soit une activation de cette expression.

- De façon préférée, les sondes ou amorces selon l'invention sont immobilisées sur un support, de manière covalente ou non covalente. En particulier, le support peut être une puce à ADN ou un filtre à haute ou moyenne densité, également objets de la présente invention (brevets WO 97/29212, WO 98/27317, WO 97/10365 et WO 92/10588).

- On entend désigner par puce à ADN ou filtre haute densité, un support sur lequel sont fixées des séquences d'ADN, chacune d'entre elles pouvant être repérée par sa localisation géographique. Ces puces ou filtres diffèrent principalement par leur taille, le matériau du support, et éventuellement le nombre de séquences d'ADN qui y sont fixées.

- On peut fixer les sondes ou amorces selon la première invention sur des supports solides, en particulier les puces à ADN, par différents procédés de fabrication. En particulier, on peut effectuer une synthèse *in situ* par adressage photochimique ou par jet d'encre. D'autres techniques consistent à effectuer une synthèse *ex situ* et à fixer les sondes sur le support de la puce à ADN par adressage mécanique, électronique ou par jet d'encre. Ces différents procédés sont bien connus de l'homme du métier.

Une séquence nucléotidique (sonde ou amorce) selon l'invention permet donc la détection et/ou l'amplification de séquences nucléiques spécifiques. En particulier, la détection de cesdites séquences est facilitée lorsque la sonde est fixée sur une puce à ADN, ou à un filtre haute densité.

L'utilisation de puces à ADN ou de filtres à haute densité permet en effet de déterminer l'expression de gènes dans un organisme présentant une séquence génomique proche de *Streptococcus agalactiae* et le typage de la souche en cause.

- La séquence génomique de *Streptococcus agalactiae*, complétée par l'identification des gènes de ces organismes, telle que présentée dans la présente invention, sert de base à la construction de ces puces à ADN ou filtre.

- La préparation de ces filtres ou puces consiste à synthétiser des oligonucléotides, correspondant aux extrémités 5' et 3' des gènes ou à des fragments plus internes pour amplifier des fragments d'une taille adaptée, par exemple comprise environ entre 300 et 800 bases. Ces oligonucléotides sont choisis en utilisant la séquence génomique et ses annotations divulguées par la présente invention. La température d'appariement des ces oligonucléotides aux places correspondantes sur l'ADN doit être approximativement la même pour chaque oligonucleotide. Ceci permet de préparer des fragments d'ADN correspondant à chaque gène par l'utilisation de conditions de PCR appropriées dans un environnement hautement automatisé. Les fragments amplifiés sont ensuite immobilisés sur des filtres ou des supports en verre, silicium ou polymères synthétiques et ces milieux sont utilisés pour l'hybridation.

- La disponibilité de tels filtres et/ou puces et de la séquence génomique correspondante annotée permet d'étudier l'expression de grands ensembles, voire de la totalité des gènes dans les micro-organismes associés à *Streptococcus agalactiae* et *Streptococcus agalactiae* CIP 82.45 (ATCC 12403), en préparant les ADN complémentaires, et en les hybridant à l'ADN ou aux oligonucléotides immobilisés sur les filtres ou les puces. De même, les filtres et/ou les puces permettent d'étudier la variabilité des souches ou des espèces, en préparant l'ADN de ces organismes et en les hybridant à l'ADN ou aux oligonucléotides immobilisés sur les filtres ou les puces.

- Les différences entre les séquences génomiques des différentes souches ou espèces peuvent grandement affecter l'intensité de l'hybridation et, par conséquent, perturber l'interprétation des résultats. Il peut donc être nécessaire d'avoir la séquence précise des gènes de la souche que l'on souhaite étudier. La méthode de détection des gènes décrite plus loin en détail, impliquant la détermination de la séquence de fragments aléatoires d'un génome, et les organisant d'après la séquence du génome de *Streptococcus agalactiae*, notamment de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) divulguée dans la présente invention, peut être très utile.

Les séquences nucléotidiques selon l'invention peuvent être utilisées dans des puces à ADN pour effectuer l'analyse de mutations. Cette analyse repose sur la constitution de puces capables d'analyser chaque base d'une séquence nucléotidique selon l'invention. On pourra notamment à cette fin mettre en œuvre les techniques de

5 microséquençage sur puce à ADN. Les mutations sont détectées par extension d'amorces immobilisées hybridant à la matrice des séquences analysées, juste en position adjacente de celle du nucléotide muté recherché. Une matrice simple brin, ARN ou ADN, des séquences à analyser sera avantageusement préparée selon des méthodes classiques, à partir de produits amplifiés selon les techniques de type PCR. Les matrices

10 d'ADN simple brin, ou d'ARN ainsi obtenues sont alors déposées sur la puce à ADN, dans des conditions permettant leur hybridation spécifique aux amorces immobilisées. Une polymérase thermostable, par exemple la Tth ou la Taq ADN polymérase, étend spécifiquement l'extrémité 3' de l'amorce immobilisée avec un analogue de nucléotide marqué complémentaire du nucléotide en position du site variable ; par exemple, un

15 cyclage thermique est réalisé en présence des didéoxyribonucléotides fluorescents. Les conditions expérimentales seront adaptées notamment aux puces employées, aux amorces immobilisées, aux polymérases employées, et au système de marquage choisi. Un avantage du microséquençage, par rapport aux techniques basées sur l'hybridation de sondes, est qu'il permet d'identifier tous les nucléotides variables avec une

20 discrimination optimale dans des conditions de réactions homogènes ; utilisé sur des puces à ADN, il permet une résolution et une spécificité optimales pour la détection routinière et industrielle de mutations en multiplex.

Une puce à ADN ou un filtre peut être un outil extrêmement intéressant pour la détermination, la détection et/ou l'identification d'un micro-organisme. Ainsi, on

25 préfère également les puces à ADN selon l'invention qui contiennent en outre au moins une séquence nucléotidique d'un micro-organisme autre que *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou *Streptococcus agalactiae*, immobilisée sur le support de ladite puce. De préférence, le micro-organisme choisi l'est parmi les bactéries du genre *Streptococcus* (ci-après désignées comme bactéries associées à *Streptococcus*

30 *agalactiae*), ou les variants de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403).

Une puce à ADN ou un filtre selon l'invention est un élément très utile de certains kits ou nécessaires pour la détection et/ou l'identification de micro-organismes, en particulier les bactéries appartenant à l'espèce *Streptococcus agalactiae* ou les micro-organismes associés, également objets de l'invention.

Par ailleurs, les puces à ADN ou les filtres selon l'invention, contenant des sondes ou amorces spécifiques de *Streptococcus agalactiae*, sont des éléments très avantageux de kits ou nécessaires pour la détection et/ou la quantification de l'expression de gènes de *Streptococcus agalactiae* (ou de micro-organismes associés).

- 5 En effet, le contrôle de l'expression des gènes est un point critique pour optimiser la croissance et le rendement d'une souche, soit en permettant l'expression d'un ou plusieurs gènes nouveaux, soit en modifiant l'expression de gènes déjà présents dans la cellule. La présente invention fournit l'ensemble des séquences naturellement actives chez *Streptococcus agalactiae* permettant l'expression des gènes. Elle permet
- 10 ainsi la détermination de l'ensemble des séquences exprimées chez *Streptococcus agalactiae*. Elle fournit également un outil permettant de repérer les gènes dont l'expression suit un schéma donné. Pour réaliser cela, l'ADN de tout ou partie des gènes de *Streptococcus agalactiae* peut être amplifié grâce à des amorces selon l'invention, puis fixé à un support comme par exemple le verre ou le nylon ou une puce à ADN, afin
- 15 de construire un outil permettant de suivre le profil d'expression de ces gènes. Cet outil, constitué de ce support contenant les séquences codantes sert de matrice d'hybridation à un mélange de molécules marquées reflétant les ARNs messagers exprimés dans la cellule (en particulier les sondes marquées selon l'invention). En répétant cette expérience à différents instants et en combinant l'ensemble de ces données par un
- 20 traitement approprié, on obtient alors les profils d'expression de l'ensemble de ces gènes. La connaissance des séquences qui suivent un schéma de régulation donné peut aussi être mise à profit pour rechercher de manière dirigée, par exemple par homologie, d'autres séquences suivant globalement, mais de manière légèrement différente le même schéma de régulation. En complément, il est possible d'isoler chaque séquence de
- 25 contrôle présente en amont des segments servant de sondes et d'en suivre l'activité à l'aide de moyen approprié comme un gène rapporteur (luciférase, β -galactosidase, GFP). Ces séquences isolées peuvent ensuite être modifiées et assemblées par ingénierie métabolique avec des séquences d'intérêt en vue de leur expression optimale.

- L'invention concerne également les polypeptides codés par une séquence
- 30 nucléotidique selon l'invention, de préférence, par un fragment représentatif des séquences précédentes et correspondant à une séquence ORF. En particulier, les polypeptides de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) de SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No. 2346 à SEQ ID No. 4481 sont objet de l'invention.

L'invention comprend également les polypeptides caractérisés en ce qu'ils comprennent un polypeptide choisi parmi :

- a) un polypeptide selon l'invention ;
- b) un polypeptide présentant au moins 80 % de préférence 85 %, 90 %, 95 % et 98 % d'identité avec un polypeptide selon l'invention ;
- 5 c) un fragment d'au moins 5 acides aminés, de préférence d'au moins 10, 15, 20, 25, 30, 40, 50, 75 et 100 acides aminés d'un polypeptide selon l'invention, ou tel que défini en b) ;
- d) un fragment biologiquement actif d'un polypeptide selon l'invention, ou tel que
- 10 défini en b) ou c) ; et
- e) un polypeptide selon l'invention, ou tel que défini en b), c) ou d) modifié et comportant au plus 10 %, 5 % ou 1 % d'acides aminés modifiés par rapport à la séquence de référence.

Les séquences nucléotidiques codant pour les polypeptides décrits

15 précédemment sont également objet de l'invention.

Dans la présente description, les termes polypeptides, séquences polypeptidiques, peptides et protéines sont interchangeables. Le terme polypeptide comprend toute séquence d'acides aminés permettant de générer une réponse anticorps.

Il doit être compris que l'invention ne concerne pas les polypeptides sous forme

20 naturelle, c'est-à-dire qu'ils ne sont pas pris dans leur environnement naturel. En revanche, elle concerne ceux qui ont pu être isolés ou obtenus par purification à partir de sources naturelles, ou bien obtenus par recombinaison génétique, ou par synthèse chimique, et qu'ils peuvent alors comporter des acides aminés non naturels comme cela sera décrit plus loin.

Par polypeptide présentant un certain pourcentage d'identité avec un autre, que l'on désignera également par polypeptide homologue, on entend désigner les polypeptides présentant par rapport aux polypeptides naturels, certaines modifications, en particulier une délétion, addition ou substitution d'au moins un acide aminé, une

30 polypeptides présentant des modifications post-traductionnelles. Parmi les polypeptides homologues, on préfère ceux dont la séquence d'acides aminés présentent au moins 80 %, de préférence 85 %, 90 %, 95 % et 98 % d'homologie avec les séquences d'acides aminés des polypeptides selon l'invention. Dans le cas d'une substitution, un ou plusieurs acide(s) aminé(s) consécutif(s) ou non consécutif(s) sont remplacés par des

acides aminés « équivalents ». L'expression « acides aminés équivalents » vise ici à désigner tout acide aminé susceptible d'être substitué à l'un des acides aminés de la structure de base sans cependant modifier essentiellement les activités biologiques des peptides correspondant telles qu'elles seront définies par la suite.

- 5 Ces acides aminés équivalents peuvent être déterminés soit en s'appuyant sur leur homologie de structure avec les acides aminés auxquels ils se substituent, soit sur des résultats d'essais comparatifs d'activité biologique entre les différents polypeptides susceptibles d'être effectués.

- 10 A titre d'exemple, on mentionne les possibilités de substitution susceptibles d'être effectuées sans qu'il résulte en une modification approfondie de l'activité biologique du polypeptide modifié correspondant. On peut remplacer ainsi la leucine par la valine ou l'isoleucine, l'acide aspartique par l'acide glutamine, la glutamine par l'asparagine, l'arginine par la lysine, etc., les substitutions inverses étant naturellement envisageables dans les mêmes conditions.

- 15 Les polypeptides homologues correspondent également aux polypeptides codés par les séquences nucléotidiques homologues ou identiques, telles que définies précédemment et comprennent ainsi dans la présente définition des polypeptides mutés ou correspondant à des variations inter ou intra espèces, pouvant exister chez *Streptococcus*, et qui correspondent notamment à des troncatures, substitutions, 20 délétions et/ou additions, d'au moins un résidu d'acides aminés.

- Il est entendu que l'on calcule le pourcentage d'identité entre deux polypeptides de la même façon qu'entre deux séquences d'acides nucléiques. Ainsi, le pourcentage d'identité entre deux polypeptides est calculé après alignement optimal de ces deux séquences, sur une fenêtre d'homologie maximale. Pour définir ladite fenêtre 25 d'homologie maximale, on peut utiliser les mêmes algorithmes que pour les séquences d'acide nucléique.

- Par fragment biologiquement actif d'un polypeptide selon l'invention, on entend désigner en particulier un fragment de polypeptide, tel que défini ci-après, présentant au moins une des caractéristiques biologiques des polypeptides selon l'invention, 30 notamment en ce qu'il est capable d'exercer de manière générale une activité même partielle, telle que par exemple :

- une activité enzymatique (métabolique) ou une activité pouvant être impliquée dans la biosynthèse ou la biodégradation de composés organiques ou inorganiques ;

- une activité structurelle (enveloppe cellulaire, molécule chaperonne, ribosome) ;
 - une activité de transport (d'énergie, d'ion) ; ou dans la sécrétion de protéine ;
 - une activité dans le processus de réplication, amplification, préparation,
- 5 transcription, traduction ou maturation, notamment de l'ADN, de l'ARN ou des protéines.

Par fragment de polypeptide selon l'invention, on entend désigner un polypeptide comportant au minimum 5 acides aminés, de préférence d'au moins 10, 15, 20, 25, 30, 40, 50, 75, 100 et 150 acides aminés.

- 10 Les fragments de polypeptides peuvent correspondre à des fragments isolés ou purifiés naturellement présents dans les souches de *Streptococcus*, ou à des fragments qui peuvent être obtenus par clivage dudit polypeptide par une enzyme protéolytique telle que la trypsine ou la chymotrypsine ou la collagénase, par un réactif chimique (bromure de cyanogène, CNBr) ou en plaçant ledit polypeptide dans un environnement
- 15 très acide (par exemple à pH = 2,5). Des fragments polypeptidiques peuvent également être préparés par synthèse chimique, à partir d'hôtes transformés par un vecteur d'expression selon l'invention qui contiennent un acide nucléique permettant l'expression dudit fragment, et placé sous le contrôle des éléments de régulation et/ou d'expression appropriés.

- 20 Par « polypeptide modifié » d'un polypeptide selon l'invention, on entend désigner un polypeptide obtenu par recombinaison génétique ou par synthèse chimique comme décrit plus loin, qui présente au moins une modification par rapport à la séquence normale. Ces modifications peuvent être notamment portées sur des acides aminés nécessaires pour la spécificité ou l'efficacité de l'activité, ou à l'origine de la
- 25 conformation structurale, de la charge, ou de l'hydrophobicité du polypeptide selon l'invention. On peut ainsi créer des polypeptides d'activité équivalente, augmentée ou diminuée, ou de spécificité équivalente, plus étroite ou plus large. Parmi les polypeptides modifiés, il faut citer les polypeptides dans lesquels jusqu'à cinq acides aminés peuvent être modifiés, tronqués à l'extrémité N ou C-terminale, ou bien délétés,
- 30 ou ajoutés.

Comme cela est indiqué, les modifications d'un polypeptide ont pour objectif notamment :

- de permettre sa mise en œuvre dans des procédés de biosynthèse ou de biodégradation de composés organiques ou inorganiques,

- de permettre sa mise en œuvre dans des procédés de réplication, d'amplification, de réparation et règle de transcription, de traduction, ou de maturation notamment de l'ADN, l'ARN, ou de protéines,
 - de permettre sa sécrétion améliorée,
- 5 - de modifier sa solubilité, l'efficacité ou la spécificité de son activité, ou encore de faciliter sa purification.

La synthèse chimique présente également l'avantage de pouvoir utiliser des acides aminés non naturels ou des liaisons non peptidiques. Ainsi, il peut être intéressant d'utiliser des acides aminés non naturels, par exemple sous forme D, ou des analogues d'acides aminés, notamment des formes souffrées.

10

La présente invention fournit la séquence nucléotidique du génome de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) sous forme de contigs, ainsi que certaines séquences polypeptidiques.

D'une manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la biosynthèse des acides aminés.

15

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs.

20

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide d'enveloppe cellulaire ou présent à la surface de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou pour un de ses fragments.

25

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la machinerie cellulaire.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme intermédiaire central.

30

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme énergétique.

- 5 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme des acides gras et des phospholipides.

- 10 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides.

- 15 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans les fonctions de régulation.

- 20 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de réplication.

- De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de transcription.

- 25 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de traduction.

- 30 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de transport et de liaison des protéines.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus*

agalactiae CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans l'adaptation aux conditions atypiques.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus*
5 *agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments dans la sensibilité aux médicaments et analogues.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus*
10 *agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans les fonctions relatives aux transposons.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide spécifique de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments.

Sous un autre aspect, de manière préférée, l'invention a pour objet un
15 polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la biosynthèse des acides aminés.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de
20 *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide d'enveloppe cellulaire ou de surface de *Streptococcus agalactiae* CIP 82.45 (ATCC
25 12403) ou un de ses fragments.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans la machinerie cellulaire.

30 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme intermédiaire central.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme énergétique.

- 5 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme des acides gras et des phospholipides.

- 10 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides.

- Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de
15 *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans les fonctions de régulation.

- Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué
20 dans le processus de réplication.

- Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué
 dans le processus de transcription.

- 25 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de traduction.

- Sous un autre aspect, de manière préférée, l'invention a pour objet un
30 polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans le processus de transport et de liaison des protéines.

 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de

Streptococcus agalactiae CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans l'adaptation aux conditions atypiques.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de
5 *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments dans la sensibilité aux médicaments et analogues.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de
10 *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments impliqué dans les fonctions relatives aux transposons.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide spécifique de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un de ses fragments.

L'invention a également pour objet les opérons impliqués dans la synthèse
15 d'antibiotiques et/ou de toxines.

Le tableau 1 fournit la liste de certains polypeptides selon l'invention, ainsi que leur localisation dans les séquences SEQ ID No. 1 à SEQ ID No. 139, et les analogies observées après comparaison dans les bases de données.

20 Il est important de noter toutefois qu'un organisme vivant est un tout et doit être pris comme tel. Ainsi, afin de pouvoir se développer et exhiber ses propriétés, tout organisme a besoin d'interactions entre les différentes voies métaboliques. Ainsi, la classification énoncée ci-dessus ne doit pas être considérée comme limitative, un gène pouvant être impliqué dans deux voies métaboliques distinctes.

25 La présente invention a également pour objet les séquences nucléotidiques et/ou de polypeptides selon l'invention, caractérisées en ce que lesdites séquences sont enregistrées sur un support d'enregistrement dont la forme et la nature facilitent la lecture, l'analyse et/ou l'exploitation de ladite ou desdites séquence(s). Ces supports peuvent également contenir d'autres informations extraites de la présente invention,
30 notamment les analogies avec des séquences déjà connues, et/ou des informations concernant les séquences nucléotidiques et/ou de polypeptides d'autres micro-organismes afin de faciliter l'analyse comparative et l'exploitation des résultats obtenus.

Parmi cesdits supports d'enregistrement, on préfère en particulier les supports lisibles par un ordinateur, tels les supports magnétiques, optiques, électriques ou

hybrides, en particulier les disquettes informatiques, les CD-ROM, les serveurs informatiques. De tels supports d'enregistrement sont également objet de l'invention.

Les supports d'enregistrement selon l'invention, avec les informations apportées, sont très utiles pour le choix d'amorces ou de sondes nucléotidiques pour la
5 détermination de gènes dans *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou souches proches de cet organisme. De même, l'utilisation de ces supports pour l'étude du polymorphisme génétique de souches proches de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403), en particulier par la détermination des régions de colinéarité, est très utile dans la mesure où ces supports fournissent non seulement la séquence
10 nucléotidique du génome de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403), mais également l'organisation génomique dans ladite séquence. Ainsi, les utilisations de supports d'enregistrement selon l'invention sont également des objets de l'invention.

L'analyse d'homologie entre différentes séquences s'effectue en effet avantageusement à l'aide de logiciels de comparaison de séquences, tels le logiciel
15 Blast, ou les logiciels de la trousse GCG, décrits précédemment.

L'invention vise également les vecteurs de clonage et/ou d'expression, qui contiennent une séquence nucléotidique selon l'invention.

Les vecteurs selon l'invention comportent de préférence des éléments qui permettent l'expression et/ou la sécrétion des séquences nucléotidiques dans une cellule
20 hôte déterminée.

Le vecteur doit alors comporter un promoteur, des signaux d'initiation et de terminaison de la traduction, ainsi que des régions appropriées de régulation de la transcription. Il doit pouvoir être maintenu de façon stable dans la cellule hôte et peut éventuellement posséder des signaux particuliers qui spécifient la sécrétion de la
25 protéine traduite. Ces différents éléments sont choisis et optimisés par l'homme du métier en fonction de l'hôte cellulaire utilisé. A cet effet, les séquences nucléotidiques selon l'invention peuvent être insérées dans des vecteurs à répllication autonome au sein de l'hôte choisi, ou être des vecteurs intégratifs de l'hôte choisi.

De tels vecteurs sont préparés par des méthodes couramment utilisées par
30 l'homme du métier, et les clones résultant peuvent être introduits dans un hôte approprié par des méthodes standards, telles que la lipofection, l'électroporation, le choc thermique, ou des méthodes chimiques.

Les vecteurs selon l'invention sont par exemple des vecteurs d'origine plasmidique ou virale. Ils sont utiles pour transformer des cellules hôtes afin de cloner ou d'exprimer les séquences nucléotidiques selon l'invention.

5 L'invention comprend également les cellules hôtes transformées par un vecteur selon l'invention.

L'hôte cellulaire peut être choisi parmi des systèmes procaryotes ou eucaryotes, par exemple les cellules bactériennes mais également les cellules de levure ou les cellules animales, en particulier les cellules de mammifères. On peut également utiliser des cellules d'insectes ou des cellules de plantes. Les cellules hôtes préférées selon
10 l'invention sont en particulier les cellules procaryotes, de préférence les bactéries appartenant au genre *Streptococcus*, à l'espèce *Streptococcus agalactiae*, plus particulièrement *Streptococcus agalactiae* CIP 82.45 (ATCC 12403), ou les micro-organismes associés à l'espèce *Streptococcus agalactiae*.

L'invention concerne également les végétaux et les animaux, excepté l'homme,
15 qui comprennent une cellule transformée selon l'invention. Les cellules transformées selon l'invention sont utilisables dans des procédés de préparation de polypeptides recombinants selon l'invention. Les procédés de préparation d'un polypeptide selon l'invention sous forme recombinante, caractérisés en ce qu'ils mettent en œuvre un vecteur et/ou une cellule transformée par un vecteur selon l'invention sont eux-mêmes
20 compris dans la présente invention. De préférence, on cultive une cellule transformée par un vecteur selon l'invention dans des conditions qui permettent l'expression dudit polypeptide et on récupère ledit peptide recombinant.

Ainsi qu'il a été dit, l'hôte cellulaire peut être choisi parmi des systèmes procaryotes ou eucaryotes. En particulier, il est possible d'identifier des séquences
25 nucléotidiques selon l'invention, facilitant la sécrétion dans un tel système procaryote ou eucaryote. Un vecteur selon l'invention portant une telle séquence peut donc être avantageusement utilisé pour la production de protéines recombinantes, destinées à être sécrétées. En effet, la purification de ces protéines recombinantes d'intérêt sera facilitée par le fait qu'elles sont présentes dans le surnageant de la culture cellulaire plutôt qu'à
30 l'intérieur des cellules hôtes.

On peut également préparer les polypeptides selon l'invention par synthèse chimique. Un tel procédé de préparation est également un objet de l'invention. L'homme du métier connaît les procédés de synthèse chimique, par exemple les techniques mettant en œuvre des phases solides (voir notamment Steward et al., 1984,

Solid phase peptides synthesis, Pierce Chem. Company, Rockford, 111, 2ème éd., (1984) ou des techniques utilisant des phases solides partielles, par condensation de fragments ou par une synthèse en solution classique. Les polypeptides obtenus par synthèse chimique et pouvant comporter des acides aminés non naturels correspondants
5 sont également compris dans l'invention.

L'invention est en outre relative à des polypeptides hybrides présentant au moins un polypeptide ou un de ses fragments selon l'invention, et une séquence d'un polypeptide susceptible d'induire une réponse immunitaire chez l'homme ou l'animal.

Avantageusement, le déterminant antigénique est tel qu'il est susceptible
10 d'induire une réponse humorale et/ou cellulaire.

Un tel déterminant pourra comprendre un polypeptide ou un de ses fragments selon l'invention sous forme glycosylée, utilisé en vue d'obtenir des compositions immunogènes susceptibles d'induire la synthèse d'anticorps dirigés contre des épitopes multiples. Lesdits polypeptides ou leurs fragments glycosylés font également partie de
15 l'invention.

Ces molécules hybrides peuvent être constituées en partie d'une molécule porteuse de polypeptides ou de leurs fragments selon l'invention, associée à une partie éventuellement immunogène, en particulier un épitope de la toxine diphtérique, la toxine tétanique, un antigène de surface du virus de l'hépatite B (brevet FR 79 21811),
20 l'antigène VP1 du virus de la poliomyélite ou toute autre toxine ou antigène viral ou bactérien.

Les procédés de synthèse des molécules hybrides englobent les méthodes utilisées en génie génétique pour construire des séquences nucléotidiques hybrides codant pour les séquences polypeptidiques recherchées. On pourra, par exemple, se
25 référer avantageusement à la technique d'obtention de gènes codant pour des protéines de fusion décrite par Minton en 1984.

Lesdites séquences nucléotidiques hybrides codant pour un polypeptide hybride ainsi que les polypeptides hybrides selon l'invention, caractérisés en ce qu'il s'agit de polypeptides recombinants obtenus par l'expression desdites séquences nucléotidiques
30 hybrides, font également partie de l'invention.

L'invention comprend également les vecteurs caractérisés en ce qu'ils contiennent une desdites séquences nucléotidiques hybrides. Les cellules hôtes transformées par lesdits vecteurs, les animaux transgéniques comprenant une desdites cellules transformées ainsi que les procédés de préparation de polypeptides

recombinants utilisant lesdits vecteurs, lesdites cellules transformées et/ou lesdits animaux transgéniques font également partie de l'invention.

Le couplage entre un polypeptide selon l'invention et un polypeptide immunogène peut être effectué par voie chimique, ou par voie biologique. Ainsi, selon 5 l'invention, il est possible d'introduire un ou plusieurs élément(s) de liaison, notamment des acides aminés pour faciliter les réactions de couplage entre le polypeptide selon l'invention, et le polypeptide immunostimulateur, le couplage covalent de l'antigène immunostimulateur pouvant être réalisé à l'extrémité N ou C-terminale du polypeptide selon l'invention. Les réactifs bifonctionnels permettant ce couplage sont déterminés en 10 fonction de l'extrémité choisie pour réaliser ce couplage, et les techniques de couplage sont bien connues de l'homme du métier.

Les conjugués issus d'un couplage de peptides peuvent être également préparés par recombinaison génétique. Le peptide hybride (conjugué) peut en effet être produit par des techniques d'ADN recombinant, par insertion ou addition à la séquence d'ADN 15 codant pour le polypeptide selon l'invention, d'une séquence codant pour le ou les peptide(s) antigène(s), immunogène(s) ou haptène(s). Ces techniques de préparation de peptides hybrides par recombinaison génétique sont bien connues de l'homme du métier (voir par exemple Makrides, 1996, *Microbiological Reviews* 60,512-538).

De préférence, ledit polypeptide immunitaire est choisi dans le groupe des 20 peptides contenant les anatoxines, notamment le toxoïde diphtérique ou le toxoïde tétanique, les protéines dérivées du Streptocoque (comme la protéine de liaison à la séralbumine humaine), les protéines membranaires OMPA et les complexes de protéines de membranes externes, les vésicules de membranes externes ou les protéines de chocs thermiques.

Les polypeptides hybrides selon l'invention sont très utiles pour obtenir des 25 anticorps monoclonaux ou polyclonaux, capables de reconnaître spécifiquement les polypeptides selon l'invention. En effet, un polypeptide hybride selon l'invention permet la potentialisation de la réponse immunitaire, contre le polypeptide selon l'invention couplé à la molécule immunogène. De tels anticorps monoclonaux ou 30 polyclonaux, leurs fragments, ou les anticorps chimériques, reconnaissant les polypeptides selon l'invention, sont également objet de l'invention.

Les anticorps monoclonaux spécifiques peuvent être obtenus selon la méthode classique de culture d'hybridome décrite par Köhler et Milstein (1975, *Nature* 256, 495).

Les anticorps selon l'invention sont par exemple des anticorps chimériques, des anticorps humanisés, des fragments Fab, ou F(ab')². Ils peuvent également se présenter sous forme d'immunoconjugués ou d'anticorps marqués afin d'obtenir un signal détectable et/ou quantifiable.

5 Ainsi, les anticorps selon l'invention peuvent être employés dans un procédé pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes:

- a) mise en contact de l'échantillon biologique avec un anticorps selon l'invention ;
- 10 b) mise en évidence du complexe antigène-anticorps éventuellement formé.

Les anticorps selon la présente invention sont également utilisables afin de détecter une expression d'un gène de *Streptococcus agalactiae* ou de micro-organismes associés. En effet, la présence du produit d'expression d'un gène reconnu par un anticorps spécifique dudit produit d'expression peut être détectée par la présence d'un

15 complexe antigène-anticorps formé après la mise en contact de la souche de *Streptococcus agalactiae* ou du micro-organisme associé avec un anticorps selon l'invention. La souche bactérienne utilisée peut avoir été « préparée », c'est-à-dire centrifugée, lysée, placée dans un réactif approprié pour la constitution du milieu propice à la réaction immunologique. En particulier, on préfère un procédé de détection

20 de l'expression dans le gène, correspondant à un Western blot, pouvant être effectué après une électrophorèse sur gel de polyacrylamide d'un lysat de la souche bactérienne, en présence ou en l'absence de conditions réductrices (SDS-PAGE). Après migration et séparation des protéines sur le gel de polyacrylamide, on transfère lesdites protéines sur une membrane appropriée (par exemple en nylon) et on détecte la présence de la

25 protéine ou du polypeptide d'intérêt, par mise en contact de ladite membrane avec un anticorps selon l'invention.

Ainsi, la présente invention comprend également les kits ou nécessaires pour la mise en œuvre d'un procédé tel que décrit (de détection de l'expression d'un gène de *Streptococcus agalactiae* ou d'un micro-organisme associé, ou pour la détection et/ou

30 l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou un micro-organisme associé), comprenant les éléments suivants :

- a) un anticorps polyclonal ou monoclonal selon l'invention ;
- b) éventuellement, les réactifs pour la constitution du milieu propice à la réaction immunologique ;

c) éventuellement, les réactifs permettant la mise en évidence des complexes antigène-anticorps produits par la réaction immunologique.

Les polypeptides et les anticorps selon l'invention peuvent avantageusement être immobilisés sur un support, notamment une puce à protéines. Une telle puce à protéines est un objet de l'invention, et peut également contenir au moins un polypeptide d'un micro-organisme autre que *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou un anticorps dirigé contre un composé d'un micro-organisme autre que *Streptococcus agalactiae* CIP 82.45 (ATCC 12403).

Les puces à protéines ou filtres à haute densité contenant des protéines selon l'invention peuvent être construites de la même manière que les puces à ADN selon l'invention. En pratique, on peut effectuer la synthèse des polypeptides directement fixés sur la puce à protéines, ou effectuer une synthèse *ex situ* suivie d'une étape de fixation sur ladite puce du polypeptide synthétisé. Cette dernière méthode est préférable, lorsque l'on désire fixer des protéines de taille importante sur le support, ces protéines étant avantageusement préparées par génie génétique. Toutefois, si l'on ne désire fixer que des peptides sur le support de ladite puce, il peut être plus intéressant de procéder à la synthèse desdits peptides directement *in situ*.

Les puces à protéines selon l'invention peuvent être avantageusement utilisées dans des kits ou nécessaires pour la détection et/ou l'identification de bactéries associées à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme, ou de façon plus générale dans des kits ou nécessaires pour la détection et/ou l'identification de micro-organismes. Lorsque l'on fixe les polypeptides selon l'invention sur les puces à ADN, on recherche la présence d'anticorps dans les échantillons testés, la fixation d'un anticorps selon l'invention sur le support de la puce à protéines permettant l'identification de la protéine dont ledit anticorps est spécifique.

De préférence, on fixe un anticorps selon l'invention sur le support de la puce à protéines, et on détecte la présence de l'antigène correspondant, spécifique de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou d'un micro-organisme associé.

Une puce à protéines ci-dessus décrite peut être utilisée pour la détection de produits de gènes, pour établir un profil d'expression desdits gènes, en complément d'une puce à ADN selon l'invention.

Les puces à protéines selon l'invention sont également extrêmement utiles pour les expériences de protéomique, qui étudie les interactions entre les différentes protéines d'un micro-organisme donné. De façon simplifiée, on fixe des peptides représentatifs

des différentes protéines d'un organisme sur un support. Puis, on met ledit support en contact avec des protéines marquées, et après une étape optionnelle de rinçage, on détecte des interactions entre lesdites protéines marquées et les peptides fixés sur la puce à protéines.

- 5 Ainsi, les puces à protéines comprenant une séquence polypeptidique selon l'invention ou un anticorps selon l'invention sont objet de l'invention, ainsi que les kits ou nécessaires les contenant.

La présente invention couvre également un procédé de détection et/ou d'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45
10 (ATCC 12403) ou à un micro-organisme associé dans un échantillon biologique, qui met en œuvre une séquence nucléotidique selon l'invention.

Il doit être entendu que le terme échantillon biologique concerne dans la présente invention les échantillons prélevés à partir d'un organisme vivant (en particulier sang, tissus, organes ou autres prélevés à partir d'un mammifère) ou un
15 échantillon contenant du matériel biologique, c'est-à-dire de l'ADN ou de l'ARN. Un tel échantillon biologique comprend aussi les compositions alimentaires contenant des bactéries (par exemple les fromages, les produits laitiers), mais également des compositions alimentaires contenant des levures (bières, pains) ou autres. Le terme échantillon biologique concerne aussi les bactéries isolées à partir de ces prélèvements
20 ou compositions alimentaires.

Le procédé de détection et/ou d'identification mettant en œuvre les séquences nucléotidiques selon l'invention peut être de diverse nature.

On préfère un procédé comportant les étapes suivantes :

- a) éventuellement, isolement de l'ADN à partir de l'échantillon biologique à analyser,
25 ou obtention d'un ADNc à partir de l'ARN de l'échantillon biologique ;
b) amplification spécifique de l'ADN de bactéries appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme associé à l'aide d'au moins une amorce selon l'invention ;
c) mise en évidence des produits d'amplification.

30 Ce procédé est basé sur l'amplification spécifique de l'ADN, en particulier par une réaction d'amplification en chaîne.

On préfère également un procédé comprenant les étapes suivantes :

- a) mise en contact d'une sonde nucléotidique selon l'invention avec un échantillon biologique, l'acide nucléique contenu dans l'échantillon biologique ayant, le cas

échéant, préalablement été rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme associé ;

- 5 b) mise en évidence de l'hybride éventuellement formé entre la sonde nucléotidique et l'ADN de l'échantillon biologique.

Un tel procédé ne doit pas être limité à la détection de la présence de l'ADN contenu dans l'échantillon biologique à tester, il peut être également mis en œuvre pour détecter l'ARN contenu dans ledit échantillon. Ce procédé englobe en particulier les

- 10 Southern et Northern blot.

Un autre procédé préféré selon l'invention comprend les étapes suivantes :

- a) mise en contact d'une sonde nucléotidique immobilisée sur un support selon l'invention avec un échantillon biologique, l'acide nucléique de l'échantillon, ayant le cas échéant, été préalablement rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme associé ;
- 15 b) mise en contact de l'hybride formé entre la sonde nucléotidique immobilisée sur un support et l'acide nucléique contenu dans l'échantillon biologique, le cas échéant après élimination de l'ADN de l'échantillon biologique n'ayant pas hybridé avec la sonde, avec une sonde nucléotidique marquée selon l'invention ;
- 20 c) mise en évidence du nouvel hybride formé à l'étape b).

Ce procédé est avantageusement utilisé avec une puce à ADN selon l'invention, l'acide nucléique recherché s'hybridant avec une sonde présente à la surface de ladite puce, et étant détecté par l'utilisation d'une sonde marquée. Ce procédé est avantageusement mis en œuvre en combinant une étape préalable d'amplification de l'ADN ou de l'ADN complémentaire obtenu éventuellement par transcription inverse, à l'aide d'amorces selon l'invention.

Ainsi, la présente invention englobe également les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique selon l'invention ;

- b) éventuellement, les réactifs nécessaires à la mise en œuvre d'une réaction d'hybridation ;
- c) éventuellement, au moins une amorce selon l'invention ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

5 De même, la présente invention englobe également les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique, dite sonde de capture, selon l'invention ;
- 10 b) une sonde oligonucléotidique, dite sonde de révélation, selon l'invention ;
- c) éventuellement, au moins une amorce selon l'invention ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

Enfin, les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) ou à un
15 micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) au moins une amorce selon l'invention ;
- b) éventuellement, les réactifs nécessaires pour effectuer une réaction d'amplification d'ADN ;
- c) éventuellement, un composant permettant de vérifier la séquence du fragment
20 amplifié, plus particulièrement une sonde oligonucléotidique selon l'invention, sont également objet de la présente invention.

De préférence, lesdites amorces et/ou sondes et/ou polypeptides et/ou anticorps selon la présente invention utilisés dans les procédés et/ou kits ou nécessaires selon la présente invention sont choisis parmi les amorces et/ou sondes et/ou polypeptides et/ou
25 anticorps spécifiques de l'espèce *Streptococcus agalactiae* CIP 82.45 (ATCC 12403). De manière préférée, ces éléments sont choisis parmi les séquences nucléotidiques codant pour une protéine sécrétée, parmi les polypeptides sécrétés, ou parmi les anticorps dirigés contre des polypeptides sécrétés de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403).

30 La présente invention a également pour objet les souches de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) et/ou de micro-organismes associés contenant une ou plusieurs mutation(s) dans une séquence nucléotidique selon l'invention, en particulier une séquence ORF, ou leurs éléments régulateurs (en particulier promoteurs).

On préfère, selon la présente invention, les souches de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) présentant une ou plusieurs mutation(s) dans les séquences nucléotidiques codant pour des polypeptides impliqués dans la machinerie cellulaire, en particulier la sécrétion, le métabolisme intermédiaire central, le métabolisme énergétique, les processus de synthèse des acides aminés, de transcription et de traduction, de synthèse des polypeptides.

Lesdites mutations peuvent mener à une inactivation du gène, ou en particulier lorsqu'elles sont situées dans les éléments régulateurs dudit gène, à une surexpression de celui-ci.

L'invention concerne en outre l'utilisation d'une séquence nucléotidique selon l'invention, d'un polypeptide selon l'invention, d'un anticorps selon l'invention, d'une cellule selon l'invention, et/ou d'un animal transformé selon l'invention, pour la sélection de composé organique ou inorganique capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la réplication cellulaire de cellules eucaryotes ou procaryotes ou capables d'induire, d'inhiber ou d'aggraver une pathologies liées à une infection par *Streptococcus agalactiae* ou un de ses micro-organismes associés.

L'invention comprend également une méthode de sélection de composés capables de se lier à un polypeptide ou un de ses fragments selon l'invention, capables de se lier à une séquence nucléotidique selon l'invention, ou capables de reconnaître un anticorps selon l'invention, et/ou capables de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la croissance ou la réplication cellulaire de cellules eucaryotes ou procaryotes, ou capables d'induire, d'inhiber ou d'aggraver chez un organisme animal ou humain une pathologie liée à une infection par *Streptococcus*, par exemple par *Streptococcus agalactiae*, ou un de ses micro-organismes associés, caractérisée en ce qu'elle comprend les étapes suivantes :

- a) mise en contact dudit composé avec ledit polypeptide, ladite séquence nucléotidique, avec une cellule transformée selon l'invention et/ou administration dudit composé à un animal transformé selon l'invention ;
- b) détermination de la capacité dudit composé à se lier avec ledit polypeptide ou ladite séquence nucléotidique, ou de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, ou de moduler la croissance ou la réplication cellulaire, ou d'induire, d'inhiber ou d'aggraver chez ledit animal transformé les pathologies liées

à une infection par *Streptococcus*, par exemple *Streptococcus agalactiae* ou un de ses micro-organismes associés.

Les cellules et/ou les animaux transformés selon l'invention, pourront avantageusement servir de modèle et être utilisés dans des procédés pour étudier, identifier et/ou sélectionner des composés susceptibles d'être responsables de pathologies induites ou aggravées par *Streptococcus agalactiae*, ou susceptibles de prévenir et/ou de traiter ces pathologies. En particulier, les cellules hôtes transformées, notamment les bactéries de la famille des *Streptococcus* dont la transformation par un vecteur selon l'invention peut par exemple accroître ou inhiber son pouvoir infectieux, ou moduler les pathologies habituellement induites ou aggravées par l'infection, pourront être utilisées pour infecter des animaux dont on suivra l'apparition des pathologies. Ces animaux non transformés, infectés par exemple avec des bactéries *Streptococcus* transformées, pourront servir de modèle d'étude. De la même manière, les animaux transformés selon l'invention pourront être utilisés dans des procédés de sélection de composés susceptibles de prévenir et/ou de traiter les maladies dues à *Streptococcus*. Lesdits procédés utilisant lesdites cellules transformées et/ou animaux transformés, font partie de l'invention.

Les composés susceptibles d'être sélectionnés peuvent être des composés organiques tels que des polypeptides ou hydrates de carbone ou tous autres composés organiques ou inorganiques déjà connus, ou des composés organiques nouveaux élaborés à partir de techniques de modélisation moléculaire et obtenus par synthèse chimique ou biochimique, ces techniques étant connues de l'homme de l'art.

Lesdits composés sélectionnés pourront être utilisés pour moduler la croissance et/ou la réplication cellulaire de *Streptococcus agalactiae* ou tout autre micro-organisme associé et ainsi pour contrôler l'infection par ces micro-organismes. Lesdits composés selon l'invention pourront également être utilisés pour moduler la croissance et/ou la réplication cellulaire de toutes cellules eucaryotes ou procaryotes, notamment les cellules tumorales et les micro-organismes infectieux, pour lesquelles lesdits composés s'avéreront actifs, les méthodes permettant de déterminer lesdites modulations étant bien connues de l'homme de l'art.

On entend désigner par composé capable de moduler la croissance d'un micro-organisme tout composé permettant d'intervenir, de modifier, de limiter et/ou de réduire le développement, la croissance, la vitesse de prolifération et/ou la viabilité dudit micro-organisme.

Cette modulation peut être réalisée par exemple par un agent capable de se lier à une protéine et ainsi d'inhiber ou de potentialiser son activité biologique, ou capable de se lier à une protéine membranaire de la surface extérieure d'un micro-organisme et de bloquer la pénétration dudit micro-organisme dans la cellule hôte ou de favoriser l'action du système immunitaire de l'organisme infecté dirigé à l'encontre dudit micro-organisme. Cette modulation peut être également réalisée par un agent capable de se lier à une séquence nucléotidique d'un ADN ou ARN d'un micro-organisme et de bloquer par exemple l'expression d'un polypeptide dont l'activité biologique ou structurelle est nécessaire à la croissance ou à la reproduction dudit micro-organisme.

On entend désigner par micro-organisme associé dans la présente invention, tout micro-organisme dont l'expression de gène peut être modulée, régulée, induite ou inhibée, ou dont la croissance ou la réplication cellulaire peut être également modulée par un composé de l'invention. On entend désigner également par micro-organisme associé dans la présente invention, tout micro-organisme comportant des séquences nucléotidiques ou des polypeptides selon l'invention. Ces micro-organismes peuvent dans certains cas comporter des polypeptides ou des séquences nucléotidiques identiques ou homologues à celles de l'invention et pourront également être détectés et/ou identifiés par les procédés ou kit de détection et/ou d'identification selon l'invention et également servir de cible pour les composés de l'invention. On entend aussi désigner par micro-organisme tout micro-organisme *Streptococcus agalactiae* de tout sérotype.

L'invention concerne les composés susceptibles d'être sélectionnés par une méthode de sélection selon l'invention.

L'invention concerne également une composition pharmaceutique comprenant un composé choisi parmi les composés suivants :

- a) une séquence nucléotidique selon l'invention ;
- b) un polypeptide selon l'invention ;
- c) un vecteur selon l'invention ;
- d) un anticorps selon l'invention ; et

e) un composé susceptible d'être sélectionné par une méthode de sélection selon l'invention, éventuellement en association avec un véhicule pharmaceutiquement acceptable.

La présente invention concerne en outre une composition pharmaceutique selon l'invention pour la prévention et le traitement d'une infection par une bactérie appartenant à l'espèce *Streptococcus agalactiae*.

- 5 L'invention, caractérisée en ce qu'elle comprend des anticorps dirigés contre les polypeptides spécifiques de *Streptococcus agalactiae*.

On entend désigner par quantité efficace, une quantité suffisante dudit composé ou anticorps, ou de polypeptide de l'invention, permettant de moduler la croissance de *Streptococcus agalactiae* ou d'un micro-organisme associé.

- 10 L'invention concerne aussi une composition pharmaceutique selon l'invention pour la prévention ou le traitement d'une infection par une bactérie appartenant au genre *Streptococcus* ou par un micro-organisme associé.

- 15 L'invention vise en outre une composition immunogène et/ou vaccinale, caractérisée en ce qu'elle comprend un ou plusieurs polypeptides selon l'invention et/ou un ou plusieurs polypeptides hybrides selon l'invention.

L'invention comprend aussi l'utilisation d'une cellule transformée selon l'invention, pour la préparation d'une composition vaccinale.

- 20 L'invention vise également une composition vaccinale, caractérisée en ce qu'elle contient une séquence nucléotidique selon l'invention, un vecteur selon l'invention et/ou une cellule transformée selon l'invention.

- L'invention concerne en outre une composition immunogène capable d'induire une réponse immunitaire cellulaire ou humorale pour la prévention ou le traitement d'une infection par une bactérie appartenant à l'espèce *Streptococcus agalactiae*, caractérisée en ce qu'elle comprend une composition immunogène ou une composition
25 vaccinale selon l'invention, en association avec un véhicule pharmaceutiquement acceptable et éventuellement un ou plusieurs adjuvants de l'immunité appropriés.

L'invention concerne également les compositions vaccinales selon l'invention, pour la prévention ou le traitement d'une infection par une bactérie appartenant au genre *Streptococcus* ou par un micro-organisme associé.

- 30 De manière préférée, les compositions immunogènes et/ou vaccinales selon l'invention destinées à la prévention et/ou au traitement d'infection par *Streptococcus* ou par un micro-organisme associé seront choisies parmi les compositions immunogènes et/ou vaccinales comprenant un polypeptide ou un de ses fragments correspondant à une protéine, ou un de ses fragments, de l'enveloppe cellulaire de *Streptococcus*. Les

compositions vaccinales comprenant des séquences nucléotidiques comprendront de préférence également des séquences nucléotidiques codant pour un polypeptide ou un de ses fragments correspondant à une protéine, ou un de ses fragments, de l'enveloppe cellulaire de *Streptococcus*.

- 5 Les polypeptides de l'invention ou leurs fragments entrant dans les compositions immunogènes selon l'invention peuvent être sélectionnés par des techniques connues de l'homme de l'art comme par exemple sur la capacité desdits polypeptides à stimuler les cellules T, qui se traduit par exemple par leur prolifération ou la sécrétion d'interleukines, ou qui aboutit à la production d'anticorps dirigés contre lesdits
10 polypeptides.

- Chez la souris, chez laquelle une dose pondérale de la composition vaccinale comparable à la dose utilisée chez l'homme est administrée, la réaction anticorps est testée par prélèvement du sérum suivi d'une étude de la formation d'un complexe entre les anticorps présents dans le sérum et l'antigène de la composition vaccinale, selon les
15 techniques usuelles.

Selon l'invention, lesdites compositions vaccinales seront de préférence en association avec un véhicule pharmaceutiquement acceptable et, le cas échéant, avec un ou plusieurs adjuvants de l'immunité appropriés.

- Aujourd'hui, divers types de vaccins sont disponibles pour protéger l'homme
20 contre des maladies infectieuses : micro-organismes vivants atténués (*M. bovis* - BCG pour la tuberculose), micro-organismes inactivés (virus de la grippe), des extraits acellulaires (*Bordetella pertussis* pour la coqueluche), protéines recombinées (antigène de surface du virus de l'hépatite B), des polysides (pneumocoques). Des vaccins préparés à partir de peptides de synthèse ou de micro-organismes génétiquement
25 modifiés exprimant des antigènes hétérologues sont en cours d'expérimentation. Plus récemment encore, des ADNs plasmidiques recombinés portant des gènes codant pour des antigènes protecteurs ont été proposés comme stratégie vaccinale alternative. Ce type de vaccination est réalisé avec un plasmide particulier dérivant d'un plasmide de *E. coli* qui ne se réplique pas *in vivo* et qui code uniquement pour la protéine vaccinnante.
- 30 Des animaux ont été immunisés en injectant simplement l'ADN plasmidique nu dans le muscle. Cette technique conduit à l'expression de la protéine vaccinnale *in situ* et à une réponse immunitaire de type cellulaire (CTL) et de type humoral (anticorps). Cette double induction de la réponse immunitaire est l'un des principaux avantages de la technique de vaccination avec de l'ADN nu.

Les compositions vaccinales comprenant des séquences nucléotidiques ou des vecteurs dans lesquels sont insérées lesdites séquences, sont notamment décrites dans la demande internationale N° WO 90/11092 et également dans la demande internationale N° WO 95/11307.

5 La séquence nucléotidique constitutive de la composition vaccinale selon l'invention peut être injectée à l'hôte après avoir été couplée à des composés qui favorisent la pénétration de ce polynucléotide à l'intérieur de la cellule ou son transport jusqu'au noyau cellulaire. Les conjugués résultants peuvent être encapsulés dans des microparticules polymères, comme décrit dans la demande internationale N° WO
10 94/27238 (Medisorb Technologies International).

Selon un autre mode de réalisation de la composition vaccinale selon l'invention, la séquence nucléotidique, de préférence un ADN, est complexée avec du DEAE-dextran, avec des protéines nucléaires, avec des lipides ou encapsulée dans des liposomes ou encore introduite sous la forme d'un gel facilitant sa transfection dans les
15 cellules. Le polynucléotide ou le vecteur selon l'invention peut aussi être en suspension dans une solution tampon ou être associé à des liposomes.

Avantageusement, un tel vaccin sera préparé conformément à la technique décrite par Tacson et al. ou Huygen et al. en 1996 ou encore conformément à la technique décrite par Davis et al. dans la demande internationale N° WO 95/11307.

20 Un tel vaccin peut être également préparé sous la forme d'une composition contenant un vecteur selon l'invention, placée sous le contrôle d'éléments de régulation permettant son expression chez l'homme ou l'animal. On pourra par exemple utiliser, en tant que vecteur d'expression *in vivo* de l'antigène polypeptidique d'intérêt, le plasmide pcDNA3 ou le plasmide pcDNA1/neo, tous les deux commercialisés par Invitrogen (R
25 & D Systems, Abingdon, Royaume-Uni). Un tel vaccin comprendra avantageusement, outre le vecteur recombinant, une solution saline, par exemple une solution de chlorure de sodium.

On entend désigner par véhicule pharmaceutiquement acceptable, un composé ou une combinaison de composés entrant dans une composition pharmaceutique ou
30 vaccinale ne provoquant pas de réactions secondaires et qui permet par exemple la facilitation de l'administration du composé actif, l'augmentation de sa durée de vie et/ou de son efficacité dans l'organisme, l'augmentation de sa solubilité en solution ou encore l'amélioration de sa conservation. Ces véhicules pharmaceutiquement acceptables sont

bien connus et seront adaptés par l'homme de l'art en fonction de la nature et du mode d'administration du composé actif choisi.

En ce qui concerne les formulations vaccinales, celles-ci peuvent comprendre des adjuvants de l'immunité appropriés qui sont connus de l'homme de l'art, comme par
5 exemple l'hydroxyde d'aluminium, un représentant de la famille des muramyl peptides comme un des dérivés peptidiques du N-acétyl-muramyl, un lysat bactérien, ou encore l'adjuvant incomplet de Freund.

De préférence, ces composés seront administrés par voie systémique, en particulier par voie intraveineuse, par voie intramusculaire, intradermique ou sous-
10 cutanée, ou par voie orale. De manière plus préférée, la composition vaccinale comprenant des polypeptides selon l'invention, sera administrée à plusieurs reprises, de manière étalée dans le temps, par voie intradermique ou sous-cutanée.

Leurs modes d'administration, posologies et formes galéniques optimaux peuvent être déterminés selon les critères généralement pris en compte dans
15 l'établissement d'un traitement adapté à un patient comme par exemple l'âge ou le poids corporel du patient, la gravité de son état général, la tolérance au traitement et les effets secondaires constatés.

Enfin, l'invention comprend l'utilisation d'une composition selon l'invention, pour le traitement ou la prévention de maladies induites ou aggravées par la présence de
20 *Streptococcus*.

Par ailleurs, la présente invention a également pour objet une banque d'ADN génomique d'une bactérie du genre *Streptococcus*, de manière préférée, *Streptococcus agalactiae*, de manière préférée la CIP 82.45 (ATCC 12403).

La banque d'ADN génomique décrite dans la présente invention, en particulier
25 la banque déposée à la CNCM le 28 décembre 2000 sous le numéro d'ordre N° I-2610, recouvre en effet *Streptococcus agalactiae* CIP 82.45 (ATCC 12403). Toutefois, si certaines régions n'ont pas pu être clonées dans ladite banque, en raison de problèmes de létalités chez *Escherichia coli*, ces régions peuvent facilement être amplifiées et identifiées par l'homme du métier, en utilisant des oligonucléotides spécifiques des
30 séquences des extrémités des différents clones qui forment les contigs.

La présente invention concerne également les méthodes pour l'isolement d'un polynucleotide d'intérêt présent chez une souche de *Streptococcus agalactiae* et absente chez une autre souche, qui utilise au moins une banque d'ADN basée par exemple sur un plasmide pSYX34 contenant un fragment du génome de *Streptococcus agalactiae*.

La méthode selon l'invention pour l'isolement d'un polynucléotide d'intérêt peut comprendre les étapes suivantes :

a) isoler au moins un polynucléotide contenu dans un clone de la banque d'ADN d'origine de *Streptococcus agalactiae*,

5 b) isoler :

- au moins un polynucléotide génomique ou ADNc d'une bactérie *Streptococcus*, ladite bactérie *Streptococcus* appartenant à une souche différente de la souche utilisée pour la construction de la banque d'ADN de l'étape a) ou, de façon alternative,

10 - au moins un polynucléotide contenu dans un clone d'une banque d'ADN préparé à partir du génome d'une *Streptococcus* qui est différente de la souche *Streptococcus agalactiae* utilisée pour la construction de la banque d'ADN de l'étape a) ;

c) hybrider le polynucléotide de l'étape a) au polynucléotide de l'étape a) ;

15 d) sélectionner les polynucléotides de l'étape a) qui n'ont pas formé de complexe d'hybridation avec les polynucléotides de l'étape b) ;

e) caractériser le polynucléotide sélectionné.

On peut préparer le polynucléotide de l'étape a) par la digestion d'au moins un clone recombinant avec une enzyme de restriction appropriée, et de façon optionnelle, l'amplification de l'insert polynucléotide qui en résulte.

20 Ainsi, la méthode de l'invention permet à l'homme du métier d'effectuer des études génomiques comparatives entre les différentes souches ou espèces du genre *Streptococcus*, par exemple entre les souches pathogéniques et leurs équivalents non pathogènes.

25 En particulier, il est possible d'étudier et de déterminer les régions de polymorphisme entre lesdites souches.

L'invention comprend aussi un procédé d'identification de séquence spécifique de *Streptococcus agalactiae*, caractérisé par l'alignement de séquences nucléotidiques de *Streptococcus agalactiae* selon l'invention et le traitement de données obtenues par cet alignement pour isoler les séquences spécifiques.

30

La présente invention concerne également l'utilisation des séquences nucléiques ou des polypeptides selon la présente invention :

- pour la sécrétion de protéines,
- comme facteurs de virulence,

- pour le contrôle par l'intermédiaire du quorum-sensing,
 - pour l'identification de cibles pour les maladies humaines dont *Streptococcus agalactiae* est un modèle, et
 - pour l'identification de cibles contre les bactéries Gram positives pathogènes
- 5 par la méthode de génomique soustractive (comme par exemple par comparaison avec des bactéries Gram positives non pathogènes).

EXEMPLES

Exemple 1 : Matériels et méthode

- 10 La stratégie de séquençage du génome de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) repose sur un séquençage alléatoire (shot-gun). La première étape de ce travail consiste à cloner l'ADN génomique de la bactérie *Streptococcus agalactiae* dans différents vecteurs (plasmides et BAC).

Matériels et méthodes.

- 15 1. Construction des banques :

a/ Banque de petits fragments dans le vecteur pcDNA2.1

- L'ADN chromosomique de la souche de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) a été préparé par une méthode classique incluant un traitement à la protéinase K et une extraction au phénol (9). Environ 10 µg d'ADN ont été cassés par
- 20 nébulisation (1 minute sous une pression de 1 bar) (4). Les extrémités des fragments d'ADN ont été rendues franches en faisant agir la DNA-polymérase du bactériophage T4 pendant 15 minutes à 37°C en présence des 4 nucléotides tri-phosphate. L'enzyme a été inactivée par une incubation de 15 mn à 75°C. Des adaptateurs (Invitrogen Cat. N° 408-18) ont ensuite été ligaturés à ces extrémités. Après ligation, les fragments
- 25 d'ADN chromosomiques ayant une taille entre 1 000 et 3 000 paires de bases ont été purifiés après électrophorèse sur gel d'agarose. Le vecteur utilisé pour la construction de la banque, pcDNA2.1 (Invitrogen), a été digéré par l'enzyme BstX1 et purifié par geneclon (BIO-101) après électrophorèse sur gel d'agarose. L'ADN chromosomique et le vecteur purifié ont été ligaturés par action de la ligase du bactériophage T4. Le
- 30 mélange de ligation a été introduit par transformation dans la souche d'*Escherichia coli* XL2-blue (Stratagene). Environ 4000 colonies sont obtenues par µl du mélange de ligation.

b/ Construction d'une banque de fragments de taille moyenne (banque déposée à la CNCM sous le numéro I-2610)

Afin de limiter la fréquence des événements de co-ligation et de clones sans insert, la méthode du remplissage partiel du site de coupure a été utilisée (7).

L'ADN chromosomique de la souche de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) a été digéré de manière partielle par l'enzyme de restriction Sau3A en utilisant une gamme de dilution de l'enzyme. La fraction présentant la gamme de tailles souhaitée (entre 2 et 12 kbases) a été précipitée et les extrémités ont été remplies partiellement par le fragment de Klenow de la DNA polymérase d'*E. coli* en présence de dITP et dCTP. Après purification sur gel d'agarose les fragments d'ADN chromosomique ayant une taille comprise entre 3 et 6 kbases ont été ligués au vecteur pSYX34 (7) digéré par l'enzyme Sall remplie partiellement par l'enzyme de Klenow en présence de dATP et dGTP. Le mélange de ligation a été introduit par transformation dans la souche d'*Escherichia coli* XL10-kan (Stratagene) et étalé sur milieu LB contenant du chloramphénicol à une concentration de 20 mg/l. Environ 500 colonies sont obtenues par µl du mélange de ligation.

2. Préparation des plasmides et séquençage

Les plasmides ont été préparés par une méthode semi-automatique de préparation développée au laboratoire GMP basé sur la méthode de lyse alcaline (2). Les inserts chromosomiques ont été séquencés à partir de leurs deux extrémités en utilisant les primer T7 et universel en suivant les recommandations du fournisseur (PE-biosystems). Les séquences ont été déterminées en utilisant un séquenceur automatique de type 3700 (PE-Biosystem).

3. Assemblage des séquences

Les séquences ont été assemblées en utilisant l'ensemble de logiciel développé à l'Université de Washington, Phred, Phrap et Consed (5, 8). La finition de la séquence a été réalisée en utilisant l'ensemble de logiciel GMPTB (7). L'étape de finition correspond au reséquençage des régions où la séquence est peu sûre et le séquençage des régions situées entre les contigs. Elle a été réalisée en séquençant des produits de PCR correspondant à ces régions identifiées par un expert en utilisant les logiciels Consed (8) et GMPTB (7). Les séquences des oligonucléotides ont été définies en utilisant les logiciels Consed et Primo (8, 10).

4. Annotation des séquences

L'identification des phases codantes (CDS) a été réalisée en utilisant l'ensemble de logiciel GMPTB (L. Frangeul et al. non publié). Ce programme combine les résultats de différentes méthodes : (i) l'identification de phases ouvertes de lecture et

leur tri en fonction de leur taille, (ii) l'analyse de la probabilité d'être codante en utilisant le logiciel Genemark (11), (iii) l'identification d'un début de traduction (codon d'initiation et séquence de fixation du ribosome), (iv) similarité de la séquence protéique déduite avec les séquences protéiques contenues dans les banques de séquence en utilisant le logiciel BLASTP.

Les fonctions des protéines codées par les phases codantes identifiées indiquées au tableau 1 ont été prédites par l'analyse des résultats de recherche de similarités dans les banques en utilisant le logiciel BLASTP (1).

Exemple 2 : Description scientifique de la banque de BAC de *Streptococcus agalactiae*

CIP 82.45 (ATCC 12403) déposée à la CNCM le 28 décembre 2000 sous le numéro I-2610.

Collection de clones d'*Escherichia coli* DH 10B™ (Calvin et al., J. Bacteriol. 170, 2796, 1988) contenant des fragments d'ADN génomique de la bactérie *Streptococcus agalactiae* souche NEM 316, CIP 82.45 (ATCC 12403), clonés dans le vecteur pSYX34 (Xu et al., Biotechniques, 17:57, 1990). Le vecteur a été digéré Sall et partiellement rempli à l'aide de l'ADN polymérase afin de produire des extrémités 5'-TC. Des fragments génomiques aléatoires de 3-6 kb provenant de *Streptococcus agalactiae* (souche NEM 316, CIP 82-45, ATCC 12403) ont été digérés partiellement par Sau3A et partiellement remplis afin de produire des extrémités 5'-GA. Après ligature *in vitro* et transformation, des clones résistants au chloromphénicol ont été sélectionnés. Environ 5000 clones ont été assemblés, suspendus dans 15 ml de milieu L et congelés.

Exemple 3 : Les protéines de surface de *Streptococcus agalactiae* NEM316

Les protéines de surface des bactéries pathogènes, et plus particulièrement les protéines dites du type LPXTG (Navarre et Schneewind, Microbial. Mol. Biol. Rev. 63 174-229), jouent un rôle crucial lors du processus infectieux en permettant notamment des interactions entre le microorganisme et les cellules de l'hôte et/ou l'échappement au système immunitaire. Les inventeurs ont donc focalisé leur étude sur ce type de protéines qui présentent la particularité d'être liées covalamment au peptidoglycane via le motif d'ancrage carboxylique LPXTG. Cette réaction est catalysée par une enzyme bifonctionnelle (endopeptidase-transpeptidase) appelée sortase. L'étude du rôle de ces protéines dans la virulence de *S. agalactiae* a été réalisée par 2 approches

complémentaires (construction d'un mutant sortase-déficient, inactivation des gènes codant pour des protéines de type LPXTG).

- Le gène *srtA* de *S. agalactiae* NEM316 (IPF N°1268).

- 5 Le mutant MEM1979, déposé le 24 avril 2002 à la CNCM sous le numéro I-2861, est une souche mutante dérivée de NEM316 (CIP 82.45, ATCC 12403) dans laquelle l'IPF 1268 a été inactivé.

L'analyse du génome de NEM316 nous a permis de caractériser un gène *srtA* présentant homologie respectivement 55 % et 30 % d'identité avec les sortases de *Streptococcus gordonii* et de *Staphylococcus aureus*. Ce gène a été inactivé par
10 insertion-inactivation et nous avons montré que le mutant ainsi construit n'adhérait plus à des cellules épithéliales humaines pulmonaires (A549) et utérines (HeLa). Ces résultats suggèrent que les protéines du type LPXTG de *S. agalactiae* jouent un rôle dans la virulence de cette bactérie, en permettant notamment son adhésion avec les cellules de l'hôte.

- 15 - Recensement des protéines du type LPXTG de *S. agalactiae* NEM316.

Une analyse *in silico* du génome de NEM316 a révélé la présence de 30 protéines de surface putatives possédant le motif d'ancrage de type LPXTG (Tableau 6). Nous avons étudié par amplification PCR, en utilisant des amorces spécifiques, la distribution des gènes codant pour 21 protéines du type LPXTG dans une collection de
20 99 souches non-redondantes de *S. agalactiae* responsables d'infections non-invasives (70 souches provenant de portage ou d'infection urinaire) et invasives (29 souches provenant d'hémoculture ou de méningite). Cette étude a montré que 6 de ces gènes (IPN N° 1503, 678, 2192, 1861, 584, 280) étaient présents dans toutes les souches de notre échantillonnage (Tableau 7). Deux de ces six gènes (IPF N°678 et 1503) ont été
25 inactivés par insertion-inactivation et les mutants correspondants NEM2056 et NEM2057 présentaient une adhérence diminuée avec les cellules épithéliales A549 (Tableau 5).

- 30 Le mutant NEM2056, déposé le 24 avril 2002 à la CNCM sous le numéro I-2862, est une souche mutante dérivée de NEM316 (CIP 82.45, ATCC 12403) dans laquelle l'IPF 678 a été inactivé.

Le mutant NEM2057, déposé le 24 avril 2002 à la CNCM sous le numéro I-2863, est une souche mutante dérivée de NEM316 (CIP 82.45, ATCC 12403) dans laquelle l'IPF 1503 a été inactivé.

- Cibles vaccinales.

La présence des gènes IPF N°1503, 678, 2192, 1861, 584, 280 chez toutes les souches de *S. agalactiae* testées font des protéines correspondantes des cibles vaccinales de choix pour le développement d'un vaccin anti-*S. agalactiae*.

5

TABLEAU 1: Liste des phases codantes annotées identifiées par l'analyse des séquences des contigs

10

Seq ID No.	Prot No.	Localisation et sens sur contig	Résultats Blastp sur des banques de protéines non redondantes & Homologie	Commentaires
SeqID 140	SA-1.2	Contig137 (42738-43340 p)	74	Identities = 129/202 (63%), Positives = 156/202 (76%), Gaps = 8/202 (3%) ref NP_072029.1 traG-related protein [Enterococcus faecalis] gb AAAG40447.1 (AE002565) traG-related protein [Enterococcus faecalis] Length = 423
SeqID 141	SA-10.1	Contig137 (33454-33681 m)	No Hits found	Identities = 220/354 (62%), Positives = 274/354 (77%), Gaps = 1/354 (0%) sp Q48677 PEPA_LACLC GLUTAMYL-AMINOPEPTIDASE emb CAA56994.1 (X81089) glutamyl-aminopeptidase [Lactococcus lactis] Length = 355
SeqID 143	SA-1001.1	Contig127 (12912-13202 p)	No Hits found	Identities = 49/100 (49%), Positives = 71/100 (71%), Gaps = 4/100 (4%) db JBAB06972.1 (AP001518) thioredoxin H1 [Bacillus halodurans] Length = 106
SeqID 144	SA-1002.1	Contig127 (12518-12802 m)	No Hits found	Identities = 79/196 (40%), Positives = 126/196 (63%), Gaps = 1/196 (0%) pir JAG6999 phenylalanyl-RNA synthetase (beta subunit) homolog ytpR - Bacillus subtilis gb AAC00291.1 (AF008220) YtpR [Bacillus subtilis] emb CAB14960.1 (Z99119) similar to phenylalanyl-RNA synthetase (beta subunit) [Bacillus subtilis] Length = 201
SeqID 145	SA-1003.1	Contig127 (12198-12407 m)	65	Identities = 69/243 (28%), Positives = 117/243 (47%), Gaps = 15/243 (6%) sp Q02148 YH16_LACLA HYPOTHETICAL 30.7 KDA PROTEIN IN HISD-HISB INTERGENIC REGION (ORF6) pir JF45734 orf6 3 to hisD - Lactococcus lactis subsp. lactis gb AAB81904.1 (U92974) unknown [Lactococcus lactis] Length = 263
SeqID 146	SA-1004.1	Contig127 (11539-12165 m)	60	
SeqID 147	SA-1006.1	Contig127 (10769-11485 p)	47	

SeqID 148	SA-1007.1	Contig127 (10293-10688 m)	69	Identities = 65/141 (46%), Positives = 93/141 (65%), Gaps = 10/141 (7%) gb AA74079.1 (AF212845) putative single stranded binding protein [Lactococcus u36] lactis bacteriophage Length = 141
SeqID 149	SA-101.1	Contig131 (21108-21947 p)	82	Identities = 201/279 (72%), Positives = 231/279 (82%) gb AAC81484.1 (AF082738) ABC transporter ATP-binding protein [Streptococcus pyogenes] Length = 296
SeqID 150	SA-1010.1	Contig127 (9526-10170 m)	33	Identities = 63/179 (35%), Positives = 91/179 (50%), Gaps = 2/179 (1%) emb CAC13072.1 (AL445503) putative hydrolase [Streptomyces coelicolor A3(2)] Length = 238
SeqID 151	SA-1012.1	Contig127 (7754-9499 m)	60	Identities = 254/585 (43%), Positives = 371/585 (63%), Gaps = 9/585 (1%) pir JAG9655 two-component sensor histidine kinase lyS-involved - Bacillus subtilis emb CAA99610.1 (Z75208) autolysin sensor kinase [Bacillus subtilis] emb CAB14853.1 (Z99118) two-component sensor histidine kinase [Bacillus subtilis] Length = 593
SeqID 152	SA-1013.1	Contig127 (7033-7779 m)	62	Identities = 105/244 (43%), Positives = 157/244 (64%), Gaps = 6/244 (2%) pir JB8655 two-component response regulator lyT-involved - Bacillus subtilis emb CAA99611.1 (Z75208) autolysin response regulator [Bacillus subtilis] emb CAB14852.1 (Z99118) two-component response regulator [Bacillus subtilis] Length = 241
SeqID 153	SA-1014.1	Contig127 (6936-7100 p)	No Hits found	
SeqID 154	SA-1016.1	Contig127 (6408-6863 m)	51	Identities = 50/110 (45%), Positives = 82/110 (74%), Gaps = 2/110 (1%) pir JC69983 conserved hypothetical protein ysbA - Bacillus subtilis emb CAA99612.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14851.1 (Z99118) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] Length = 146

SeqID 155	SA-1017.1	Contig127 (5678-6405 m)	64	Identities = 120/240 (50%), Positives = 159/240 (66%), Gaps = 10/240 (4%) pir D99983 conserved hypothetical protein yabB - Bacillus subtilis emb CAA9613.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14850.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 231
SeqID 156	SA-1018.1	Contig127 (3807-5435 m)	90	Identities = 498/542 (91%), Positives = 518/542 (94%) gb AAC67217.1 (U78968) surface lipoprotein DppA [Streptococcus pyogenes] Length = 542
SeqID 157	SA-1019.1	Contig127 (2717-3694 m)	96	Identities = 302/325 (92%), Positives = 317/325 (96%) gb AAC67218.1 (U78968) transmembrane transport protein DppB [Streptococcus pyogenes] Length = 325
SeqID 158	SA-102.1	Contig131 (20566-21108 p)	69	Identities = 119/165 (72%), Positives = 134/165 (81%), Gaps = 5/165 (3%) gb AAC61483.1 (AF082738) phosphotidylglycerophosphate synthase [Streptococcus pyogenes] Length = 165
SeqID 159	SA-1020.1	Contig127 (1899-2720 m)	92	Identities = 255/274 (93%), Positives = 263/274 (95%), Gaps = 1/274 (0%) gb AAC67219.1 (U78968) transmembrane transport protein DppC [Streptococcus pyogenes] Length = 274
SeqID 160	SA-1021.1	Contig127 (1084-1887 m)	95	Identities = 254/267 (95%), Positives = 262/267 (97%) gb AAC67220.1 (U78968) ATPase protein DppD [Streptococcus pyogenes] Length = 267
SeqID 161	SA-1022.1	Contig127 (474-1100 m)	91	Identities = 185/205 (90%), Positives = 195/205 (94%) gb AAC67221.1 (U78968) ATPase protein DppE [Streptococcus pyogenes] Length = 208

SeqID 162	SA-1023.1	Contig1127 (1-192 m)	62	<p>Identities = 35/58 (60%), Positives = 44/58 (75%) splP36672 PTTB_ECOLI PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-TRE) pir C65236 phosphotransferase system trehalose permease - Escherichia coli (strain K-12) gb AAC77197.1 (AE000495) PTS system enzyme II, trehalose specific [Escherichia coli K12] Length = 473</p>
SeqID 163	SA-1024.2	Contig113 (19147-19281 p)	No Hits found	
SeqID 164	SA-1025.2	Contig113 (18773-19144 p)	53	<p>Identities = 37/124 (29%), Positives = 67/124 (53%), Gaps = 2/124 (1%) gb AAC98903.1 (AF023181) DivIC homolog [Listeria monocytogenes] Length = 128</p>
SeqID 165	SA-1026.1	Contig113 (18514-18786 p)	75	<p>Identities = 49/84 (58%), Positives = 70/84 (83%) splP37557 YABO_BACSU HYPOTHETICAL 9.7 KDA PROTEIN IN MFD-DIVIC INTERGENIC REGION pir S66089 conserved hypothetical protein yabo - Bacillus subtilis db BAA05294.1 (D26185) unknown [Bacillus subtilis] emb CAB11835.1 (Z39104) similar to hypothetical proteins [Bacillus subtilis] Length = 86</p>
SeqID 166	SA-1028.1	Contig113 (14726-18223 p)	62	<p>Identities = 523/1051 (49%), Positives = 733/1051 (68%), Gaps = 20/1051 (1%) gb AAD03810.1 (AF054624) transcription-repair coupling factor [Lactobacillus sakei] Length = 1045</p>
SeqID 167	SA-1029.1	Contig113 (14154-14729 p)	60	<p>Identities = 89/187 (47%), Positives = 127/187 (67%), Gaps = 2/187 (1%) db BAG03787.1 (AP001507) stage V sporulation protein C (peptidyl-tRNA hydrolase) [Bacillus halodurans] Length = 185</p>
SeqID 168	SA-103.1	Contig131 (19160-20443 p)	62	<p>Identities = 207/424 (48%), Positives = 277/424 (64%), Gaps = 3/424 (0%) gb AAC61481.1 (AF082738) unknown [Streptococcus pyogenes] Length = 429</p>

SeqID 169	SA-1030.1	Contig113 (12855-14070 p)	84	Identities = 261/371 (70%), Positives = 313/371 (84%), Gaps = 5/371 (1%) gb BA007770.1 (AP001520) GTP-binding protein [Bacillus halodurans] Length = 366
SeqID 170	SA-1031.1	Contig113 (12592-12795 p)	No Hits found	
SeqID 171	SA-1032.1	Contig113 (12183-12390 p)	82	Identities = 46/63 (73%), Positives = 57/63 (90%) gb AAC45338.1 (AF000658) ORFX [Streptococcus pneumoniae] Length = 64
SeqID 172	SA-1033.1	Contig113 (11290-12183 p)	43	Identities = 83/298 (27%), Positives = 138/298 (45%), Gaps = 35/298 (11%) pr JH6995 hypothetical protein yJIR - Bacillus subtilis gb AAC00282.1 (AF008220) YIR [Bacillus subtilis] emb CAB14972.1 (Z99119) yJIR [Bacillus subtilis] Length = 308
SeqID 173	SA-1034.1	Contig113 (10098-11232 p)	80	Identities = 278/378 (73%), Positives = 324/378 (85%) sp O6072 DP3B_STRPN DNA POLYMERASE III, BETA CHAIN gb AAC45337.1 (AF000658) beta subunit of DNA polymerase III [Streptococcus pneumoniae] Length = 378
SeqID 174	SA-1035.1	Contig113 (8580-8941 p)	82	Identities = 353/455 (77%), Positives = 401/455 (87%), Gaps = 6/455 (1%) gb AAAF71535.1 (AF255728_1) (AF255728) chromosomal initiator protein DnaA [Streptococcus pyogenes] Length = 451
SeqID 175	SA-1036.1	Contig113 (7608-8381 p)	71	Identities = 138/257 (53%), Positives = 188/257 (72%), Gaps = 5/257 (1%) gb AAC45335.1 (AF000658) SP-SpoJ [Streptococcus pneumoniae] Length = 252
SeqID 176	SA-1037.1	Contig113 (6275-7510 p)	70	Identities = 222/396 (56%), Positives = 230/396 (73%), Gaps = 27/396 (6%) gb AAC45334.1 (AF000658) putative serine protease [Streptococcus pneumoniae] Length = 397
SeqID 177	SA-1038.1	Contig113 (5601-6080 m)	80	Identities = 111/159 (69%), Positives = 136/159 (84%) gb AAC44894.1 (U76218) unknown [Streptococcus pneumoniae] gb AAC45340.1 (AF000658) ORF1 [Streptococcus pneumoniae] Length = 159

SeqID 178	SA-1039.1	Contig113 (2443-5022 p)	21	<p>Identities = 140/260 (53%), Positives = 182/260 (69%), Gaps = 6/260 (2%) gblAAC14608.1 U05840) transmembrane protein Tmp5 [Lactococcus lactis] Length = 273</p> <p>Identities = 228/413 (55%), Positives = 307/413 (74%) gblAAC61480.1 (AF082738) unknown [Streptococcus pyogenes] Length = 414</p>
SeqID 179	SA-104.1	Contig131 (17914-19158 p)	73	<p>Identities = 354/542 (65%), Positives = 452/542 (83%), Gaps = 4/542 (0%) pifIE9861 ABC transporter (ATP-binding protein) homolog YpA - Bacillus subtilis embICAB13316.1 (Z99111) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] gblAAC24918.1 (AF012285) Ykpa [Bacillus subtilis] Length = 540</p>
SeqID 180	SA-1041.1	Contig113 (701-2320 p)	82	<p>Identities = 70/193 (36%), Positives = 119/193 (61%) pifID70042 conserved hypothetical protein yjA - Bacillus subtilis gblAAC67260.1 (AF017113) YjA [Bacillus subtilis] embICAB15545.1 (Z99122) similar to hypothetical proteins [Bacillus subtilis] Length = 281</p>
SeqID 181	SA-1042.1	Contig113 (111-635 p)	56	<p>Identities = 98/200 (49%), Positives = 139/200 (69%), Gaps = 1/200 (0%) gblAAF25544.1 AF109218_4 (AF109218) Thle [Staphylococcus carnosus] Length = 212</p>
SeqID 182	SA-1044.2	Contig130 (3069-3740 p)	62	<p>Identities = 242/412 (58%), Positives = 303/412 (72%), Gaps = 2/412 (0%) gblAAF86297.1 (AF072894) UDP-N-acetylglucosamine-1-carboxyvinyl transferase [Listeria monocytogenes] Length = 439</p>
SeqID 183	SA-1045.1	Contig130 (3867-5128 p)	70	<p>Identities = 56/185 (30%), Positives = 86/185 (46%), Gaps = 4/185 (2%) dbjBAB04556.1 (AP001510) unknown conserved protein [Bacillus halodurans] Length = 197</p>
SeqID 184	SA-1046.1	Contig130 (5210-5782 p)	44	<p>Identities = 158/431 (36%), Positives = 270/431 (61%), Gaps = 6/431 (1%) dbjBAB06894.1 (AP001518) unknown conserved protein [Bacillus halodurans] Length = 435</p>
SeqID 185	SA-1047.1	Contig130 (5763-7068 p)	62	

SeqID 186	SA-1048.1	Contig130 (7081-7941 p)	44	Identities = 101/207 (48%), Positives = 128/207 (61%), Gaps = 31/207 (14%) gb AAC35914.1 (AF071085) methionine aminopeptidase A [Enterococcus faecalis] Length = 178
SeqID 187	SA-1048.1	Contig130 (7943-8863 p)	49	Identities = 83/276 (30%), Positives = 157/276 (56%), Gaps = 3/276 (1%) gb AAC35915.1 (AF071085) Orfde2 [Enterococcus faecalis] Length = 302
SeqID 188	SA-105.1	Contig131 (17322-17675 m)	61	Identities = 56/116 (48%), Positives = 74/116 (63%), Gaps = 3/116 (2%) pir JC4754 hypothetical 13.6k protein - Lactococcus lactis emb CAA61548.1 (X89367) orf121 [Lactococcus lactis] Length = 120
SeqID 189	SA-1050.1	Contig130 (8880-9314 m)	50	Identities = 52/161 (32%), Positives = 78/161 (48%), Gaps = 26/161 (16%) gb AAD54224.1 AF143443_3 (AF143443) MesH [Leuconostoc mesenteroides] Length = 160
SeqID 190	SA-1051.1	Contig130 (9517-10026 p)	47	Identities = 56/158 (35%), Positives = 91/158 (57%), Gaps = 8/158 (5%) emb CAA68244.1 (X99978) citrulline cluster-linked gene [Lactobacillus plantarum] Length = 186
SeqID 191	SA-1053.1	Contig130 (10186-12124 p)	70	Identities = 345/657 (52%), Positives = 462/657 (69%), Gaps = 8/657 (1%) sp O31498 DNLJ_BACSU DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+)) pir F69794 DNA ligase (NAD+) (EC 6.5.1.2) - Bacillus subtilis emb CAB12482.1 (Z99107) similar to DNA ligase [Bacillus subtilis] Length = 668
SeqID 192	SA-1054.1	Contig130 (12138-13155 p)	54	Identities = 151/293 (51%), Positives = 193/293 (65%), Gaps = 5/293 (1%) pir F69795 conserved hypothetical protein yerQ - Bacillus subtilis emb CAB12492.1 (Z99107) similar to hypothetical proteins [Bacillus subtilis] Length = 303
SeqID 193	SA-1055.1	Contig130 (13159-15459 p)	47	Identities = 227/669 (33%), Positives = 363/669 (53%), Gaps = 66/669 (9%) pir 1808262A thermostable pullulanase [Bacillus stearothermophilus] Length = 658

SeqID 194	SA-1056.1	Contig130 (15565-17533 p)	60	<p>Identities = 276/628 (43%), Positives = 377/628 (59%), Gaps = 20/628 (3%) spP30537[GLGB_BACCL 1,4-ALPHA-GLUCAN BRANCHING ENZYME (GLYCOGEN BRANCHING ENZYME)] prjIB56539 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - <i>Bacillus caldolyticus</i> emb CAA78440.1 (Z14057) 1,4-alpha-glucan branching enzyme [<i>Bacillus caldolyticus</i>] Length = 666</p>
SeqID 195	SA-1057.1	Contig130 (17575-18714 p)	65	<p>Identities = 195/352 (55%), Positives = 259/352 (72%) spO08328[GLGC_BACST GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) dbjBAA19689.1] (D87026) subunit of ADP-glucose pyrophosphorylase [<i>Bacillus stearothermophilus</i>] Length = 387</p>
SeqID 196	SA-1058.1	Contig130 (18704-18837 p)	47	<p>Identities = 105/353 (29%), Positives = 180/353 (50%), Gaps = 9/353 (2%) dbjBAA04805.1 (AP001510) required for glycogen biosynthesis [<i>Bacillus halodurans</i>] Length = 368</p>
SeqID 197	SA-1059.2	Contig130 (19834-21264 p)	65	<p>Identities = 221/475 (46%), Positives = 313/475 (65%), Gaps = 1/475 (0%) spO08328[GLGA_BACST GLYCOGEN SYNTHASE (STARCH [BACTERIAL GLYCOGEN SYNTHASE) dbjBAA19591.1] (D87026) bacterial glycogen synthase [<i>Bacillus stearothermophilus</i>] Length = 485</p>
SeqID 198	SA-106.1	Contig131 (16210-17319 m)	78	<p>Identities = 249/364 (68%), Positives = 300/364 (82%), Gaps = 1/364 (0%) spP49999[RECF_STRPY RECF PROTEIN prjJUC4077 recF protein - <i>Streptococcus pyogenes</i> gb AA485783.1 (U07342) RecF protein [<i>Streptococcus pyogenes</i>] Length = 368</p>
SeqID 199	SA-1060.1	Contig108 (28847-29194 m)	64	<p>Identities = 71/87 (81%), Positives = 75/87 (85%) emb CAA13587.1 (A1233894) xanthine phosphoribosyltransferase [<i>Streptococcus pneumoniae</i>] Length = 152</p>
SeqID 200	SA-1061.1	Contig109 (28169-28557 p)	No Hits found	

SeqID 201	SA-1062.1	Contig109 (27573-28847 m)	68	<p>Identities = 213/412 (51%), Positives = 292/412 (70%), Gaps = 5/412 (1%) spIP42068 PBUX_BACSU XANTHINE PERMEASE pir S1310 xanthine transport protein pbuX - Bacillus subtilis emb CAA58759.1 (X83878) xanthine permease [Bacillus subtilis] gb AAA96812.1 (L77246) transport protein [Bacillus subtilis] emb CAB14123.1 (Z99115) xanthine permease [Bacillus subtilis] Length = 438</p>
SeqID 202	SA-1063.1	Contig109 (26686-27474 p)	44	<p>Identities = 82/253 (32%), Positives = 119/253 (46%), Gaps = 10/253 (3%) spIP39608 YWCJ_BACSU HYPOTHETICAL 28.4 KD PROTEIN IN SACT-SACP INTERGENIC REGION pir S39703 nitrite transport protein homolog ywcJ - Bacillus subtilis emb CAA51604.1 (X73124) ipa-48r [Bacillus subtilis] emb CAB15632.1 (Z99123) alternate gene name: ipa-48r~similar to nitrite transporter [Bacillus subtilis] Length = 256</p>
SeqID 203	SA-1064.1	Contig109 (25352-26587 p)	26	<p>Identities = 80/162 (49%), Positives = 112/162 (68%) gb AAG18632.1 (AY007504) unknown [Streptococcus mitis] Length = 173</p>
SeqID 204	SA-1065.1	Contig109 (24726-25328 p)	54	<p>Identities = 93/160 (58%), Positives = 120/160 (74%), Gaps = 1/160 (0%) gb AAG18632.1 (AY007504) unknown [Streptococcus mitis] Length = 173</p>
SeqID 205	SA-1066.1	Contig109 (23755-24708 p)	50	<p>Identities = 103/317 (32%), Positives = 165/317 (51%), Gaps = 15/317 (4%) spIO83774 APBE_TREPA THIAMINE BIOSYNTHESIS LIPOPROTEIN APBE PRECURSOR pir C71281 conserved hypothetical protein TP0796 - syphilis spirochete gb AAC65759.1 (AE001250) conserved hypothetical protein [Treponema pallidum] Length = 362</p>

SeqID 206	SA-1067.1	Contig109 (23439-23621 p)	55	<p>Identities = 27/60 (45%), Positives = 36/60 (60%) spQ01468 XYLH_PSEPU 4-OXALOCROTONATE TAUTOMERASE (4-OT) pir A43397 4-oxalocrotonate tautomerase (EC 5.3.2.-) xylH - Pseudomonas putida plasmid TOL pWW0 gb AA25694.1 (M94186) 4- oxalocrotonate tautomerase [Pseudomonas putida] gb AA26046.1 (M9550) 4-oxalocrotonate tautomerase [Plasmid pWW0] pir 1916401D 4-oxalocrotonate tautomerase [Pseudomonas putida] Length = 63</p>
SeqID 207	SA-1068.1	Contig109 (22732-23301 m)	89	<p>Identities = 157/189 (83%), Positives = 175/189 (92%) spP47846 KITH_STRGC THYMIDINE KINASE gb AA80289.1 (L40415) thymidine kinase [Streptococcus gordonii] Length = 191</p>
SeqID 208	SA-1069.1	Contig109 (21618-22697 m)	76	<p>Identities = 211/351 (60%), Positives = 281/351 (79%), Gaps = 1/351 (0%) spP46872 RF1_BACSU PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) pir S55437 translation releasing factor RF-1 - Bacillus subtilis emb CAA89884.1 (Z49782) peptide chain release factor 1 [Bacillus subtilis] emb CAB15718.1 (Z99122) peptide chain release factor 1 [Bacillus subtilis] Length = 356</p>
SeqID 209	SA-107.1	Contig131 (15332-16198 p)	78	<p>Identities = 195/277 (70%), Positives = 236/277 (84%) gb AA556773.1 (U17382) putative multiple membrane domain protein; possible TTG initiation codon at position 1084, near putative RBS at position 1052 [Streptococcus pyogenes] Length = 277</p>
SeqID 210	SA-1071.1	Contig109 (20788-21618 m)	47	<p>Identities = 94/236 (39%), Positives = 132/236 (55%), Gaps = 12/236 (5%) dbj BA07493.1 (AP001519) protoerythrogen oxidase [Bacillus halodurans] Length = 289</p>
SeqID 211	SA-1072.1	Contig109 (20199-20795 m)	57	<p>Identities = 71/199 (35%), Positives = 115/199 (57%), Gaps = 4/199 (2%) pir E72324 conserved hypothetical protein - Thermotoga maritima (strain MS88) gb AA435934.1 AE001752.1 (AE001752) conserved hypothetical protein [Thermotoga maritima] Length = 335</p>

SeqID 212	SA-1073.1	Contig109 (18851-20107 m)	73	<p>Identities = 242/417 (58%), Positives = 308/417 (73%), Gaps = 7/417 (1%) spIQWZH9IGLYA_THEME SERINE HYDROXYMETHYLTRANSFERASE (SERINE METHYLASE) (SHMT) pilJF72341 glycine hydroxymethyltransferase (EC 2.1.2.1) - Thermotoga maritima (strain MSB8) gblAAD35802.1 AE001743_4 (AE001743) serine hydroxymethyltransferase [Thermotoga maritima] Length = 427</p>
SeqID 213	SA-1074.1	Contig109 (17869-18846 m)	15	<p>Identities = 32/95 (33%), Positives = 53/95 (55%), Gaps = 1/95 (1%) emb CAB71302.1 (AJ130879) hypothetical protein [Clostridium sticklandii] Length = 95</p>
SeqID 214	SA-1075.1	Contig109 (17265-17867 m)	38	<p>Identities = 53/140 (37%), Positives = 78/140 (54%), Gaps = 2/140 (1%) pilJF69900 hypothetical protein yocA [imported] - Bacillus subtilis gblAAB84433.1 (AF027868) RAS-related protein [Bacillus subtilis] emb CAB13803.1 (Z99114) similar to transposon-related protein [Bacillus subtilis] Length = 225</p>
SeqID 215	SA-1076.1	Contig109 (15532-17253 m)	55	<p>Identities = 196/570 (34%), Positives = 327/570 (56%), Gaps = 5/570 (0%) pilJF72396 ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) gblAAD35376.1 AE001710_10 (AE001710) ABC transporter, ATP-binding protein [Thermotoga maritima] Length = 577</p>
SeqID 216	SA-1077.1	Contig109 (13798-15531 m)	58	<p>Identities = 219/552 (39%), Positives = 337/552 (60%), Gaps = 3/552 (0%) spIQWYCY288_THEME HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN TM0288 pilJF72396 ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) gblAAD35376.1 AE001710_11 (AE001710) ABC transporter, ATP-binding protein [Thermotoga maritima] Length = 598</p>
SeqID 217	SA-1078.2	Contig109 (13587-13841 m)	No Hits found	

SeqID 218	SA-1079.1	Contig109 (11805-13523 p)	91	Identities = 486/573 (84%), Positives = 527/573 (91%), Gaps = 1/573 (0%) emb CAB396418.1 (A243290) phosphoglucosyltransferase [Streptococcus thermophilus] Length = 572
SeqID 219	SA-108.1	Contig131 (14614-15276 p)	45	Identities = 512/515 (23%), Positives = 102/215 (46%), Gaps = 9/215 (4%) gb AA04237.1 (AF007761) MurR [Streptococcus mutans] Length = 287
SeqID 220	SA-1080.1	Contig108 (11246-11695 p)	43	Identities = 49/190 (25%), Positives = 84/190 (43%), Gaps = 33/190 (17%) emb CAA80247.1 (Z22520) membrane protein [Bacillus acidopullulyticus] Length = 183
SeqID 221	SA-1081.1	Contig108 (10535-11077 p)	66	Identities = 101/145 (69%), Positives = 122/145 (83%) sp Q54433 DFF_STRIMU DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG gb AAC4502.1 (U48885) DNA/pantothenate metabolism flavoprotein [Streptococcus mutans] Length = 145
SeqID 222	SA-1082.1	Contig109 (9841-10542 p)	46	Identities = 74/232 (31%), Positives = 122/232 (51%), Gaps = 36/232 (15%) sp Q58323 DFF_METJA DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG pri jA64414 pantothenate metabolism flavoprotein MJ0913 - Methanococcus jannaschii gb AAB88918.1 (U67535) pantothenate metabolism flavoprotein (dfr) [Methanococcus jannaschii] Length = 403
SeqID 223	SA-1083.1	Contig109 (8666-9702 m)	43	Identities = 94/221 (42%), Positives = 134/221 (60%), Gaps = 2/221 (0%) dbj BAB07541.1 (AP001520) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 276
SeqID 224	SA-1084.1	Contig109 (7674-8873 m)	54	Identities = 162/311 (52%), Positives = 218/311 (70%), Gaps = 1/311 (0%) pri S49950 probable trimethylamine dehydrogenase (EC 1.5.99.7) - Mycoplasma capricolum (SGC3) (fragment) pri J577803 hypothetical protein MC012 - Mycoplasma capricolum emb CAA483700.1 (Z33015) similar to trimethylamine DH [Mycoplasma capricolum] Length = 311

SeqID 230	SA-109.1	Contig131 (13055-14539 p)	93	<p>Identities = 481/493 (93%), Positives = 478/493 (95%) <i>spiP50099</i>[IMDH_STRPY INOSINE-5-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE (IMPDH) (IMPD) <i>pir</i>[JCA372 IMP dehydrogenase (EC 1.1.1.205) - Streptococcus pyogenes <i>gb</i>[AAB03846.1] (U26056) inosine monophosphate dehydrogenase [Streptococcus pyogenes] Length = 493</p>
SeqID 231	SA-1090.1	Contig138 (11341-11670 m)	60	<p>Identities = 42/102 (41%), Positives = 70/102 (68%) <i>gb</i>[AA23551.1] (M93570) PTS enzyme III cel [Escherichia coli] Length = 116</p>
SeqID 232	SA-1091.2	Contig138 (11868-12857 m)	53	<p>Identities = 98/309 (31%), Positives = 178/309 (58%), Gaps = 1/309 (0%) <i>dbj</i>[BAB04498.1] (AP001509) transcriptional regulator [Bacillus halodurans] Length = 316</p>
SeqID 233	SA-1092.2	Contig138 (12970-13725 m)	56	<p>Identities = 96/243 (39%), Positives = 148/243 (60%), Gaps = 1/243 (0%) <i>spiP76034</i>[YCIT_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN OSMB-RNB INTERGENIC REGION <i>pir</i>[G54876 hypothetical protein b1284 - Escherichia coli <i>gb</i>[AAC74386.1] (AE000228) putative DEOR-type transcriptional regulator [Escherichia coli K12] Length = 249</p>
SeqID 234	SA-1093.1	Contig138 (13846-14622 p)	54	<p>Identities = 106/289 (36%), Positives = 146/289 (49%), Gaps = 50/289 (17%) <i>spiP75794</i>[PFLE_ECOLI PUTATIVE PYRUVATE FORMATE-LYASE 3 ACTIVATING ENZYME <i>pir</i>[H64819 probable pyruvate formate-lyase activating enzyme (EC 1.97.1.4) 3 - Escherichia coli <i>gb</i>[AAC73911.1] (AE000184) putative pyruvate formate-lyase 2 activating enzyme [Escherichia coli K12] <i>dbj</i>[BAA35512.1] (D90720) iron-dependent pyruvate formate-lyase-activating enzyme [Escherichia coli] Length = 308</p>

SeqID 235	SA-1094.1	Contig138 (14669-15025 m)	56	Identities = 46/120 (38%), Positives = 71/120 (58%), Gaps = 11/120 (9%) dbj BAB07066.1 (AP001518) polyribonucleotide nucleosyltransferase (general stress protein 13) [Bacillus halodurans] Length = 138
SeqID 236	SA-1095.1	Contig138 (15027-16385 m)	23	Identities = 81/174 (46%), Positives = 109/174 (62%), Gaps = 30/174 (17%) sp P87051 YDJ3_SCHPO PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C57A10.03 pf T38930 peptidylprolyl isomerase (EC 5.2.1.8) SPAC57A10.03 [similarity]-fission yeast (Schizosaccharomyces pombe) emb CAB08166.1 (Z94864) putative peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe] Length = 155
SeqID 237	SA-1096.1	Contig138 (16469-17122 m)	83	Identities = 155/209 (74%), Positives = 184/209 (87%) emb CAB54571.1 (AJ006393) response regulator [Streptococcus pneumoniae] Length = 210
SeqID 238	SA-1097.1	Contig138 (17103-18122 m)	70	Identities = 159/234 (47%), Positives = 239/334 (70%), Gaps = 5/334 (1%) emb CAB54570.1 (AJ006393) histidine kinase [Streptococcus pneumoniae] Length = 331
SeqID 239	SA-1098.1	Contig138 (18119-18814 m)	43	Identities = 53/230 (23%), Positives = 104/230 (45%), Gaps = 14/230 (6%) dbj BAB03323.1 (AB035448) hypothetical protein [Staphylococcus aureus] Length = 233
SeqID 240	SA-1099.1	Contig138 (18989-19231 p)	No Hits found	
SeqID 241	SA-11.1	Contig137 (32951-36100 p)	27	Identities = 170/605 (28%), Positives = 289/605 (47%), Gaps = 105/605 (17%) ref NP_053171.1 pX02-16 [Bacillus anthracis] gb AAAF13621.1 AF188935_19 (AF188935) pX02-16 [Bacillus anthracis] Length = 611
SeqID 242	SA-110.1	Contig131 (12416-12801 p)	56	Identities = 63/144 (43%), Positives = 93/144 (65%), Gaps = 4/144 (2%) emb CA09426.1 (AJ010954) arginine repressor [Bacillus stearothermophilus] Length = 149

SeqID 243	SA-1100.1	Contig138 (18973-20928 m)	43	Identities = 219/380 (57%), Positives = 284/380 (74%), Gaps = 8/380 (2%) emb CAA10713.1 (AJ132604) hypothetical protein [Lactococcus lactis] Length = 378
SeqID 244	SA-1101.1	Contig138 (20928-21665 m)	69	Identities = 131/245 (53%), Positives = 177/245 (71%), Gaps = 4/245 (1%) emb CAA10712.1 (AJ132604) ppL protein [Lactococcus lactis] Length = 258
SeqID 245	SA-1102.1	Contig138 (21703-23025 m)	68	Identities = 222/434 (51%), Positives = 305/434 (70%), Gaps = 15/434 (3%) emb CAA10711.1 (AJ132604) sunL protein [Lactococcus lactis] Length = 424
SeqID 246	SA-1103.1	Contig138 (23015-23950 m)	67	Identities = 158/314 (50%), Positives = 215/314 (68%), Gaps = 5/314 (1%) dbj BAB06227.1 (AP001515) methionyl-tRNA formyltransferase [Bacillus halodurans] Length = 317
SeqID 247	SA-1104.1	Contig138 (23987-26387 m)	66	Identities = 377/807 (46%), Positives = 529/807 (64%), Gaps = 21/807 (2%) sp P94461 PRIA_BACSU PRIMOSOMAL PROTEIN N (REPLICATION FACTOR Y) priI A69682 primosomal replication factor Y priA - Bacillus subtilis emb CAA74261.1 (Y13937) putative PriA protein [Bacillus subtilis] emb CAB13444.1 (Z59112) primosomal replication factor Y (primosomal protein N%) [Bacillus subtilis] Length = 805
SeqID 248	SA-1105.2	Contig138 (26461-26775 m)	35	Identities = 25/57 (43%), Positives = 40/57 (69%), Gaps = 1/57 (1%) priI C69878 hypothetical protein yioH - Bacillus subtilis emb CAA74272.1 (Y13937) putative rpoZ protein [Bacillus subtilis] emb CAB13442.1 (Z59112) yioH [Bacillus subtilis] Length = 67
SeqID 249	SA-1107.1	Contig105 (16384-17661 p)	75	Identities = 260/416 (62%), Positives = 324/416 (77%) dbj BAB06905.1 (AP001518) argininosuccinate lyase [Bacillus halodurans] Length = 458

SeqID 250	SA-1108.1	Contig105 (15175-16365 p)	79	Identities = 262/366 (66%), Positives = 321/366 (80%), Gaps = 1/366 (0%) dbj BA06505.1 (AP001518) argininosuccinate synthase (citulline-aspartate ligase) [Bacillus halodurans] Length = 409
SeqID 251	SA-1109.1	Contig105 (14002-15021 p)	46	Identities = 97/307 (31%), Positives = 170/307 (54%), Gaps = 16/307 (5%) gij AAC62214.1 (AF049873) sensor protein [Lactococcus lactis] Length = 464
SeqID 252	SA-1111.1	Contig131 (11879-12405 p)	60	Identities = 102/174 (58%), Positives = 141/174 (80%) pir JH0364 hypothetical protein 176 (SAGP 5 region) - Streptococcus pyogenes Length = 176
SeqID 253	SA-1110.1	Contig105 (13287-13958 p)	58	Identities = 86/231 (37%), Positives = 133/231 (57%), Gaps = 10/231 (4%) emb CAB84972.1 (AJ012050) VicR protein [Enterococcus faecalis] Length = 283
SeqID 264	SA-1111.1	Contig105 (12570-13255 p)	62	Identities = 87/225 (38%), Positives = 145/225 (64%), Gaps = 1/225 (0%) emb CA405977.1 (AJ003195) ATP-binding subunit [Anaerobaculum variabilis] Length = 244
SeqID 255	SA-1112.1	Contig105 (11482-12570 p)	50	Identities = 103/352 (29%), Positives = 191/352 (54%), Gaps = 9/352 (2%) pir JF75581 hypothetical protein - Deinococcus radiodurans (strain R1) db AAF12525.1 AE001863_150 (AE001863) hypothetical protein [Deinococcus radiodurans] Length = 353
SeqID 256	SA-1113.1	Contig105 (10314-11300 m)	61	Identities = 141/327 (43%), Positives = 204/327 (62%), Gaps = 4/327 (1%) sp P39444 RRSR_BACSU RIBOSE OPERON REPRESSOR pir IE95960 transcription repressor of ribose operon - Bacillus subtilis emb CAB07457.1 (Z282953) repressor [Bacillus subtilis] emb CAB19508.1 (Z99122) transcriptional regulator (LacI family) [Bacillus subtilis] Length = 326

SeqID 257	SA-11114.1	Contig105 (9410-10321 m)	57	<p>Identities = 132/293 (45%), Positives = 176/293 (60%), Gaps = 4/293 (1%) sp P36949 RBRSK_BACSU RIBOKINASE pir J069690 ribokinase (EC 2.7.1.15) - Bacillus subtilis emb CAB07465.1 (Z92953) ribokinase [Bacillus subtilis] emb CAB15609.1 (Z92962) ribokinase [Bacillus subtilis] Length = 293</p>
SeqID 258	SA-11115.1	Contig105 (9037-9435 m)	60	<p>Identities = 74/131 (56%), Positives = 96/131 (72%), Gaps = 1/131 (0%) sp P36949 RBSD_BACSU HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD pir J04064 ribose ABC transporter (membrane protein) rnsD - Bacillus subtilis emb CAA81050.1 (Z25798) Membrane Ribose Binding Protein [Bacillus subtilis] emb CAB07464.1 (Z92953) membrane transport protein [Bacillus subtilis] emb CAB15610.1 (Z99122) ribose ABC transporter (membrane protein) [Bacillus subtilis] Length = 131</p>
SeqID 259	SA-11116.1	Contig105 (7543-9021 m)	76	<p>Identities = 298/493 (60%), Positives = 377/493 (76%), Gaps = 1/493 (0%) sp P36949 RBBSA_BACSU RIBOSE TRANSPORT ATP-BINDING PROTEIN RBBSA pir J069689 ribose ABC transporter (ATP-binding protein) rbsA - Bacillus subtilis emb CAB07463.1 (Z92953) ATP-binding transport protein [Bacillus subtilis] emb CAB15611.1 (Z99122) ribose ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 493</p>
SeqID 260	SA-11118.1	Contig105 (6500-7541 m)	78	<p>Identities = 198/305 (64%), Positives = 252/305 (81%), Gaps = 1/305 (0%) pir J069690 ribose ABC transporter (permease) rbsC - Bacillus subtilis emb CAB07462.1 (Z92953) membrane transport protein [Bacillus subtilis] emb CAB15612.1 (Z99122) ribose ABC transporter (permease) [Bacillus subtilis] Length = 322</p>

SeqID 261	SA-1119.1	Contig105 (6579-6547 m)	59	<p>Identities = 143/301 (47%), Positives = 204/301 (67%), Gaps = 1/301 (0%) sp P36949 RBSS_BACSU D-RIBOSE-BINDING PROTEIN PRECURSOR pir A69690 ribose ABC transporter (ribose-binding protein) rnsB - Bacillus subtilis emb CA807461.1 (Z92953) periplasmic substrate-binding protein [Bacillus subtilis] emb CAB15613.1 (Z99122) ribose ABC transporter (ribose-binding protein) [Bacillus subtilis] Length = 305</p>
SeqID 262	SA-112.1	Contig131 (10814-11482 m)	31	<p>Identities = 42/132 (31%), Positives = 74/132 (55%), Gaps = 3/132 (2%) pir H81323 hypothetical protein PA4181 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb AAAG07568.1 AE004834.8 (AE004834) hypothetical protein [Pseudomonas aeruginosa] Length = 239</p>
SeqID 263	SA-1120.1	Contig105 (4086-5539 p)	69	<p>Identities = 273/491 (55%), Positives = 353/491 (71%), Gaps = 19/491 (3%) sp P22250 SYE_BACSU GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE-TRNA LIGASE) (GLURS) pir SY3SET glutamate-TRNA ligase (EC 6.1.1.17) glx - Bacillus subtilis gb AA22495.1 (M55073) transfer RNA-Gln synthetase [Bacillus subtilis] gb AA21796.1 (L14580) glutamyl-tRNA synthetase [Bacillus subtilis] db BA005328.1 (D26185) glutamyl-tRNA synthetase [Bacillus subtilis] emb CAB11868.1 (Z99104) glutamyl-tRNA synthetase [Bacillus subtilis] gb AAC31971.1 (U49789) glutamyl-tRNA synthetase [Bacillus subtilis] Length = 483</p>
SeqID 264	SA-1121.1	Contig105 (2557-3876 p)	65	<p>Identities = 201/443 (45%), Positives = 290/443 (65%) sp P77212 YKGC_ECOLI PROBABLE PYRIDINE NUCLEOTIDE-DISULFIDE OXIDOREDUCTASE IN EAEH-BETA INTERGENIC REGION pir H64755 probable mercury(II) reductase (EC 1.16.1.1) - Escherichia coli gb AA818031.1 (U73857) similar to S. aureus mercury(II) reductase [Escherichia coli] gb AAC73407.1 (AE000137) putative oxidoreductase [Escherichia coli K12] Length = 450</p>

SeqID 265	SA-1122.1	Contig105 (1905-2403 p)	56	<p>Identities = 69/162 (42%), Positives = 100/162 (61%), Gaps = 2/162 (1%) sp Q10612 YC84_MYCTU HYPOTHETICAL 18.2 KIA PROTEIN RV1284 p H70771 hypothetical protein RV1284 - Mycobacterium tuberculosis (strain H37RV) emb CAA97750.1 (Z73419) hypothetical protein RV1284 [Mycobacterium tuberculosis] Length = 163</p>
SeqID 266	SA-1123.1	Contig105 (406-1770 p)	78	<p>Identities = 284/453 (62%), Positives = 358/453 (78%), Gaps = 4/453 (0%) sp P37572 IRADA_BACSU DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG) p H586116 DNA repair protein sms - Bacillus subtilis dbj BA053271.1 (D26185) unknown [Bacillus subtilis] emb CAB11863.1 (Z99104) DNA repair protein homolog [Bacillus subtilis] Length = 458</p>
SeqID 267	SA-1124.1	Contig105 (2-244 p)	64	<p>Identities = 41/80 (51%), Positives = 52/80 (64%), Gaps = 5/80 (6%) gb AAAF74088.1 (AF212845) putative dUTPase [Lactococcus lactis bacteriophage u136] Length = 139</p>
SeqID 268	SA-1125.2	Contig120 (17546-17980 p)	44	<p>Identities = 48/128 (35%), Positives = 70/128 (53%), Gaps = 5/128 (3%) gb AAK05804.1 AE006401.5 (AE006401) mannose-specific PTS system component IAB (EC 2.7.1.69) [Lactococcus lactis subsp. lactis] Length = 329</p>
SeqID 269	SA-1126.2	Contig120 (17983-19179 p)	54	<p>Identities = 156/370 (42%), Positives = 219/370 (59%), Gaps = 3/370 (0%) dbj BAB05773.1 (AP001514) unsaturated glucuronyl hydrolase [Bacillus halodurans] Length = 375</p>
SeqID 270	SA-1127.1	Contig120 (19234-19728 p)	52	<p>Identities = 63/125 (50%), Positives = 89/125 (70%), Gaps = 1/125 (0%) gb AAAC44679.1 (U65015) PTS permease for mannose subunit IIIMan C terminal domain [Vibrio furnissii] Length = 157</p>
SeqID 271	SA-1129.1	Contig120 (19764-20630 p)	45	<p>Identities = 93/295 (31%), Positives = 140/295 (46%), Gaps = 48/295 (16%) gb AAAF81084.1 AF228498.4 (AF228498) Agaw [Escherichia coli] Length = 259</p>

SeqID 272	SA-113.1	Contig131 (9315-10547 m)	95	Identities = 375/411 (91%), Positives = 395/411 (95%), Gaps = 1/411 (0%) sp P16921ARCA_STRPY ARGININE DEIMINASE (AD) (ARGININE DIHYDROLASE) (AD) (STREPTOCOCCAL ACID GLYCOPROTEIN) pir A38833 streptococcal antitumor protein - Streptococcus pyogenes emb CAA39192.1 (X55659) antitumor protein [Streptococcus pyogenes] dbj BA02938.1 (D13790) acid glycoprotein [Streptococcus pyogenes] Length = 411
SeqID 273	SA-1131.1	Contig120 (20617-21432 p)	54	Identities = 101/278 (36%), Positives = 164/278 (58%), Gaps = 6/278 (2%) gb AA57943.1 (U18997) ORF_0290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli] Length = 290
SeqID 274	SA-1132.1	Contig120 (21512-23416 p)	19	Identities = 76/206 (36%), Positives = 124/206 (59%), Gaps = 1/206 (0%) emb CAB01924.1 (Z79691) OrfA [Streptococcus pneumoniae] Length = 207
SeqID 275	SA-1134.1	Contig120 (23466-24497 p)	79	Identities = 222/333 (66%), Positives = 279/333 (83%) emb CAB01925.1 (Z79691) RegR [Streptococcus pneumoniae] Length = 333
SeqID 276	SA-1135.1	Contig120 (24568-25182 m)	87	Identities = 169/204 (82%), Positives = 192/204 (93%), Gaps = 1/204 (0%) emb CAC15392.1 (A278785) polypeptide deformylase [Streptococcus pneumoniae] Length = 203
SeqID 277	SA-1136.1	Contig120 (25248-25760 m)	42	Identities = 58/191 (30%), Positives = 98/191 (50%) sp P33023YEIL_ECOLI HYPOTHETICAL 25.3 KD PROTEIN IN INFO-FRUA INTERGENIC REGION pir IB64985 hypothetical 25.3 kD protein in info-frua intergenic region - Escherichia coli (strain K-12) gb AA60515.1 (U00007) yeil [Escherichia coli] gb AAC75224.1 (AE000305) putative transcriptional regulator [Escherichia coli K12] prt J2014253BJ yeil gene [Escherichia coli] Length = 219

SeqID 272	SA-113.1	Contig131 (9315-10547 m)	95	<p>Identities = 375/411 (91%), Positives = 395/411 (95%), Gaps = 1/411 (0%) sp P18621ARCA_STRYP ARGININE DEIMINASE (AD) (ARGININE DIHYDROLASE) (AD) (STREPTOCOCCAL ACID GLYCOPROTEIN) pir J38833 streptococcal antitumor protein - Streptococcus pyogenes emb CAA39192.1 (X55659) antitumor protein [Streptococcus pyogenes] db BA042938.1 (U13790) acid glycoprotein [Streptococcus pyogenes] Length = 411</p>
SeqID 273	SA-1131.1	Contig120 (20617-21432 p)	54	<p>Identities = 101/278 (36%), Positives = 164/278 (58%), Gaps = 6/278 (2%) gb AA57943.1 (U18997) ORF_0290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli] Length = 290</p>
SeqID 274	SA-1132.1	Contig120 (21512-23416 p)	19	<p>Identities = 76/206 (36%), Positives = 124/206 (59%), Gaps = 1/206 (0%) emb CAB01924.1 (Z79691) OrfA [Streptococcus pneumoniae] Length = 207</p>
SeqID 275	SA-1134.1	Contig120 (23496-24497 p)	79	<p>Identities = 222/333 (66%), Positives = 279/333 (83%) emb CAB01925.1 (Z79691) RegR [Streptococcus pneumoniae] Length = 333</p>
SeqID 276	SA-1135.1	Contig120 (24568-25182 m)	87	<p>Identities = 169/204 (82%), Positives = 192/204 (93%), Gaps = 1/204 (0%) emb CAC15392.1 (AJ278785) polypeptide deformylase [Streptococcus pneumoniae] Length = 203</p>
SeqID 277	SA-1136.1	Contig120 (25248-25760 m)	42	<p>Identities = 58/191 (30%), Positives = 98/191 (50%) sp P33023YEIL_ECOLI HYPOTHETICAL 25.3 KD PROTEIN IN INFO-FRUA INTERGENIC REGION pir J864985 hypothetical 25.3 kD protein in nfo-frua intergenic region - Escherichia coli (strain K-12) gb AA60515.1 (U00007) yeil [Escherichia coli] gb AAC75224.1 (AE000305) putative transcriptional regulator [Escherichia coli K12] prf J2014253BJ yeil gene [Escherichia coli] Length = 219</p>

SeqID 278	SA-1137.1	Contig120 (26052-27167 p)	43	<p>Identities = 95/382 (24%), Positives = 174/382 (44%), Gaps = 30/382 (7%) pirJID75094 transport protein, permease PAB0761 - <i>Pyrococcus abyssi</i> (strain Orsay) emb CAB50057.1 (AJ248286) TRANSPORT PROTEIN, permease [<i>Pyrococcus abyssi</i>] Length = 372</p>
SeqID 279	SA-1138.1	Contig120 (27213-28196 m)	50	<p>Identities = 101/327 (30%), Positives = 169/327 (50%), Gaps = 12/327 (3%) pirJF50594 probable oxidoreductase [imported] - <i>Streptomyces coelicolor</i> emb CAB61731.1 (AL133220) putative oxidoreductase. [<i>Streptomyces coelicolor</i> A3(2)] Length = 351</p>
SeqID 280	SA-1139.1	Contig120 (28344-30239 p)	88	<p>Identities = 504/631 (79%), Positives = 563/631 (88%) emb CAC14579.1 (AJ249396) oligopeptidase [<i>Streptococcus thermophilus</i>] Length = 631</p>
SeqID 281	SA-114.1	Contig131 (8878-9219 m)	57	<p>Identities = 68/114 (57%), Positives = 85/114 (73%) sp P16963 YSA1_STRPY_HYPOTHETICAL 16.6 KD PROTEIN IN SAGP 3 REGION pir JE0081 hypothetical 16.5K protein (SAGP 5 region) - <i>Streptococcus pyogenes</i> db BAA02939.1 (D13790) ORF2 [<i>Streptococcus pyogenes</i>] Length = 146</p>
SeqID 282	SA-1140.1	Contig120 (30289-31242 m)	61	<p>Identities = 133/309 (43%), Positives = 197/309 (63%), Gaps = 5/309 (1%) sp O35046 YOC_D_BACSU_HYPOTHETICAL 36.4 KDA PROTEIN IN CSAA-DES INTERGENIC REGION pir JA69901 immunity to bacteriotoxins homolog yocD - <i>Bacillus subtilis</i> gbl AAB84435.1 (AF027868) YocD [<i>Bacillus subtilis</i>] emb CAB13809.1 (Z99114) similar to immunity to bacteriotoxins [<i>Bacillus subtilis</i>] Length = 325</p>
SeqID 283	SA-1141.1	Contig120 (31400-31645 p)	No Hits found	
SeqID 284	SA-1143.2	Contig120 (31746-33716 p)	39	<p>Identities = 174/524 (33%), Positives = 275/524 (52%), Gaps = 13/524 (2%) pir JE70040 conserved hypothetical protein yvgP - <i>Bacillus subtilis</i> emb CAB15347.1 (Z99121) similar to hypothetical proteins [<i>Bacillus subtilis</i>] Length = 670</p>

SeqID 285	SA-1144.1	Contig120 (33993-35525 m)	86	<p>Identities = 393/509 (75%), Positives = 441/509 (86%) dbj BA25696.1 (AB010712) NADH oxidase/alkyl hydroperoxidase reductase [Streptococcus mutans] Length = 510</p>
SeqID 286	SA-1145.1	Contig120 (35543-36103 m)	92	<p>Identities = 188/186 (90%), Positives = 180/186 (96%) dbj BA25695.1 (AB010712) alkyl hydroperoxidase [Streptococcus mutans] Length = 186</p>
SeqID 287	SA-1146.1	Contig124 (43925-44143 m)	67	<p>Identities = 36/72 (50%), Positives = 49/72 (68%) sp P54457 YOEL_BACSU HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION prj H69951.yoeB protein homolog yqeL - Bacillus subtilis dbj BA12449.1 (D84432) YqeL [Bacillus subtilis] emb CAB14504.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 118</p>
SeqID 288	SA-1148.1	Contig124 (43125-43859 m)	61	<p>Identities = 86/242 (35%), Positives = 155/242 (63%), Gaps = 4/242 (1%) sp P54458 YQEM_BACSU HYPOTHETICAL 28.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION prj A89952 conserved hypothetical protein yqeM - Bacillus subtilis dbj BA12450.1 (D84432) YqeM [Bacillus subtilis] emb CAB14503.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 247</p>
SeqID 289	SA-1149.1	Contig124 (42851-43075 m)	No Hits found	
SeqID 290	SA-115.1	Contig131 (7849-8862 m)	86	<p>Identities = 244/333 (73%), Positives = 294/333 (88%), Gaps = 1/333 (0%) prj 146742 ornithine carbamoyltransferase (EC 2.1.3.3) [validated] - Lactobacillus sakei emb CAA04683.1 (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei] Length = 337</p>
SeqID 291	SA-1150.1	Contig124 (41745-42854 m)	49	<p>Identities = 131/367 (35%), Positives = 185/367 (49%), Gaps = 45/367 (12%) dbj BA060304.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 416</p>

SeqID 292	SA-1151.1	Contig124 (40939-41652 m)	56	<p>Identities = 92/246 (37%), Positives = 143/246 (57%) Gaps = 14/246 (5%) pjl1C9861 transcription activator of multidrug-efflux transporter genes rntA - <i>Bacillus subtilis</i> emb CAA69863.1 (Y08559) Unknown [Bacillus subtilis] emb CAB15677.1 (Z99122) transcriptional regulator [Bacillus subtilis] Length = 257</p>
SeqID 293	SA-1152.1	Contig124 (40396-40800 m)	49	<p>Identities = 56/129 (43%), Positives = 74/129 (56%), Gaps = 7/129 (5%) s9IP64430YRK_C_BACSU HYPOTHETICAL 21.3 KD PROTEIN IN BLTR-SPOILIC INTERGENIC REGION pjl1A69876 hypothetical protein yrkC - <i>Bacillus subtilis</i> dbj BAA12358.1 (D84432) YrkC [Bacillus subtilis] emb CAB14597.1 (Z99117) yrkC [Bacillus subtilis] Length = 186</p>
SeqID 294	SA-1153.1	Contig124 (39417-40130 p)	70	<p>Identities = 136/230 (59%), Positives = 171/230 (74%) dbj BAC04811.1 (AP001510) glycerol uptake facilitator [Bacillus halodurans] Length = 276</p>
SeqID 295	SA-1154.1	Contig124 (39033-39407 p)	63	<p>Identities = 64/118 (54%), Positives = 85/118 (71%) dbj BAB07114.1 (AP001518) unknown conserved protein in others [Bacillus halodurans] Length = 128</p>
SeqID 296	SA-1155.1	Contig124 (38455-39033 p)	68	<p>Identities = 99/193 (51%), Positives = 138/193 (71%), Gaps = 2/193 (1%) dbj BAB07115.1 (AP001518) unknown conserved protein in others [Bacillus halodurans] Length = 196</p>
SeqID 297	SA-1156.1	Contig124 (37428-38417 p)	76	<p>Identities = 205/329 (62%), Positives = 261/329 (79%) dbj BAB07116.1 (AP001518) dihydroxyacetone kinase [Bacillus halodurans] Length = 330</p>
SeqID 298	SA-1157.1	Contig124 (36718-37254 m)	44	<p>Identities = 59/142 (41%), Positives = 81/142 (56%), Gaps = 5/142 (3%) dbj BAB07113.1 (AP001518) unknown [Bacillus halodurans] Length = 186</p>
SeqID 299	SA-1158.1	Contig124 (35722-36708 m)	59	<p>Identities = 142/285 (49%), Positives = 197/285 (68%), Gaps = 1/285 (0%) dbj BAB07112.1 (AP001518) dihydroxyacetone kinase [Bacillus halodurans] Length = 331</p>

SeqID 292	SA-1151.1	Contig124 (40939-41652 m)	56	<p>Identities = 92/246 (37%), Positives = 143/246 (57%), Gaps = 14/246 (5%) pif[C69661 transcription activator of multidrug-efflux transporter genes nta - Bacillus subtilis emb CAA69863.1 (Y08569) Unknown [Bacillus subtilis] emb CAB15677.1 (Z99122) transcriptional regulator [Bacillus subtilis] Length = 257</p>
SeqID 293	SA-1152.1	Contig124 (40396-40800 m)	49	<p>Identities = 56/129 (43%), Positives = 74/129 (56%), Gaps = 7/129 (5%) spiP6430YRKC-BACSU HYPOTHETICAL 21.3 KD PROTEIN IN BLTR-SPOIC INTERGENIC REGION pif A69976 hypothetical protein yrkC - Bacillus subtilis dbj BAA12358.1 (D84432) YrkC [Bacillus subtilis] emb CAB14597.1 (Z99117) yrkC [Bacillus subtilis] Length = 186</p>
SeqID 294	SA-1153.1	Contig124 (39417-40130 p)	70	<p>Identities = 136/230 (59%), Positives = 171/230 (74%) dbj BAB04811.1 (AP001510) glycerol uptake facilitator [Bacillus halodurans] Length = 276</p>
SeqID 295	SA-1154.1	Contig124 (39033-39407 p)	63	<p>Identities = 64/118 (54%), Positives = 85/118 (71%) dbj BAB07114.1 (AP001518) unknown conserved protein in others [Bacillus halodurans] Length = 128</p>
SeqID 296	SA-1155.1	Contig124 (38455-39033 p)	68	<p>Identities = 99/193 (51%), Positives = 138/193 (71%), Gaps = 2/193 (1%) dbj BAB07115.1 (AP001518) unknown conserved protein in others [Bacillus halodurans] Length = 196</p>
SeqID 297	SA-1156.1	Contig124 (37428-38417 p)	76	<p>Identities = 205/329 (62%), Positives = 261/329 (79%) dbj BAB07116.1 (AP001518) dihydroxyacetone kinase [Bacillus halodurans] Length = 330</p>
SeqID 298	SA-1157.1	Contig124 (36718-37254 m)	44	<p>Identities = 59/142 (41%), Positives = 81/142 (56%), Gaps = 5/142 (3%) dbj BAB07113.1 (AP001518) unknown [Bacillus halodurans] Length = 186</p>
SeqID 299	SA-1158.1	Contig124 (35722-36708 m)	59	<p>Identities = 142/285 (49%), Positives = 197/285 (68%), Gaps = 1/285 (0%) dbj BAB07112.1 (AP001518) dihydroxyacetone kinase [Bacillus halodurans] Length = 331</p>

SeqID 300	SA-116.1	Contig131 (6359-7766 m)	72	Identities = 265/470 (56%), Positives = 347/470 (73%), Gaps = 34/70 (0%) embICA76779.1 (Y17554) permease [Bacillus licheniformis] Length = 468
SeqID 301	SA-1160.1	Contig124 (34888-35604 m)	72	Identities = 182/237 (76%), Positives = 201/237 (84%) spJ76351YEEN_ECOLI HYPOTHETICAL 25.9 KDA PROTEIN IN AMN-CBL INTERGENIC REGION piriJ64963 conserved hypothetical protein b1983 - Escherichia coli gblAAC75047.1 (AE000290) ori, hypothetical protein [Escherichia coli K12] Length = 238
SeqID 302	SA-1161.1	Contig124 (34044-34733 m)	43	Identities = 72/178 (40%), Positives = 101/178 (56%), Gaps = 2/178 (1%) piriJT36850 hypothetical protein SC135.37 - Streptomyces coelicolor embICA20826.1 (AL031541) hypothetical protein SC135.37 [Streptomyces coelicolor A3(2)] Length = 242
SeqID 303	SA-1162.1	Contig124 (33109-33942 m)	46	Identities = 83/264 (31%), Positives = 133/264 (49%), Gaps = 13/264 (4%) gblAAC45332.1 (U97348) basic surface protein [Lactobacillus fermentum] Length = 264
SeqID 304	SA-1163.1	Contig124 (32144-32968 m)	58	Identities = 110/284 (38%), Positives = 176/284 (61%), Gaps = 13/284 (4%) embICAB59825.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 287
SeqID 305	SA-1165.1	Contig124 (30634-32010 m)	46	Identities = 132/419 (31%), Positives = 212/419 (50%), Gaps = 144/419 (3%) piriJ75327 ArgE/DapE/acy1 family protein - R1 Dienococcus radiodurans (strain gbIAAF11560.1)AE002038_9 (AE002038) ArgE/DapE/acy1 family protein [Dienococcus radiodurans] Length = 463
SeqID 306	SA-1166.1	Contig124 (29833-30207 p)	38	Identities = 43/115 (37%), Positives = 52/115 (44%), Gaps = 2/115 (1%) piriJH72617 hypothetical protein APE1401 - Aeropyrum pernix (strain K1) dbjJBA480398.1 (AP000061) 123aa long hypothetical protein [Aeropyrum pernix] Length = 123

SeqID 307	SA-1167.1	Contig124 (29571-30641 m)	71	Identities = 187/338 (55%), Positives = 256/338 (75%), Gaps = 12/338 (3%) emb CAB59828.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 368
SeqID 308	SA-1169.1	Contig124 (28882-29574 m)	73	Identities = 137/231 (59%), Positives = 171/231 (73%), Gaps = 1/231 (0%) emb CAB59829.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 231
SeqID 309	SA-117.1	Contig131 (5382-6338 m)	76	Identities = 199/311 (63%), Positives = 254/311 (80%), Gaps = 3/311 (0%) sp O53090 ARCC_LACSK CARBAMATE KINASE prf T46743 carbamate kinase (EC 2.7.2.2) [validated] - Lactobacillus sakei. emb CAA04684.1 (AJ001330) carbamate kinase [Lactobacillus sakei] Length = 314
SeqID 310	SA-1170.1	Contig124 (27776-28633 p)	72	Identities = 196/347 (56%), Positives = 257/347 (73%), Gaps = 1/347 (0%) prf C81088 alcohol dehydrogenase, zinc-containing NIMB1395 [imported] - Neisseria meningitidis (group B strain MD58) gb AAE41759.1 (AE002488) alcohol dehydrogenase, zinc-containing [Neisseria meningitidis MC58] Length = 346
SeqID 311	SA-1171.2	Contig124 (26284-27664 p)	55	Identities = 182/453 (40%), Positives = 265/453 (58%), Gaps = 29/453 (6%) prf C59596 branched-chain amino acid transporter brab - Bacillus subtilis gb AAC00400.1 (AF008220) branched-chain amino acid transporter [Bacillus subtilis] emb CAB14938.1 (Z99119) branched-chain amino acid transporter [Bacillus subtilis] Length = 445
SeqID 312	SA-1173.3	Contig136 (3489-3797 m)	No Hits found	
SeqID 313	SA-1174.1	Contig136 (3794-4186 m)	No Hits found	
SeqID 314	SA-1175.1	Contig136 (4104-4676 m)	No Hits found	
SeqID 315	SA-1176.1	Contig136 (4677-5165 m)	No Hits found	
SeqID 316	SA-1177.1	Contig136 (5180-5494 m)	No Hits found	
SeqID 317	SA-1178.1	Contig136 (5729-6937 m)	No Hits found	
SeqID 318	SA-1179.1	Contig136 (6986-7477 m)	No Hits found	

SeqID 319	SA-118.1	Contig131 (4247-5272 p)	78	<p>Identities = 225/340 (66%), Positives = 271/340 (79%), Gaps = 3/340 (0%) sp Q46127 SW_CLO4O TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS) gb AAC05711.1 (L49336) tryptophanyl-RNA synthetase [Clostridium longisporum] Length = 341</p>
SeqID 320	SA-1180.2	Contig136 (7491-11102 m)	52	<p>Identities = 405/1293 (31%), Positives = 636/1293 (48%), Gaps = 175/1293 (13%) pf JID71610 probable type II DNA modification enzyme (methyltransferase) - Helicobacter pylori (strain J99) gb AAO09887.1 (AE001563) putative TYPE II DNA MODIFICATION ENZYME (METHYLTRANSFERASE) [Helicobacter pylori J99] Length = 1252</p>
SeqID 321	SA-1182.1	Contig136 (11439-12641 m)	40	<p>Identities = 90/357 (25%), Positives = 162/357 (45%), Gaps = 33/357 (9%) ref NP_049990.1 orf359 gp [Streptococcus thermophilus bacteriophage Sf21] emb CAA64931.1 (X95646) integrase [Streptococcus thermophilus bacteriophage Sf21] gb AAC03454.1 (AF020798) integrase homolog [Streptococcus thermophilus bacteriophage TP-J34] gb AAD44095.1 (AF115103_25) (AF115103) orf359 gp [Streptococcus thermophilus bacteriophage Sf21] Length = 359</p>
SeqID 322	SA-1183.1	Contig136 (12641-12952 m)	No Hits found	<p>Identities = 183/298 (61%), Positives = 234/298 (78%), Gaps = 1/298 (0%) sp P23496 LAXP_LACLA LACX PROTEIN, PLASMID pf JID23896 lacX protein - Lactococcus lactis gb AAZ5184.1 (M60447) ORF [Lactococcus lactis] Length = 299</p>
SeqID 323	SA-1184.1	Contig136 (13606-14501 m)	74	<p>Identities = 442/468 (94%), Positives = 459/468 (97%) gb AAA26949.1 (M19454) phospho-beta-D-galactosidase (EC 3.2.1.85) [Lactococcus lactis subsp. cremoris] Length = 477</p>
SeqID 324	SA-1187.1	Contig136 (14601-16007 m)	96	
SeqID 325	SA-1188.1	Contig136 (16587-17003 p)	No Hits found	

SeqID 326	SA-1189.1	Contig136 (16094-17800 m)	94	<p>Identities = 520/568 (91%), Positives = 547/568 (95%), Gaps = 1/568 (0%) sp P23532 PTLA_LACLA PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIBC-LAC) (LACTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EIL-LAC) p B23696 phosphotransferase system enzyme II (EC 2.7.1.69) - Lactococcus lactis gb AA25182.1 (M60447) enzyme III [Lactococcus lactis] Length = 568</p>
SeqID 327	SA-119.1	Contig131 (4008-4139 p)	No Hits found	<p>Identities = 89/105 (84%), Positives = 97/105 (91%) sp P23532 PTLA_LACLA PTS SYSTEM, LACTOSE-SPECIFIC IIA COMPONENT (EIIA-LAC) (LACTOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EII-LAC) p B23696 phosphotransferase system enzyme III (EC 2.7.-.-) - Lactococcus lactis p B1E2A/A Chain A, Enzyme IIA From The Lactose Specific Pts From Lactococcus lactis p B1E2A/B Chain B, Enzyme IIA From The Lactose Specific Pts From Lactococcus lactis p B1E2A/C Chain C, Enzyme IIA From The Lactose Specific Pts From Lactococcus lactis gb AA25181.1 (M60447) enzyme III [Lactococcus lactis] Length = 105</p>
SeqID 328	SA-1190.1	Contig136 (17800-18117 m)	78	
SeqID 329	SA-1191.1	Contig136 (18148-18879 m)	56	<p>Identities = 104/278 (37%), Positives = 169/278 (60%), Gaps = 1/278 (0%) sp P24401 LACT_LACCA TRANSCRIPTION ANTI-TERMINATOR LACT emb CAB02555.1 (Z80834) Lact [Lactobacillus casei] gb AAB49331.1 (U21391) Lact [Lactobacillus casei] Length = 292</p>

SeqID 330	SA-1192.1	Contig136 (19372-20352 m)	92	<p>Identities = 279/326 (85%), Positives = 308/326 (93%) spiP28593 LACC_LACLA TAGATOSE 1,6-DIPHOSPHATE ALDOLASE (TAGATOSE-BISPHOSPHATE ALDOLASE) (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE) pif J39778 Lacc tagatose-1,6-diphosphate aldolase - Lactococcus lactis gb AA25171.1 (M65190) lacD [Lactococcus lactis] gb AA25180.1 (M60447) tagatose 1,6-dip aldolase [Lactococcus lactis] Length = 326</p>
SeqID 331	SA-1193.1	Contig136 (20357-21266 m)	78	<p>Identities = 207/310 (66%), Positives = 245/310 (78%), Gaps = 1/310 (0%) spiP23391 LACC_LACLA TAGATOSE-6- PHOSPHATE KINASE (PHOSPHOTAGATOKINASE) pif J39778 tagatose-6-phosphate kinase (EC 2.7.1.-) LacC - Lactococcus lactis gb AA25170.1 (M65190) lacC [Lactococcus lactis] gb AA25179.1 (M60447) tagatose 6-P kinase [Lactococcus lactis] Length = 310</p>
SeqID 332	SA-1194.3	Contig136 (21299-21814 m)	85	<p>Identities = 142/171 (83%), Positives = 156/171 (91%) spiP23495 LACB_LACLA GALACTOSE-6-PHOSPHATE ISOMERASE LACB SUBUNIT pif J39778 galactose-6- phosphate isomerase (EC 5.3.1.-) component LacB - Lactococcus lactis gb AA25169.1 (M65190) lacB [Lactococcus lactis] gb AA25178.1 (M60447) galactose 6-P isomerase [Lactococcus lactis] Length = 171</p>
SeqID 333	SA-1195.3	Contig136 (21831-22256 m)	76	<p>Identities = 120/141 (85%), Positives = 134/141 (94%) spiP23494 LACA_LACLA GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT pif J39778 galactose-6- phosphate isomerase (EC 5.3.1.-) component LacA - Lactococcus lactis gb AA25168.1 (M65190) lacA [Lactococcus lactis] gb AA25177.1 (M60447) galactose 6-P isomerase [Lactococcus lactis] Length = 141</p>
SeqID 334	SA-1196.2	Contig111 (10300-10728 p)	No Hits found	

SeqID 335	SA-1197.1	Contig111 (9929-10219 p)	49	<p>Identities = 35/91 (38%), Positives = 51/91 (55%) splP34159YHS1_CLOAB HYPOTHETICAL 11.0 KD PROTEIN IN HSP18 3 REGION (ORF1) embICA446375.1 (X65276) ORF1 [Clostridium acetobutylicum] Length = 96</p>
SeqID 336	SA-1198.1	Contig111 (9134-9421 m)	No Hits found	
SeqID 337	SA-1199.1	Contig111 (8609-9144 m)	No Hits found	
SeqID 338	SA-120.1	Contig110 (1487-1594 p)	No Hits found	
SeqID 339	SA-1200.1	Contig111 (8449-8687 m)	No Hits found	
SeqID 340	SA-1201.1	Contig111 (8034-8504 p)	No Hits found	
SeqID 341	SA-1202.1	Contig111 (6984-7439 m)	34	<p>Identities = 36/89 (40%), Positives = 52/89 (57%), Gaps = 3/89 (3%) pflT39903 serine-rich protein - fission yeast (Schizosaccharomyces pombe) embICA22127.1 (AL033534) hypothetical serine-rich secreted protein [Schizosaccharomyces pombe] Length = 534</p>
SeqID 342	SA-1203.1	Contig111 (6610-7866 p)	59	<p>Identities = 171/402 (42%), Positives = 248/402 (61%), Gaps = 46/402 (11%) pflA33952 58K mobilization protein - Streptococcus pneumoniae plasmids gblAA26387.1 (M28538) mobilization peptide [Plasmid pMV158] Length = 494</p>
SeqID 343	SA-1205.1	Contig111 (5659-6293 p)	No Hits found	
SeqID 344	SA-1207.1	Contig111 (4967-5755 p)	51	<p>Identities = 90/264 (34%), Positives = 139/264 (52%), Gaps = 22/264 (8%) pflJ1405330A repli gene [Staphylococcus aureus] Length = 314</p>
SeqID 345	SA-1208.1	Contig111 (4028-4687 p)	No Hits found	
SeqID 346	SA-1209.1	Contig111 (3684-4022 p)	49	<p>Identities = 34/102 (33%), Positives = 56/102 (54%) gblAAD41248.1AF106927_1 (AF106927) unknown [Streptococcus suis] Length = 272</p>
SeqID 347	SA-121.1	Contig131 (3142-3447 m)	No Hits found	
SeqID 348	SA-1210.1	Contig111 (3409-3650 p)	No Hits found	
SeqID 349	SA-1211.1	Contig111 (2975-3288 p)	No Hits found	
SeqID 350	SA-1212.1	Contig111 (2259-2810 m)	15	<p>Identities = 23/63 (36%), Positives = 36/63 (56%) dbj BAB05162.1 (AP001512) transcriptional regulator [Bacillus halodurans] Length = 107</p>

SeqID 351	SA-1213.1	Contig111 (1036-2190 m)	53	Identities = 128/386 (33%), Positives = 208/386 (53%). Gaps = 18/386 (4%) db AAG28618.1 (AF217235) integrase-like protein [Staphylococcus aureus] Length = 378
SeqID 352	SA-1214.1	Contig111 (516-908 p)	73	Identities = 90/129 (69%), Positives = 106/129 (81%) sp P07842 RS9_BACST_30S RIBOSOMAL PROTEIN S9 (BS10) pr P3859 ribosomal protein S9 - Bacillus stearothermophilus Length = 129
SeqID 353	SA-1215.1	Contig111 (49-495 p)	68	Identities = 89/144 (61%), Positives = 113/144 (77%) db BAB03887.1 (AP001507) ribosomal protein L13 [Bacillus halodurans] Length = 145
SeqID 354	SA-1216.2	Contig130 (62901-63572 p)	24	Identities = 27/119 (22%), Positives = 54/119 (44%), Gaps = 10/119 (8%) emb CAC12088.1 (AL445066) NADH dehydrogenase, chain M related protein [Thermoplasma acidophilum] Length = 503
SeqID 355	SA-1217.1	Contig130 (62156-62926 p)	66	Identities = 121/249 (48%), Positives = 172/249 (68%) pr H70023 N-acetyl-glucosamine catabolism homolog yufB - Bacillus subtilis emb CAB15219.1 (Z99120) similar to N-acetyl-glucosamine catabolism [Bacillus subtilis] Length = 256
SeqID 356	SA-1218.1	Contig130 (61418-62155 p)	42	Identities = 59/248 (23%), Positives = 104/248 (41%), Gaps = 30/248 (12%) pr J51688 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana pr J56919 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) (clone TE 1-7) - Arabidopsis thaliana emb CAA85389.1 (Z36912) acyl-[acyl-carrier protein] thioesterase [Arabidopsis thaliana] db BAB02069.1 (AB026647) acyl carrier protein thioesterase [Arabidopsis thaliana] Length = 362
SeqID 357	SA-1219.1	Contig130 (60284-61414 p)	65	Identities = 173/375 (46%), Positives = 248/375 (66%), Gaps = 5/375 (1%) db BAB05062.1 (AP001511) coproporphyrinogen III oxidase [Bacillus halodurans] Length = 385
SeqID 358	SA-1220.1	Contig130 (59812-60192 p)	No Hits found	

SeqID 359	SA-1221.1	Contig130 (59416-59787 p)	26	<p>Identities = 20/68 (29%), Positives = 35/68 (51%) sp P24252 YBGA_ECOLI HYPOTHETICAL 20.2 KDA PROTEIN IN RHSC-PHRB INTERGENIC REGION (TKP) [ORF169] prij B64806 ygaA protein - Escherichia coli gb AA24387.1 (K01299) unidentified protein ORF-169 [Escherichia coli] gb AAC73801.1 (AE000174) orf, hypothetical protein [Escherichia coli K12] dbj BAA35366.1 (D90709) Hypothetical 20.2 kd protein in phrB 5 region (tkp) (orf169) [Escherichia coli] dbj BAA35371.1 (D90710) Hypothetical 20.2 kd protein in phrB 5 region (tkp) (orf169) [Escherichia coli] Length = 169</p>
SeqID 360	SA-1222.1	Contig130 (57941-59293 p)	77	<p>Identities = 284/451 (62%), Positives = 353/451 (77%), Gaps = 4/451 (0%) pri B69745 phosphoglucosyltransferase (glycolysis) homolog ybbT - Bacillus subtilis emb CAB11953.1 (Z99104) similar to phosphoglucosyltransferase (glycolysis) [Bacillus subtilis] emb CAB11970.1 (Z99105) similar to phosphoglucosyltransferase (glycolysis) [Bacillus subtilis] Length = 448</p>
SeqID 361	SA-1223.1	Contig130 (57018-57887 p)	50	<p>Identities = 90/324 (27%), Positives = 167/324 (50%), Gaps = 18/324 (5%) pri A69745 hypothetical protein ybbR - Bacillus subtilis emb CAB11952.1 (Z99104) ybbR [Bacillus subtilis] emb CAB11969.1 (Z99105) ybbR [Bacillus subtilis] Length = 483</p>
SeqID 362	SA-1225.1	Contig130 (56011-56925 p)	60	<p>Identities = 125/253 (49%), Positives = 186/253 (73%), Gaps = 5/253 (1%) pri H69744 conserved hypothetical protein ybbP - Bacillus subtilis dbj BAA19509.1 (AB002150) YbbP [Bacillus subtilis] emb CAB11951.1 (Z99104) alternate gene name: ybbQ~similar to hypothetical proteins [Bacillus subtilis] emb CAB11966.1 (Z99105) alternate gene name: ybbQ~similar to hypothetical proteins [Bacillus subtilis] Length = 273</p>

SeqID 363	SA-1226.1	Contig130 (54591-55910 m)	50	Identities = 144/442 (32%), Positives = 229/442 (51%), Gaps = 17/442 (3%) pili[T31440 UDP-N-acetylmuramyl tripeptide synthetase homolog murC - Helicobacillus mobilis gb AAC84012.1 (AF080002) UDP-N-acetylmuramyl tripeptide synthetase MurC [Helicobacillus mobilis] Length = 455
SeqID 364	SA-1227.1	Contig130 (53806-54477 m)	47	Identities = 89/250 (35%), Positives = 129/250 (51%), Gaps = 9/250 (3%) pili[T31438 probable cobyric acid synthase CobQ - Helicobacillus mobilis gb AAC84011.1 (AF080002) cobyric acid synthase CobQ [Helicobacillus mobilis] Length = 252
SeqID 365	SA-1228.1	Contig130 (52710-53699 p)	63	Identities = 153/316 (48%), Positives = 212/316 (66%), Gaps = 3/316 (0%) dbj BAB04402.1 (AP001509) lipocate-protein ligase [Bacillus halodurans] Length = 330
SeqID 366	SA-123.1	Contig131 (1559-1945 p)	79	Identities = 95/128 (74%), Positives = 105/128 (81%), Gaps = 9/128 (6%) sp P20277 RL17_BACSU 50S RIBOSOMAL PROTEIN L17 (BL15) (BL21) pili[F32307 ribosomal protein L17 - Bacillus subtilis gb AA02218.1 (M26414) ribosomal protein L17 [Bacillus subtilis] gb AAB08827.1 (L47971) ribosomal protein L17 [Bacillus subtilis] emb CAB11820.1 (Z99104) ribosomal protein L17 (BL15) [Bacillus subtilis] Length = 120
SeqID 367	SA-1230.1	Contig130 (50855-52612 p)	57	Identities = 229/589 (38%), Positives = 339/589 (56%), Gaps = 25/589 (4%) pili 40794 dihydroliopamide dehydrogenase (EC 1.8.1.4) [validated] - Clostridium magnum gb AA021748.1 (L31844) dihydroliopamide dehydrogenase [Clostridium magnum] Length = 578
SeqID 368	SA-1231.1	Contig130 (49407-50795 p)	57	Identities = 187/462 (40%), Positives = 267/462 (57%), Gaps = 26/462 (5%) dbj BA04497.1 (AP001509) dihydroliopamide S-acetyltransferase [Bacillus halodurans] Length = 436

SeqID 369	SA-1232.1	Contig130 (48282-49280 p)	72	Identities = 189/319 (59%), Positives = 249/319 (77%), Gaps = 1/319 (0%) dbj BA04496.1 (AP001509) acetoin dehydrogenase (TPP-dependent) beta chain Length = 327
SeqID 370	SA-1233.1	Contig130 (48230-48595 m)	40	Identities = 45/97 (46%), Positives = 50/97 (51%) pir G72548 hypothetical protein APE1675 - Aeropyrum pernix (strain K1) dbj BAA80676.1 (AP000062) 155aa long hypothetical protein Length = 155 [Aeropyrum pernix]
SeqID 371	SA-1234.1	Contig130 (47238-48207 p)	64	Identities = 148/317 (46%), Positives = 214/317 (66%), Gaps = 1/317 (0%) dbj BA04495.1 (AP001509) acetoin dehydrogenase (TPP-dependent) alpha chain Length = 326 [Bacillus halodurans]
SeqID 372	SA-1236.3	Contig130 (45180-47090 p)	75	Identities = 397/641 (61%), Positives = 488/641 (75%), Gaps = 17/641 (2%) gb AAK05160.1 AE006339_3 (AE006339) ABC transporter ATP binding protein [Lactococcus lactis subsp. lactis] Length = 635
SeqID 373	SA-1238.1	Contig135 (95462-95566 p)	No Hits found	
SeqID 374	SA-1239.1	Contig135 (94858-95316 p)	No Hits found	
SeqID 375	SA-1240.1	Contig135 (94570-94797 p)	No Hits found	
SeqID 376	SA-1241.1	Contig135 (94477-94533 p)	No Hits found	
SeqID 377	SA-1242.1	Contig135 (93778-94036 m)	No Hits found	
SeqID 378	SA-1243.1	Contig135 (93763-94326 p)	No Hits found	
SeqID 379	SA-1244.1	Contig135 (93063-93815 p)	No Hits found	
SeqID 380	SA-1245.1	Contig135 (92528-93014 p)	No Hits found	
SeqID 381	SA-1246.1	Contig135 (92196-92423 p)	No Hits found	
SeqID 382	SA-1247.1	Contig135 (89123-91921 p)	22	Identities = 157/406 (38%), Positives = 216/406 (52%), Gaps = 28/406 (6%) gb AAB30711.1 (S70345) SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, MUCOB 263, Peptide, 1566 aa] Length = 1566

SeqID 369	SA-1232.1	Contig130 (49282-49280 p)	72	Identities = 189/319 (59%), Positives = 249/319 (77%), Gaps = 1/319 (0%) dbj BA04496.1 (AP001509) acetoin dehydrogenase (TPP-dependent) beta chain Length = 327
SeqID 370	SA-1233.1	Contig130 (48230-48595 m)	40	Identities = 45/97 (46%), Positives = 50/97 (51%) pir G72548 hypothetical protein APE1675 - Aeropyrum pernix (strain K1) dbj BAA80676.1 (AP000082) 155aa long hypothetical protein [Aeropyrum pernix] Length = 155
SeqID 371	SA-1234.1	Contig130 (47239-48207 p)	64	Identities = 148/317 (46%), Positives = 214/317 (66%), Gaps = 1/317 (0%) dbj BA04495.1 (AP001509) acetoin dehydrogenase (TPP-dependent) alpha chain Length = 326
SeqID 372	SA-1235.3	Contig130 (45180-47090 p)	75	Identities = 357/641 (51%), Positives = 488/641 (75%), Gaps = 17/641 (2%) gb AAK05160.1 (AE006339) ABC transporter ATP binding protein [Lactococcus lactis subsp. lactis] Length = 635
SeqID 373	SA-1238.1	Contig135 (95462-95596 p)	No Hits found	
SeqID 374	SA-1239.1	Contig135 (94858-95316 p)	No Hits found	
SeqID 375	SA-1240.1	Contig135 (94570-94787 p)	No Hits found	
SeqID 376	SA-1241.1	Contig135 (94477-94533 p)	No Hits found	
SeqID 377	SA-1242.1	Contig135 (93779-94036 m)	No Hits found	
SeqID 378	SA-1243.1	Contig135 (93763-94326 p)	No Hits found	
SeqID 379	SA-1244.1	Contig135 (93063-93815 p)	No Hits found	
SeqID 380	SA-1245.1	Contig135 (92529-93014 p)	No Hits found	
SeqID 381	SA-1246.1	Contig135 (92196-92423 p)	No Hits found	
SeqID 382	SA-1247.1	Contig135 (89123-91921 p)	22	Identities = 157/406 (38%), Positives = 216/406 (52%), Gaps = 28/406 (6%) gb AA030711.1 (S70345) SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus, MUCOB 263, Peptide, 1566 aa] Length = 1566

SeqID 383	SA-1248.1	Contig135 (88346-89056 p)	53	<p>Identities = 85/268 (31%), Positives = 129/268 (47%), Gaps = 35/268 (13%) prf[S45091] hypothetical protein lta - Streptococcus pyogenes plasmid pDB101 prf[S68125] hypothetical protein lta - Streptococcus pyogenes plasmid pSM19035 embiCAA47087.1 (X68468) orf lta [Streptococcus pyogenes] Length = 268</p>
SeqID 384	SA-1249.1	Contig135 (88324-88794 m)	30	<p>Identities = 37/104 (35%), Positives = 48/104 (45%), Gaps = 5/104 (4%) refjXP_007094.1 collagen, type IV, alpha 1 [Homo sapiens] Length = 1669</p>
SeqID 385	SA-125.1	Contig131 (606-1544 p)	79	<p>Identities = 190/314 (60%), Positives = 249/314 (78%), Gaps = 2/314 (0%) spjO50634[RPOA_BACHD DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (TRANSCRIPTASE ALPHA CHAIN)] RNA POLYMERASE ALPHA SUBUNIT prf[T44410] DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain rpoA [imported] - Bacillus halodurans dbj[BAA24194.1] (AB010082) RNA polymerase alpha subunit [Bacillus halodurans] dbj[BAA75288.1] (AB017508) rpoA homologue (identity of 85 to B. subtilis%) [Bacillus halodurans] dbj[BAB03881.1] (AP001507) DNA-directed RNA polymerase alpha subunit [Bacillus halodurans] Length = 314</p>
SeqID 386	SA-1250.1	Contig135 (86100-86331 p)	45	<p>Identities = 185/839 (22%), Positives = 342/839 (40%), Gaps = 124/839 (14%) prf[G41662] 130K surface exclusion protein Sec10 precursor - Enterococcus faecalis plasmid pCF10 gb AAA65847.1 (M54978) surface exclusion protein [Plasmid pCF10] Length = 891</p>
SeqID 387	SA-1251.1	Contig135 (85784-86083 p)	No Hits found	<p>Identities = 29/58 (50%), Positives = 41/58 (70%) ref NP_049430.1 unknown [Streptococcus thermophilus bacteriophage DT1] gb AAD21918.1 (AF085222) unknown [Streptococcus thermophilus bacteriophage DT1] Length = 165</p>
SeqID 388	SA-1252.1	Contig135 (85204-85401 p)	60	
SeqID 389	SA-1253.1	Contig135 (85022-85207 p)	No Hits found	

SeqID 390	SA-1254.1	Contig135 (83986-85020 p)	36	Identities = 95/192 (49%), Positives = 128/192 (66%), Gaps = 7/192 (3%) refNP_038742.1 IFN-response element binding factor 1 [Mus musculus] sp P22560 RBF-1_MOUSE IFN-RESPONSE BINDING FACTOR 1 (RBF-1) p I A38558 interferon response element-binding factor 1 - mouse gb AA37884.1 (M55290) IFN-response element binding factor 1 [Mus musculus] Length = 311
SeqID 391	SA-1255.1	Contig135 (83829-83983 p)	No Hits found	
SeqID 392	SA-1256.1	Contig135 (83345-83722 p)	No Hits found	
SeqID 393	SA-1257.1	Contig135 (82756-83013 p)	50	Identities = 28/81 (34%), Positives = 46/81 (56%), Gaps = 3/81 (3%) sp P2318 YR7D_ECOLI_HYPOTHETICAL_11.0_KD PROTEIN (ORF) (RETRON EC67) p I JQ0859 hypothetical 11K protein - Escherichia coli retron Ec67 gb AA23395.1 (M55249) unknown [Escherichia coli] Length = 100
SeqID 394	SA-1258.1	Contig135 (82201-82572 p)	No Hits found	
SeqID 395	SA-1261.1	Contig135 (81104-82087 p)	82	Identities = 244/321 (76%), Positives = 286/321 (89%), Gaps = 2/321 (0%) p I C70015_probable_GMP_reductase_(EC_1.6.6.8) yumD - Bacillus subtilis emb CAB07955.1 (Z93939) unknown [Bacillus subtilis] emb CAB15203.1 (Z99120) similar to GMP reductase [Bacillus subtilis] Length = 326
SeqID 396	SA-1265.2	Contig125 (17134-18261 m)	75	Identities = 209/376 (55%), Positives = 266/376 (75%), Gaps = 3/376 (0%) gp AAK06013.1 AEO06422_2 (AE006422) Na ⁺ /H ⁺ antiporter [Lactococcus lactis subsp. lactis] Length = 379
SeqID 397	SA-1266.1	Contig125 (16108-17070 p)	45	Identities = 86/319 (26%), Positives = 147/319 (45%), Gaps = 34/319 (10%) sp P31847 YPUA_BACSU_HYPOTHETICAL_31.3_KD_PROTEIN_IN_LYSA-PPIE_INTERGENIC_REGION (ORF19) p I JQ0473 ypuA protein - Bacillus subtilis gp AA67474.1 (L09228) ORF-X19 [Bacillus subtilis] emb CAB14269.1 (Z99116) ypuA [Bacillus subtilis] Length = 290

SeqID 398	SA-1267.1	Contig125 (15541-15554 p)	64	<p>Identities = 76/139 (54%), Positives = 92/139 (65%), Gaps = 12/139 (8%) spP45871YWKD_BACSU HYPOTHETICAL 14.8 KD PROTEIN IN TDK-PRFA INTERGENIC REGION pir S55436 conserved hypothetical protein ywkD - Bacillus subtilis emb CAA89883.1 (Z49782) unknown [Bacillus subtilis] emb CAB15719.1 (Z99122) similar to hypothetical proteins [Bacillus subtilis] Length = 128</p>
SeqID 399	SA-1268.1	Contig125 (14782-15525 p)	35	<p>Identities = 85/126 (51%), Positives = 89/126 (70%), Gaps = 1/126 (0%) gb AAA73122.1 (M77279) alpha-amylase [unidentified cloning vector] Length = 137</p>
SeqID 400	SA-127.1	Contig131 (173-556 p)	87	<p>Identities = 107/123 (86%), Positives = 115/123 (92%) spP04969 RS11_BACSU 30S RIBOSOMAL PROTEIN S11 (BS11) pir R3BS1 ribosomal protein S11 - Bacillus subtilis gb AA422216.1 (M26414) ribosomal protein S11 [Bacillus subtilis] gb AA422707.1 (M13957) ribosomal protein S11 [Bacillus subtilis] gb AAB06825.1 (L47971) ribosomal protein S11 [Bacillus subtilis] emb CAB11918.1 (Z99104) ribosomal protein S11 (BS11) [Bacillus subtilis] Length = 131</p>
SeqID 401	SA-1271.1	Contig125 (12316-14775 p)	92	<p>Identities = 71/2819 (86%), Positives = 769/819 (92%) gb AAF63266.1 (AF220945) DNA gyrase A subunit [Streptococcus pyogenes] Length = 828</p>
SeqID 402	SA-1273.1	Contig125 (11088-12077 m)	90	<p>Identities = 290/329 (88%), Positives = 313/329 (94%), Gaps = 1/329 (0%) sp O33734 LDH_STRPN L-LACTATE DEHYDROGENASE emb CAA04010.1 (AJ003036) L-lactate dehydrogenase [Streptococcus pneumoniae] Length = 328</p>
SeqID 403	SA-1274.1	Contig125 (9598-10968 p)	88	<p>Identities = 363/458 (79%), Positives = 408/458 (88%), Gaps = 3/458 (0%) gb AAC26485.2 (AF014458) NADH oxidase [Streptococcus pneumoniae] Length = 459</p>

SeqID 404	SA-1275.1	Contig125 (8436-9392 p)	72	<p>Identities = 172/318 (54%), Positives = 234/318 (73%) pir F70009 conserved hypothetical protein yuQ - <i>Bacillus subtilis</i> emb CAB07939.1 (Z99120) unknown [Bacillus subtilis] emb CAB15146.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] Length = 319</p>
SeqID 405	SA-1278.1	Contig125 (7373-8434 p)	80	<p>Identities = 154/349 (44%), Positives = 220/349 (62%), Gaps = 6/349 (1%) pir E70009 conserved hypothetical protein yuP - <i>Bacillus subtilis</i> emb CAB07938.1 (Z53937) unknown [Bacillus subtilis] emb CAB15145.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] Length = 348</p>
SeqID 406	SA-1279.1	Contig125 (5845-7380 p)	76	<p>Identities = 311/497 (62%), Positives = 396/497 (79%), Gaps = 1/497 (0%) pir D70009 probable ABC transporter yuO - <i>Bacillus</i> subtilis emb CAB07937.1 (Z93937) unknown [Bacillus subtilis] emb CAB15144.1 (Z99120) similar to ABC transporter (ATP- binding protein) [Bacillus subtilis] Length = 510</p>
SeqID 407	SA-128.1	Contig131 (3-155 p)	86	<p>Identities = 41/50 (82%), Positives = 44/50 (88%) sp P15757 RS13_BACST 30S RIBOSOMAL PROTEIN S13 pir R3BS3F ribosomal protein S13 - <i>Bacillus stearothermophilus</i> Length = 119</p>
SeqID 408	SA-1280.1	Contig125 (4651-5700 p)	61	<p>Identities = 164/337 (48%), Positives = 225/337 (66%), Gaps = 10/337 (2%) sp O0522 YUFN_BACSU HYPOTHETICAL LIPOPROTEIN YUFN PRECURSOR pir C70009 ABC transporter (lipoprotein) homolog yuN - <i>Bacillus subtilis</i> emb CAB07938.1 (Z53937) unknown [Bacillus subtilis] emb CAB15143.1 (Z99120) similar to ABC transporter (lipoprotein) [Bacillus subtilis] Length = 350</p>
SeqID 409	SA-1281.1	Contig125 (4197-4586 p)	52	<p>Identities = 66/114 (57%), Positives = 81/114 (70%) emb CAB51906.1 (A1237978) cytidine deaminase [Bacillus psychrophilus] Length = 136</p>

SeqID 410	SA-1282.1	Contig125 (3281-3871 p)	69	<p>Identities = 90/201 (44%), Positives = 144/201 (70%), Gaps = 5/201 (2%) sp P37872 YBXB_BACSU HYPOTHETICAL 22.5 KDA PROTEIN IN RPIL-RPOB INTERGENIC REGION (P23) (ORF23) p P37872 conserved hypothetical protein yxb8 - - Bacillus subtilis g AAB00971.1 (L24376) hypothetical protein [Bacillus subtilis] emb CAB11882.1 (Z99104) alternate gene name: ybaA-similar to hypothetical proteins [Bacillus subtilis] Length = 201</p>
SeqID 411	SA-1283.1	Contig125 (2255-3175 m)	65	<p>Identities = 140/307 (45%), Positives = 203/307 (65%), Gaps = 5/307 (1%) sp Q9K8X7 COAA_BACHD PANTOTHENATE KINASE (PANTOTHENIC ACID KINASE) db BAB06594.1 (AP001516) pantothenate kinase [Bacillus halodurans] Length = 316</p>
SeqID 412	SA-1284.1	Contig125 (1953-2195 m)	69	<p>Identities = 47/86 (54%), Positives = 59/86 (67%), Gaps = 7/86 (8%) db BAB05058.1 (AP001511) ribosomal protein S20 (BS20) [Bacillus halodurans] Length = 91</p>
SeqID 413	SA-1285.1	Contig125 (1035-1868 p)	66	<p>Identities = 170/269 (63%), Positives = 203/269 (75%), Gaps = 2/269 (0%) gb AAC35851.1 (AF086736) amino acid-binding protein Alp [Streptococcus uberis] Length = 277</p>
SeqID 414	SA-1286.1	Contig125 (392-1021 p)	63	<p>Identities = 94/210 (44%), Positives = 145/210 (68%), Gaps = 3/210 (1%) gb AAB49429.1 (U73111) glutamine transport ATP-binding protein GLNQ [Salmonella typhimurium] Length = 240</p>
SeqID 415	SA-1287.1	Contig125 (196-381 p)	64	<p>Identities = 54/125 (43%), Positives = 82/125 (65%), Gaps = 1/125 (0%) db BA98402.1 (AP002545) ABC amino acid transporter permease [Chlamydomonas reinhardtii] Length = 217</p>
SeqID 416	SA-1288.3	Contig139 (155214-156659 m)	21	<p>Identities = 60/268 (22%), Positives = 107/268 (39%), Gaps = 4/268 (1%) gb AAG44891.1 (AF286595.1) (AF286595) flavin-containing monooxygenase FMO3 [Rattus norvegicus] Length = 531</p>

SeqID 417	SA-1289.1	Contig139 (154486-155157 p)	66	Identities = 116/213 (54%), Positives = 152/213 (70%) gb AAD47593.1 AF140784.2 (AF140784) Vexp2 [Streptococcus pneumoniae] Length = 215
SeqID 418	SA-1290.1	Contig139 (154080-154274 p)	No Hits found	
SeqID 419	SA-1291.1	Contig139 (153049-154071 p)	45	Identities = 100/348 (28%), Positives = 158/348 (44%), Gaps = 17/348 (4%) gb AAD47594.1 AF140784.3 (AF140784) Vexp3 [Streptococcus pneumoniae] Length = 459
SeqID 420	SA-1292.1	Contig139 (152386-153039 p)	42	Identities = 61/210 (29%), Positives = 105/210 (49%), Gaps = 18/210 (8%) pif F69762 transporter homolog ycdI - Bacillus subtilis dbj BAA09006.1 D50453) homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis] emb CAB12182.1 (Z39106) similar to transporter [Bacillus subtilis] Length = 486
SeqID 421	SA-1293.1	Contig139 (151707-152243 p)	83	Identities = 175/178 (98%), Positives = 176/178 (98%) gb AAF01071.1 (AF157015) CyfK [Streptococcus agalactiae] Length = 178
SeqID 422	SA-1295.1	Contig139 (150488-151699 p)	94	Identities = 398/403 (98%), Positives = 400/403 (98%) gb AAF01070.1 (AF157015) CyfJ [Streptococcus agalactiae] Length = 403
SeqID 423	SA-1296.1	Contig139 (148288-150483 p)	95	Identities = 730/731 (99%), Positives = 731/731 (99%) gb AAF89495.1 (AF093787) CyfI [Streptococcus agalactiae] Length = 731
SeqID 424	SA-1297.1	Contig139 (147338-148291 p)	99	Identities = 317/317 (100%), Positives = 317/317 (100%) gb AAF89494.1 (AF093787) CyfF [Streptococcus agalactiae] Length = 317
SeqID 425	SA-1298.1	Contig139 (145338-147341 p)	99	Identities = 666/667 (99%), Positives = 667/667 (99%) gb AAD32040.1 AF093787_8 (AF093787) CyfE [Streptococcus agalactiae] Length = 667
SeqID 426	SA-1299.1	Contig139 (144463-145341 p)	94	Identities = 291/292 (99%), Positives = 292/292 (99%) gb AAD32039.1 AF093787_7 (AF093787) ABC transporter homolog CyfB [Streptococcus agalactiae] Length = 292
SeqID 427	SA-13.1	Contig137 (32737-32958 p)	No Hits found	

SeqID 417	SA-1289.1	Contig139 (154486-155157 p)	66	Identities = 116/213 (54%), Positives = 152/213 (70%) gb AAD47593.1 AF140784.2 (AF140784) Vexp2 [Streptococcus pneumoniae] Length = 215
SeqID 418	SA-1290.1	Contig139 (154080-154274 p)	No Hits found	
SeqID 419	SA-1291.1	Contig139 (153049-154071 p)	45	Identities = 100/348 (28%), Positives = 158/348 (44%), Gaps = 17/348 (4%) gb AAD47594.1 AF140784.3 (AF140784) Vexp3 [Streptococcus pneumoniae] Length = 459
SeqID 420	SA-1292.1	Contig139 (152386-153039 p)	42	Identities = 61/210 (29%), Positives = 105/210 (49%), Gaps = 18/210 (8%) pf JF69762 transporter homolog yclI - Bacillus subtilis db JBA09006.1 (D50453) homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis] emb CAB12182.1 (Z99106) similar to transporter [Bacillus subtilis] Length = 486
SeqID 421	SA-1293.1	Contig139 (151707-152243 p)	83	Identities = 175/178 (98%), Positives = 176/178 (98%) gb AAF01071.1 (AF157015) CyJ [Streptococcus agalactiae] Length = 178
SeqID 422	SA-1295.1	Contig139 (150488-151689 p)	94	Identities = 395/403 (98%), Positives = 400/403 (98%) gb AAF01070.1 (AF157015) CyJ [Streptococcus agalactiae] Length = 403
SeqID 423	SA-1296.1	Contig139 (148288-150483 p)	95	Identities = 730/731 (99%), Positives = 731/731 (99%) gb AAF89495.1 (AF093787) CyJ [Streptococcus agalactiae] Length = 731
SeqID 424	SA-1297.1	Contig139 (147338-148291 p)	99	Identities = 317/317 (100%), Positives = 317/317 (100%) gb AAF89494.1 (AF093787) CyJ [Streptococcus agalactiae] Length = 317
SeqID 425	SA-1298.1	Contig139 (145338-147341 p)	99	Identities = 565/667 (99%), Positives = 667/667 (99%) gb AAD32040.1 AF093787.8 (AF093787) CyJ [Streptococcus agalactiae] Length = 667
SeqID 426	SA-1299.1	Contig139 (144463-145341 p)	94	Identities = 291/292 (99%), Positives = 292/292 (99%) gb AAD32039.1 AF093787.7 (AF093787) ABC transporter homolog CyB [Streptococcus agalactiae] Length = 292
SeqID 427	SA-13.1	Contig137 (32737-32958 p)	No Hits found	

SeqID 428	SA-130.1	Contig138 (96433-96687 p)	No Hits found	
SeqID 429	SA-1300.1	Contig139 (143541-144470 p)	92	Identities = 368/309 (99%), Positives = 308/309 (99%) gb AAD32038.1 AF093787_5 (AF093787) ABC transporter homolog CyaA [Streptococcus agalactiae] Length = 309
SeqID 430	SA-1301.1	Contig139 (143075-143551 p)	75	Identities = 120/120 (100%), Positives = 120/120 (100%) gb AAD32037.1 AF093787_5 (AF093787) CytZ [Streptococcus agalactiae] Length = 131
SeqID 431	SA-1302.1	Contig139 (142786-143091 p)	98	Identities = 101/101 (100%), Positives = 101/101 (100%) gb AAD32036.1 AF093787_4 (AF093787) acyl carrier protein homolog ApcC [Streptococcus agalactiae] Length = 101
SeqID 432	SA-1303.1	Contig139 (142071-142793 p)	94	Identities = 239/240 (99%), Positives = 240/240 (99%) gb AAD32035.1 AF093787_3 (AF093787) CytG [Streptococcus agalactiae] Length = 240
SeqID 433	SA-1304.2	Contig139 (141226-142074 p)	99	Identities = 282/282 (100%), Positives = 282/282 (100%) gb AAD32034.1 AF093787_2 (AF093787) CytD [Streptococcus agalactiae] Length = 282
SeqID 434	SA-1305.2	Contig139 (140921-141226 p)	93	Identities = 101/101 (100%), Positives = 101/101 (100%) gb AAD32033.1 AF093787_1 (AF093787) CytX [Streptococcus agalactiae] Length = 101
SeqID 435	SA-1308.2	Contig128 (27763-28422 p)	40	Identities = 54/181 (29%), Positives = 95/181 (51%), Gaps = 1/181 (0%) emb CAA65740.1 (X97014) PflA [Listeria seeligeri] Length = 237
SeqID 436	SA-1309.1	Contig128 (28446-30731 p)	65	Identities = 386/767 (50%), Positives = 502/767 (65%), Gaps = 21/767 (2%) sp P22083 PEPX_LACLC XAA-PRO DIPEPTIDYL- PEPTIDASE (X-PRO DIPEPTIDYL-PEPTIDASE) (X- PROLYL-DIPEPTIDYL AMINOPEPTIDASE) (X-PDAP) pfl A43747 X-Pro dipeptidyl-peptidase (EC 3.4.14.1) - Lactococcus lactis subsp. cremoris gb AA25232.1 (M58315) dipeptidyl peptidase IV [Lactococcus lactis] Length = 763
SeqID 437	SA-1310.1	Contig128 (30735-31094 p)	No Hits found	

SeqID 438	SA-1311.1	Contig128 (31140-32120 p)	56	<p>Identities = 101/318 (31%), Positives = 184/318 (57%), Gaps = 5/318 (1%) spIP31114[HEP2_BACSU HEPTAPRENYL DIPHOSPHATE SYNTHASE COMPONENT II (HEPPP SYNTHASE SUBUNIT 2) (SPORE GERMINATION PROTEIN C3) pirIE69630 heptaprenyl diphosphate synthase component II gerCC - Bacillus subtilis gbAA208566.1] (M80245) GerC3 [Bacillus subtilis] embICAB14190.1] (Z391116) heptaprenyl diphosphate synthase component II [Bacillus subtilis] Length = 348</p>
SeqID 439	SA-1312.1	Contig128 (32205-33953 m)	66	<p>Identities = 264/577 (45%), Positives = 391/577 (67%), Gaps = 14/577 (2%) spIP94387[CYDD_BACSU TRANSPORT ATP-BINDING PROTEIN CYDD pirID69611 ABC transporter required for expression of cytochrome bd (ATP-) cydC - Bacillus subtilis dbjBAA11730.1] (D83026) homologous to many ATP-binding transport proteins: hypothetical [Bacillus subtilis] embICAB15699.1] (Z39123) ABC membrane transporter (ATP-binding protein) [Bacillus subtilis] Length = 575</p>
SeqID 440	SA-1313.1	Contig128 (33946-35664 m)	67	<p>Identities = 278/569 (48%), Positives = 399/569 (69%), Gaps = 6/569 (1%) spIP94366[CYDC_BACSU TRANSPORT ATP-BINDING PROTEIN CYDC pirIC69611 ABC transporter required for expression of cytochrome bd (ATP-) cydC - Bacillus subtilis dbjBAA11728.1] (D83026) homologous to many ATP-binding transport proteins including SwissProt CYDD_ECOLI: hypothetical [Bacillus subtilis] embICAB15900.1] (Z39123) ABC membrane transporter (ATP-binding protein) [Bacillus subtilis] Length = 567</p>

SeqID 441	SA-1314.1	Contig128 (35664-36683 m)	65	<p>Identities = 158/331 (47%), Positives = 223/331 (66%), Gaps = 173/31 (0%) sp P94365 CYDB_BACSU CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II pir B69611 cytochrome d ubiquinol oxidase (EC 1.10.3.-) chain II cydB - Bacillus subtilis dbj BAA11728.1 (D83026) homologous to cytochrome d ubiquinol oxidase subunit II; hypothetical [Bacillus subtilis] emb CAB15901.1 (Z99123) cytochrome bd ubiquinol oxidase (subunit I) [Bacillus subtilis] Length = 338</p>
SeqID 442	SA-1316.1	Contig128 (36684-38111 m)	65	<p>Identities = 246/470 (52%), Positives = 319/470 (67%), Gaps = 12/470 (2%) sp P94364 ICYDA_BACSU CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I pir A69611 cytochrome bd ubiquinol oxidase (subunit I) cydA - Bacillus subtilis dbj BAA11727.1 (D83026) homologous to cytochrome d ubiquinol oxidase subunit I; hypothetical [Bacillus subtilis] emb CAB15902.1 (Z99123) cytochrome bd ubiquinol oxidase (subunit I) [Bacillus subtilis] Length = 488</p>
SeqID 443	SA-1318.1	Contig128 (38214-39422 m)	61	<p>Identities = 178/403 (44%), Positives = 249/403 (61%), Gaps = 7/403 (1%) pir A70015 probable NADH dehydrogenase (EC 1.6.99.3) ynmB - Bacillus subtilis emb CAB07953.1 (Z93939) unknown [Bacillus subtilis] emb CAB15200.1 (Z99120) similar to NADH dehydrogenase [Bacillus subtilis] Length = 406</p>

SeqID 444	SA-1319.2	Contig128 (39435-40334 m)	44	<p>Identities = 74/290 (25%), Positives = 138/290 (47%), Gaps = 15/290 (5%) s p 3582 IMENA_BACSU PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (DHNA-OCTAPRENYLTRANSFERASE) p r S38661 menaquinone biosynthesis protein homolog ywab - Bacillus subtilis emb CAA51562.1 (X73124) lpa-6d [Bacillus subtilis] emb CAB15875.1 (Z99123) alternate gene name: lpa-6d--similar to quinone biosynthesis [Bacillus subtilis] Length = 311</p>
SeqID 445	SA-132.2	Contig138 (94727-95020 m)	42	<p>Identities = 35/72 (48%), Positives = 42/72 (57%) p r S59084 hypothetical protein 29.1 - red alga (Chondrus crispus) mitochondrion emb CAA87600.1 (Z47547) unique orf [Chondrus crispus] Length = 79</p>
SeqID 446	SA-1320.1	Contig100 (14165-14662 p)	No Hits found	
SeqID 447	SA-1322.1	Contig100 (13666-14115 p)	No Hits found	
SeqID 448	SA-1323.1	Contig100 (13349-13642 p)	No Hits found	
SeqID 449	SA-1324.1	Contig100 (12954-13271 p)	67	<p>Identities = 70/96 (72%), Positives = 83/96 (85%) gb AA852379.1 (U31811) immunogenic secreted protein precursor [Streptococcus pyogenes] Length = 534</p>
SeqID 450	SA-1325.1	Contig100 (12107-13018 p)	60	<p>Identities = 142/298 (47%), Positives = 185/298 (61%), Gaps = 11/298 (3%) gb AA852379.1 (U31811) immunogenic secreted protein precursor [Streptococcus pyogenes] Length = 534</p>
SeqID 451	SA-1326.1	Contig100 (11805-12203 p)	32	<p>Identities = 35/112 (31%), Positives = 49/112 (43%), Gaps = 12/112 (10%) p r T07945 probable arabinogalactan protein (clone Sta 39-3) - rape gb AAC37509.1 (L47351) arabinogalactan protein [Brassica napus] Length = 136</p>
SeqID 452	SA-1327.1	Contig100 (11394-11648 p)	57	<p>Identities = 32/76 (42%), Positives = 54/76 (70%) db JBA04699.1 (AP001510) unknown conserved protein [Bacillus halodurans] Length = 102</p>

SeqID 453	SA-1328.1	Contig100 (10783-11373 p)	55	Identities = 72/259 (27%), Positives = 112/259 (42%), Gaps = 64/259 (24%) pilJCB2882 ABC Transporter UUS10 [Imported] - Ureaplasma urealyticum gb AAAF30922.1 AE002149.7 (AE002149) ABC Transporter [Ureaplasma urealyticum] Length = 668
SeqID 454	SA-1329.1	Contig100 (10314-10786 p)	No Hits found	Identities = 62/104 (59%), Positives = 68/104 (64%) pilJF81516 hypothetical protein CP0987 [Imported] - Chlamydomonas pneumoniae (strain AR39) Length = 216
SeqID 455	SA-133.1	Contig138 (95173-95493 p)	63	Identities = 59/254 (23%), Positives = 108/254 (42%), Gaps = 14/254 (5%) emb CAC16670.1 (AJ302696) hypothetical protein [Staphylococcus haemolyticus] Length = 373
SeqID 456	SA-1330.1	Contig100 (9421-10335 p)	34	Identities = 452/1058 (42%), Positives = 664/1058 (62%), Gaps = 39/1058 (3%) pilJCT0013 conserved hypothetical protein yuka - Bacillus subtilis emb CAB15175.1 (Z99120) alternate gene name: yueA-similar to hypothetical proteins [Bacillus subtilis] Length = 1207
SeqID 457	SA-1331.1	Contig100 (9062-9418 p)	No Hits found	
SeqID 458	SA-1332.1	Contig100 (8700-9050 p)	No Hits found	
SeqID 459	SA-1333.2	Contig100 (8666-8776 m)	No Hits found	
SeqID 460	SA-1334.1	Contig100 (4757-8686 p)	50	Identities = 83/323 (25%), Positives = 163/323 (49%), Gaps = 1/323 (0%) obj BAB04693.1 (AP001510) unknown conserved protein [Bacillus halodurans] Length = 440
SeqID 461	SA-1335.1	Contig100 (4279-4782 p)	No Hits found	
SeqID 462	SA-1336.1	Contig100 (2999-4272 p)	37	Identities = 101/501 (20%), Positives = 213/501 (42%), Gaps = 54/501 (10%) pilJPC6003 surface membrane protein imp4 - Mycoplasma hominis (fragment) Length = 624
SeqID 463	SA-1337.1	Contig100 (2756-2998 p)	No Hits found	
SeqID 464	SA-1338.1	Contig100 (2344-2772 p)	No Hits found	
SeqID 465	SA-1339.1	Contig100 (2-2280 p)	27	
SeqID 466	SA-134.1	Contig138 (94535-94964 m)	No Hits found	

SeqID 467	SA-1340.2	Contig120 (16456-17268 m)	58	<p>Identities = 116/260 (44%), Positives = 165/260 (62%), Gaps = 6/260 (2%) gpIP39345 IDNO_ECOLI_GLUCONATE 5-DEHYDROGENASE (5-KETO-D-GLUCONATE 5-REDUCTASE) pIIIS59492 hypothetical 27.6K protein (pepa-gntv intergenic region) - Escherichia coli gpIAAA97163.1 (U14003) ORF_1254 [Escherichia coli] gpIAAC77223.1 (AE000497) 5-keto-D-glucuronate 5-reductase [Escherichia coli K12] Length = 254</p>
SeqID 468	SA-1341.1	Contig120 (15801-16439 m)	38	<p>Identities = 47/189 (24%), Positives = 81/189 (41%), Gaps = 20/189 (10%) pIIID43258 galactose-6-phosphate isomerase subunit LacB - Streptococcus mutans Length = 171</p>
SeqID 469	SA-1342.1	Contig120 (14768-15775 m)	48	<p>Identities = 94/329 (28%), Positives = 169/329 (50%), Gaps = 7/329 (2%) pIIIG72422 2-keto-3-deoxygluconate kinase - Thermotoga maritima (strain MSB8) gpIAAD35161.1 AE001693.7 (AE001693) 2-keto-3-deoxygluconate kinase [Thermotoga maritima] Length = 339</p>
SeqID 470	SA-1343.1	Contig120 (14118-14766 m)	51	<p>Identities = 78/192 (40%), Positives = 118/192 (60%), Gaps = 6/192 (3%) pIIIF72422 KHG-KDPG bifunctional aldolase TM0066 [similarity] - Thermotoga maritima (strain MSB8) gpIAAD35160.1 AE001693.6 (AE001693) 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Thermotoga maritima] Length = 205</p>
SeqID 471	SA-1344.2	Contig120 (11557-13410 m)	35	<p>Identities = 112/529 (21%), Positives = 218/529 (41%), Gaps = 67/529 (12%) emb CAB62846.2 (AL035475) hypothetical protein [Plasmodium falciparum] Length = 1734</p>
SeqID 472	SA-1345.1	Contig120 (10772-11386 p)	67	<p>Identities = 115/203 (56%), Positives = 143/203 (69%), Gaps = 7/203 (3%) pIIIA83323 hypothetical protein PA2575 [Imported] - Pseudomonas aeruginosa (strain PAO1) gpIAAG05963.1 AE004686.1 (AE004686) hypothetical protein [Pseudomonas aeruginosa] Length = 200</p>

SeqID 473	SA-1347.1	Contig120 (10214-10639 p)	48	Identities = 49/124 (39%), Positives = 73/124 (58%) pir A69860 transcription regulator MarR family homolog ykOm - Bacillus subtilis emb CAA05611.1 (AJ002571) YkOm [Bacillus subtilis] emb CAB1319.1 (Z99110) similar to transcriptional regulator (MarR family) [Bacillus subtilis] emb CAB13207.1 (Z99111) similar to transcriptional regulator (MarR family) [Bacillus subtilis] Length = 154
SeqID 474	SA-1348.1	Contig120 (5681-10087 p)	91	Identities = 1238/1468 (84%), Positives = 1346/1468 (91%), Gaps = 3/1468 (0%) gb AA098345.1 (AF280761) DNA polymerase III alpha chain [Streptococcus pyogenes] Length = 1465
SeqID 475	SA-1349.1	Contig120 (4974-5558 p)	61	Identities = 101/201 (50%), Positives = 122/201 (60%), Gaps = 9/201 (4%) emb CAB94815.1 (AJ245582) peptidoglycan hydrolase [Streptococcus thermophilus] Length = 218
SeqID 476	SA-135.1	Contig138 (93460-93819 p)	No Hits found	
SeqID 477	SA-1350.1	Contig120 (2996-4849 p)	65	Identities = 300/608 (49%), Positives = 410/608 (67%), Gaps = 52/608 (8%) sp O31759 SYP_BACSU PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS) pir G99682 proline--RNA ligase (EC 6.1.1.15) proS - Bacillus subtilis emb CAB13530.1 (Z99112) poly-RNA synthetase [Bacillus subtilis] Length = 564
SeqID 478	SA-1351.1	Contig120 (1845-2904 p)	70	Identities = 229/425 (53%), Positives = 298/425 (69%), Gaps = 9/425 (2%) gb AA047948.1 (AF152237) Esp [Enterococcus faecalis] Length = 422
SeqID 479	SA-1352.1	Contig120 (820-1614 p)	63	Identities = 116/266 (43%), Positives = 172/266 (64%), Gaps = 6/266 (2%) dbj BAB06141.1 (AF001515) phosphatidate cytidyltransferase [Bacillus halodurans] Length = 264

SeqID 480	SA-1353.1	Contig120 (53-805 p)	63	Identities = 134/235 (57%), Positives = 170/235 (72%), Gaps = 4/235 (1%) sp O31751 UPPS_BACSU UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLTRANSFERASE) (UNDECAPRENYL DIPHOSPHATE SYNTHASE) (UDS) pir A56881 conserved hypothetical protein yluA - Bacillus subtilis emb CAB13526.1 (Z99112) similar to hypothetical proteins [Bacillus subtilis] Length = 260
SeqID 481	SA-1354.1	Contig99 (17810-18058 p)	No Hits found	
SeqID 482	SA-1355.1	Contig99 (16154-17593 p)	76	Identities = 289/478 (60%), Positives = 368/478 (76%), Gaps = 2/478 (0%) gb AAAG9226.1 (U29579) 6-phospho-beta-glucosidase [Escherichia coli] Length = 476
SeqID 483	SA-1356.1	Contig99 (15380-15994 p)	40	Identities = 43/177 (24%), Positives = 84/177 (47%), Gaps = 9/177 (5%) sp O35264 IPA1B_RAT PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (PAF ACETYLHYDROLASE 30 KDA SUBUNIT) (PAF-AH 30 KDA SUBUNIT) (PAF-AH BETA SUBUNIT) (PAFAH BETA SUBUNIT) (PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE ALPHA 2 SUBUNIT) (PAF-AH ALPHA 2) gb AAC27974.1 (AF016048) platelet-activating factor acetylhydrolase alpha 2 subunit [Rattus norvegicus] Length = 229
SeqID 484	SA-1357.1	Contig99 (14458-15279 p)	55	Identities = 103/255 (38%), Positives = 154/265 (57%), Gaps = 4/265 (1%) sp P75809 YBJI_ECOLI PROTEIN YBJI Length = 271
SeqID 485	SA-1358.1	Contig99 (12904-13836 m)	75	Identities = 197/296 (66%), Positives = 240/296 (80%) gb AAAF9977.1 AF206272.3 (AF206272) transcriptional regulator [Streptococcus mutans] Length = 301
SeqID 486	SA-1359.1	Contig99 (11315-12847 p)	46	Identities = 141/143 (31%), Positives = 241/143 (53%), Gaps = 20/143 (4%) pir JC8249 conserved hypothetical protein VCA0526 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAAF96429.1 (AE004383) conserved hypothetical protein [Vibrio cholerae] Length = 468

SeqID 487	SA-136.1	Contig138 (92309-93091 m)	No Hits found	
SeqID 488	SA-1361.1	Contig99 (10178-11206 p)	50	<p>Identities = 131/336 (38%), Positives = 188/336 (54%), Gaps = 7/336 (2%) spIP23861POTD_ECOLI SPERMIDINE/PUTRESCINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (SPBP) pIIID40840 spermidine/putrescine-binding protein precursor [validated] - Escherichia coli gb AAC37041.1 (M64519) transport protein [Escherichia coli] dbj BAA35943.1 (D90747) Spermidine/putrescine transport protein D [Escherichia coli] gb AAC74207.1 (AE000212) spermidine/putrescine periplasmic transport protein [Escherichia coli K12] Length = 348</p>
SeqID 489	SA-1362.1	Contig99 (9364-10140 p)	55	<p>Identities = 97/249 (38%), Positives = 159/249 (62%), Gaps = 3/249 (1%) pIIIG70179 spermidine/putrescine ABC transporter, permease protein (potC) homolog - Lyme disease spirochete gb AAB91527.1 (AE001165) spermidine/putrescine ABC transporter, permease protein (potC) [Borrelia burgdorferi] Length = 263</p>
SeqID 490	SA-1363.1	Contig99 (8573-9387 p)	56	<p>Identities = 90/255 (35%), Positives = 153/255 (59%), Gaps = 11/255 (4%) spIP45170POTB_HAEIN SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTB pIIIA64118 spermidine/putrescine transport system permease potb - Haemophilus influenzae (strain Rd KW20) gb AAC22950.1 (U32813) spermidine/putrescine ABC transporter, permease protein (potB) [Haemophilus influenzae Rd] Length = 286</p>
SeqID 491	SA-1364.1	Contig99 (7435-8589 p)	62	<p>Identities = 165/345 (47%), Positives = 240/345 (68%), Gaps = 1/345 (0%) pIIIA70180 spermidine/putrescine ABC transporter, ATP-binding protein (potA) homolog - Lyme disease spirochete gb AAB91525.1 (AE001165) spermidine/putrescine ABC transporter, ATP-binding protein (potA) [Borrelia burgdorferi] Length = 347</p>

SeqID 492	SA-1365.1	Contig99 (5484-7385 p)	53	<p>Identities = 119/286 (41%), Positives = 166/286 (57%), Gaps = 1/286 (0%) dbj BA006283.1 (AP001515) UDP-N-acetylglucosamine reductase [Bacillus halodurans] Length = 301</p> <p>Identities = 65/131 (49%), Positives = 86/131 (65%) sp P29252 HPPK_BACSU 2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (7,8-DIHYDRO-6-HYDROXYMETHYLPTERIN-PYROPHOSPHOKINASE) (HPPK) (6-HYDROXYMETHYL-7,8-DIHYDROPTERIN PYROPHOSPHOKINASE) (PPPK) p IJS68109 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3) - Bacillus subtilis dbj BAA05314.1 (D26185) 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase [Bacillus subtilis] emb CAB11855.1 (Z99104) 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase [Bacillus subtilis] Length = 167</p>
SeqID 493	SA-1365.1	Contig99 (5852-6340 p)	50	
SeqID 494	SA-1367.1	Contig99 (5493-5855 p)	70	<p>Identities = 72/119 (60%), Positives = 90/119 (75%) sp O33725 FOLB_STRPY DIHYDRONEOPTERIN ALDOLASE (DHNA) emb CAA04239.1 (AJ000685) dihydroneopterin aldolase [Streptococcus pyogenes] Length = 119</p>
SeqID 495	SA-1368.1	Contig99 (4688-5491 p)	83	<p>Identities = 182/287 (63%), Positives = 224/287 (78%), Gaps = 1/287 (0%) emb CAA04242.1 (AJ000686) dihydropteroate synthase [Streptococcus pyogenes] Length = 266</p>
SeqID 496	SA-137.1	Contig138 (91179-92312 p)	59	<p>Identities = 154/382 (40%), Positives = 224/382 (58%), Gaps = 19/382 (4%) p I A69774 integrate homolog ydcL - Bacillus subtilis dbj BAA19318.1 (AB001468) PROBABLY INTEGRASE. [Bacillus subtilis] emb CAB12287.1 (Z99106) similar to integrate [Bacillus subtilis] Length = 368</p>

SeqID 492	SA-1365.1	Contig99 (6484-7386 p)	53	<p>Identities = 119/286 (41%), Positives = 165/286 (57%), Gaps = 1/286 (0%) dbj BAB06283.1 (AP001515) UDP-N-acetylglucosamine reductase [Bacillus halodurans] Length = 301</p> <p>Identities = 65/131 (49%), Positives = 86/131 (65%) sp P29252 HPPK_BACSU.2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (7,8-DIHYDRO-6-HYDROXYMETHYLPTERIN-PYROPHOSPHOKINASE) (HPPK) (6-HYDROXYMETHYL-7,8-DIHYDROPTERIN PYROPHOSPHOKINASE) (PPPK) piri S66109.2-amino-4-hydroxy-6-hydroxymethylhydrotetrine pyrophosphokinase (EC 2.7.6.3) - Bacillus subtilis dbj BA005314.1 (D26185) 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase [Bacillus subtilis] emb CAB11855.1 (Z99104) 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase [Bacillus subtilis] Length = 167</p>
SeqID 493	SA-1366.1	Contig99 (5852-6340 p)	50	
SeqID 494	SA-1367.1	Contig99 (5493-5855 p)	70	<p>Identities = 72/119 (60%), Positives = 90/119 (75%) sp O33725 FOLB_STRPY.DIHYDRONEOPTERIN ALDOLASE (DHNA) emb CAA04239.1 (AJ000685) dihydroneopterin aldolase [Streptococcus pyogenes] Length = 119</p>
SeqID 495	SA-1368.1	Contig99 (4688-5491 p)	83	<p>Identities = 182/267 (68%), Positives = 224/267 (83%), Gaps = 1/267 (0%) emb CAA04242.1 (AJ000686) dihydropyruvate synthase [Streptococcus pyogenes] Length = 266</p>
SeqID 496	SA-137.1	Contig138 (91179-92312 p)	59	<p>Identities = 154/382 (40%), Positives = 224/382 (58%), Gaps = 19/382 (4%) piri A69774 integrate homolog ycdL - Bacillus subtilis dbj BAA19318.1 (AB001488) PROBABLE INTEGRASE. [Bacillus subtilis] emb CAB12287.1 (Z99106) similar to integrase [Bacillus subtilis] Length = 388</p>

SeqID 487	SA-1370.1	Contig99 (4121-4684 p)	87	<p>Identities = 148/184 (80%), Positives = 168/184 (90%) spO33729[GCH1_STRPY GTP CYCLOHYDROLASE] (GTP-CH1) emb CAA04237.1 (AJ000685) GTP cyclohydrolase [Streptococcus pyogenes] Length = 194</p>
SeqID 488	SA-1371.1	Contig99 (2840-4102 p)	57	<p>Identities = 154/426 (36%), Positives = 245/426 (57%), Gaps = 17/426 (3%) sp Q65865 FOLC_BACSU FOLYL POLYGLUTAMATE SYNTHASE (FOLYL POLY-GAMMA-GLUTAMATE SYNTHETASE) (FPG) p JBA0646 oly-polyglutamate synthetase fblC - Bacillus subtilis gb AA85021.1 (L04520) folyl-polyglutamate synthetase [Bacillus subtilis] emb CAB14768.1 (Z99118) folyl-polyglutamate synthetase [Bacillus subtilis] Length = 430</p>
SeqID 499	SA-1372.1	Contig99 (1951-2638 p)	63	<p>Identities = 110/295 (37%), Positives = 188/295 (63%), Gaps = 6/295 (2%) dbj BAB07585.1 (AP001520) unknown conserved protein [Bacillus halodurans] Length = 308</p>
SeqID 500	SA-1373.2	Contig99 (1098-1964 p)	79	<p>Identities = 188/289 (65%), Positives = 232/289 (80%), Gaps = 1/289 (0%) sp P72535 KHSE_STRPN HOMOSERINE KINASE (HK) gb AAC44297.1 (U41735) homoserine kinase homolog [Streptococcus pneumoniae] Length = 289</p>
SeqID 501	SA-1374.2	Contig99 (2-1096 p)	71	<p>Identities = 187/368 (50%), Positives = 261/368 (70%), Gaps = 11/368 (2%) sp P52985 DHOM_LACLA HOMOSERINE DEHYDROGENASE (HDH) p JJC6049 homoserine dehydrogenase (EC 1.1.1.3) - Lactococcus lactis emb CAA65713.1 (X96988) hom [Lactococcus lactis] Length = 428</p>
SeqID 502	SA-1377.1	Contig134 (51276-52901 p)	59	<p>Identities = 210/541 (38%), Positives = 328/541 (59%), Gaps = 1/541 (2%) dbj BAB04286.1 (AP001509) nickel transport system (nickel-binding protein) [Bacillus halodurans] Length = 539</p>

SeqID 503	SA-1378.1	Contig134 (52888-53832 p)	55	<p>Identities = 121/304 (39%), Positives = 176/304 (57%) dbj BAB04287.1 (AP001509) nickel transport system (permease) [Bacillus halodurans] Length = 314</p>
SeqID 504	SA-1379.1	Contig134 (53871-54638 p)	58	<p>Identities = 106/255 (41%), Positives = 164/255 (63%) dbj BAB04288.1 (AP001509) nickel transport system (permease) [Bacillus halodurans] Length = 277</p>
SeqID 505	SA-138.1	Contig138 (90969-91175 p)	No Hits found	
SeqID 506	SA-1380.1	Contig134 (54614-55414 p)	57	<p>Identities = 85/253 (33%), Positives = 154/253 (60%) Gaps = 2/253 (0%) gbl AAE73561.1 (AE002315) peptide ABC transporter, ATP-binding protein [Chlamydia muridarum] Length = 281</p>
SeqID 507	SA-1381.1	Contig134 (55401-56081 p)	55	<p>Identities = 81/199 (40%), Positives = 131/199 (65%), Gaps = 2/199 (1%) dbj BAB05797.1 (AP001514) oligopeptide ABC transporter (ATP-binding protein) [Bacillus halodurans] Length = 244</p>
SeqID 508	SA-1382.1	Contig134 (56202-56930 p)	76	<p>Identities = 143/238 (60%), Positives = 193/238 (81%) sp O31749 PYRH_BACSU URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) pif F69708 uridylate kinase smba - Bacillus subtilis emb CAB13524.1 (Z99112) uridylate kinase [Bacillus subtilis] Length = 240</p>
SeqID 509	SA-1383.1	Contig134 (56946-57503 p)	78	<p>Identities = 112/185 (60%), Positives = 149/185 (80%) dbj BAB06143.1 (AP001515) ribosome recycling factor [Bacillus halodurans] Length = 185</p>
SeqID 510	SA-1384.1	Contig134 (57621-58475 p)	49	<p>Identities = 107/269 (39%), Positives = 155/269 (56%) Gaps = 6/269 (2%) pif F69840 hypothetical protein yitL - Bacillus subtilis emb CAB12943.1 (Z99109) yitL [Bacillus subtilis] Length = 298</p>
SeqID 511	SA-1385.1	Contig134 (58601-59122 p)	67	<p>Identities = 102/175 (58%), Positives = 127/175 (72%), Gaps = 2/175 (1%) dbj BAB05167.1 (AP001512) peptide methionine sulfoxide reductase [Bacillus halodurans] Length = 179</p>

SeqID 512	SA-1386.1	Contig134 (59143-59334 p)	50	<p>Identities = 24/66 (36%), Positives = 42/66 (63%) pti A69931 hypothetical protein yocE - Bacillus subtilis emb CAB13859.1 (Z99114) yocE [Bacillus subtilis] Length = 74</p> <p>Identities = 47/2590 (80%), Positives = 535/550 (90%) gb AAAS1870.1 (U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes] Length = 590</p>
SeqID 513	SA-1388.1	Contig134 (59492-61264 p)	89	<p>Identities = 191/305 (62%), Positives = 241/305 (78%), Gaps = 1/305 (0%) sp P46343 PHOL_BACSU PHOH-LIKE PROTEIN pti E69576 phosphate starvation-induced protein phoH - Bacillus subtilis db BAA12477.1 (D84432) YqfE [Bacillus subtilis] emb CAB14476.1 (Z99117) phosphate starvation-induced protein [Bacillus subtilis] Length = 319</p>
SeqID 514	SA-1389.1	Contig134 (61388-62374 p)	65	
SeqID 515	SA-1390.2	Contig134 (62465-63288 m)	25	<p>Identities = 42/161 (25%), Positives = 72/161 (44%), Gaps = 19/161 (11%) gb AAC95491.1 (U73025) unknown [Staphylococcus aureus] gb AAG42230.1 (AF299292_4 (AF299292) ORFX [Staphylococcus intermedius] Length = 289</p>
SeqID 516	SA-1391.2	Contig133 (46310-47965 m)	56	<p>Identities = 176/589 (29%), Positives = 315/589 (52%), Gaps = 47/589 (7%) dbj BAB06875.1 (AP001517) two-component sensor histidine kinase involved in phosphate regulation [Bacillus halodurans] Length = 589</p>
SeqID 517	SA-1392.1	Contig133 (47958-48635 m)	59	<p>Identities = 98/224 (43%), Positives = 138/224 (60%), Gaps = 2/224 (0%) sp P45606 PHOB_SHIDY PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB pti A44753 phoB protein - Shigella dysenteriae db AA426535.1 (M31793) phosphate regulatory protein phoB [Shigella dysenteriae] Length = 229</p>

SeqID 518	SA-1393.1	Contig133 (48635-49291 m)	51	<p>Identities = 66/213 (30%), Positives = 119/213 (54%), Gaps = 4/213 (1%) sp Q51547 PHOU_PSEAE PHOSPHATE TRANSPORT SYSTEM PROTEIN PHOU prf S65576 negative regulator Phou - Pseudomonas aeruginosa prf S68596 negative regulator Phou - Pseudomonas aeruginosa prf H82975 phosphate uptake regulatory protein Phou PA5365 [imported] - Pseudomonas aeruginosa (strain PAO1) db BAA08138.1 (D45195) a negative regulator of the iron regulon [Pseudomonas aeruginosa] gb AA008750.1 AE004948.6 (AE004948) phosphate uptake regulatory protein Phou [Pseudomonas aeruginosa] Length = 242</p>
SeqID 519	SA-1394.1	Contig133 (49288-50037 m)	82	<p>Identities = 166/245 (67%), Positives = 211/245 (85%), Gaps = 1/245 (0%) gb AAD22041.1 (AF118229) ATP-binding cassette protein PstB [Streptococcus pneumoniae] Length = 250</p>
SeqID 520	SA-1395.1	Contig133 (50030-50908 m)	66	<p>Identities = 135/263 (51%), Positives = 203/263 (76%) gb AAD22040.1 (AF118229) transmembrane protein PstA [Streptococcus pneumoniae] Length = 271</p>
SeqID 521	SA-1396.1	Contig133 (50910-51755 m)	74	<p>Identities = 162/266 (60%), Positives = 212/266 (78%), Gaps = 3/266 (1%) gb AAD22039.1 (AF118229) transmembrane protein PstC [Streptococcus pneumoniae] Length = 271</p>
SeqID 522	SA-1398.2	Contig133 (52368-52664 p)	No Hits found	
SeqID 523	SA-1399.1	Contig133 (51770-52651 m)	77	<p>Identities = 230/230 (100%), Positives = 230/230 (100%) prf A61607 probable hemolysin precursor - Streptococcus agalactiae (strain 74-360) Length = 230</p>
SeqID 524	SA-14.1	Contig137 (32042-32473 p)	32	<p>Identities = 31/118 (26%), Positives = 51/118 (42%), Gaps = 3/118 (2%) prf S67490 single-stranded DNA-binding protein - Eubacterium sp. gb AA09866.1 (U12515) single-stranded DNA binding protein [uncultured eubacterium] prf 2108276A ssDNA-binding protein [Rattus norvegicus] Length = 181</p>

SeqID 525	SA-140.1	Contig138 (90097-90963 p)	47	Identities = 86/278 (30%), Positives = 137/278 (48%), Gaps = 36/278 (12%) dbj BAA07788.1 (D43692) rep protein [Brevibacillus borstelensis] Length = 281
SeqID 526	SA-1400.1	Contig133 (52862-53439 m)	No Hits found	Identities = 119/250 (47%), Positives = 149/250 (59%), Gaps = 9/250 (3%) dbj BAA05069.1 (AP001511) unknown conserved protein [Bacillus halodurans] Length = 250
SeqID 527	SA-1401.1	Contig133 (53436-54176 m)	58	Identities = 138/309 (44%), Positives = 193/309 (61%), Gaps = 5/309 (1%) pir J143740 probable ribosomal protein L11 methyltransferase (EC 2.1.1.-) [imported] - Listeria monocytogenes dbj BAA82791.1 (AB023064) orf35 [Listeria monocytogenes] Length = 314
SeqID 528	SA-1403.1	Contig133 (54176-55129 m)	59	
SeqID 529	SA-1404.1	Contig133 (55126-55434 m)	No Hits found	Identities = 87/246 (35%), Positives = 140/246 (56%), Gaps = 13/246 (5%) pir C69661 transcription activator of multidrug-efflux transporter genes mta - Bacillus subtilis emb CAA6863.1 (Y08559) Unknown [Bacillus subtilis] emb CAB15677.1 (Z99122) transcriptional regulator [Bacillus subtilis] Length = 257
SeqID 530	SA-1405.1	Contig133 (55708-56424 p)	57	
SeqID 531	SA-1406.1	Contig133 (56463-56933 m)	36	Identities = 38/136 (27%), Positives = 60/136 (43%), Gaps = 3/136 (2%) sp P54444 YRK_N_BACSU HYPOTHETICAL 21.3 KD PROTEIN IN BLTR-SPOILIC INTERGENIC REGION pir J08977 hypothetical protein yrkN - Bacillus subtilis dbj BAA12369.1 (D84432) YrkN [Bacillus subtilis] emb CAB14586.1 (Z59117) yrkN [Bacillus subtilis] Length = 185
SeqID 532	SA-1407.1	Contig133 (56905-57363 m)	52	Identities = 57/131 (43%), Positives = 82/131 (62%) pir F83247 hypothetical protein PA3180 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA06568.1 (AE004742_4) (AE004742) hypothetical protein [Pseudomonas aeruginosa] Length = 145
SeqID 533	SA-1408.1	Contig133 (57350-57496 m)	No Hits found	
SeqID 534	SA-141.1	Contig138 (89680-89994 p)	No Hits found	

SeqID 535	SA-1410.1	Contig133 (57499-57969 m)	No Hits found	
SeqID 536	SA-1413.1	Contig97 (10056-12434 p)	61	Identities = 360/785 (45%), Positives = 498/785 (62%), Gaps = 15/785 (1%) pir S76896 hypothetical protein - <i>Synechocystis</i> sp. (strain PCC 6803) dbj BAA18808.1 (D90917) hypothetical protein [<i>Synechocystis</i> sp.] Length = 821
SeqID 537	SA-1414.1	Contig97 (8875-9866 p)	73	Identities = 211/363 (58%), Positives = 270/363 (74%), Gaps = 9/363 (2%) sp P39300 YJFR_ECOLI_HYPOTHETICAL_40.1 KD PROTEIN IN AIDB-SGAT INTERGENIC REGION Length = 354
SeqID 538	SA-1415.1	Contig97 (6879-8558 p)	41	Identities = 136/511 (26%), Positives = 234/511 (45%), Gaps = 29/511 (5%) dbj BAB03939.1 (AP001507) unknown conserved protein [<i>Bacillus halodurans</i>] Length = 701
SeqID 539	SA-1416.1	Contig97 (6052-6813 p)	39	Identities = 58/235 (24%), Positives = 104/235 (43%), Gaps = 9/235 (3%) pir C83362 hypothetical protein PA2260 [imported] - <i>Pseudomonas aeruginosa</i> (strain PAO1) gb AAG05648.1 AE004652.1 (AE004652) hypothetical protein [<i>Pseudomonas aeruginosa</i>] Length = 260
SeqID 540	SA-1417.1	Contig97 (5766-6032 p)	40	Identities = 28/89 (31%), Positives = 44/89 (48%), Gaps = 3/89 (3%) sp P44991 LYXK_HAEIN_PROBABLE_L-XYLULOSE KINASE (L-XYLULOKINASE) pir JH64164 hypothetical protein H1027 - <i>Haemophilus influenzae</i> (strain Rd KW20) gb AAC22687.1 (U32783) L-xylose kinase (lyx) [<i>Haemophilus influenzae</i> Rd] Length = 485
SeqID 541	SA-1418.1	Contig97 (4513-5727 p)	48	Identities = 126/393 (32%), Positives = 212/393 (53%), Gaps = 16/393 (4%) sp P37677 LYXK_ECOLI_CRYPTIC_L-XYLULOSE KINASE (L-XYLULOKINASE) pir J47801 L-xylokinase (EC 2.7.1.53) - <i>Escherichia coli</i> gb AAB18557.1 (U00039) No definition line found [<i>Escherichia coli</i>] gb AAC76604.1 (AE000435) L-xyloose kinase, cryptic [<i>Escherichia coli</i> K12] Length = 488
SeqID 542	SA-1419.1	Contig97 (3458-4447 p)	No Hits found	

SeqID 543	SA-1421.1	Contig97 (1985-3436 p)	40	Identities = 106/402 (26%), Positives = 196/402 (48%), Gaps = 15/402 (3%) dbj BAAY75340.1 (AB011837) PTS system galactitol-specific enzyme IIC component [Bacillus halodurans] dbj BA001507.1 (AP001507) PTS system, galactitol-specific enzyme II, C component [Bacillus halodurans] Length = 419
SeqID 544	SA-1424.1	Contig97 (831-1887 p)	59	Identities = 123/326 (37%), Positives = 193/326 (58%), Gaps = 8/326 (2%) pir B75057 glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay) emb CA850351.1 (A0248287) GLYCERATE DEHYDROGENASE [Pyrococcus abyssi] Length = 335
SeqID 545	SA-1425.1	Contig97 (1-912 p)	No Hits found	
SeqID 546	SA-1427.1	Contig115 (8540-9379 p)	57	Identities = 101/275 (36%), Positives = 165/275 (59%), Gaps = 22/275 (8%) gb AAD50462.1 (AF169967) BacA [Flavobacterium johnsoniae] Length = 265
SeqID 547	SA-1429.1	Contig115 (9499-10254 p)	80	Identities = 188/248 (67%), Positives = 205/248 (81%), Gaps = 9/248 (3%) dbj BA482113.1 (AB022909) negative regulator of genetic competence [Streptococcus mutans] Length = 240
SeqID 548	SA-143.1	Contig138 (88238-89581 p)	40	Identities = 103/460 (22%), Positives = 191/460 (41%), Gaps = 72/460 (15%) pir JF69774 hypothetical protein ydcQ [imported] - Bacillus subtilis dbj BA18323.1 (AB001488) SIMILAR TO ORF21 OF ENTEROCOCCUS FAECALIS TRANSPOSON TN916 [Bacillus subtilis] emb CAB12293.1 (Z99106) similar to transposon protein [Bacillus subtilis] Length = 480
SeqID 549	SA-1430.1	Contig115 (10400-11416 p)	80	Identities = 267/382 (69%), Positives = 317/382 (82%) dbj BA482114.1 (AB022909) RgpG [Streptococcus mutans] Length = 388

SeqID 543	SA-1421.1	Contig97 (1985-3436 p)	40	<p>Identities = 106/402 (26%), Positives = 196/402 (48%), Gaps = 15/402 (3%) dbj BAA75340.1 (AB011837) PTS system galactitol-specific enzyme IIC component [Bacillus halodurans]</p> <p>dbj BAB03908.1 (AP001507) PTS system, galactitol-specific enzyme II, C component [Bacillus halodurans]</p> <p>Length = 419</p>
SeqID 544	SA-1424.1	Contig97 (931-1887 p)	59	<p>Identities = 123/326 (37%), Positives = 193/326 (58%), Gaps = 8/326 (2%) pir J575057 glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay) emb CAB50351.1 (AJ248287) GLYCERATE DEHYDROGENASE [Pyrococcus abyssi]</p> <p>Length = 335</p>
SeqID 545	SA-1425.1	Contig97 (1-912 p)	No Hits found	
SeqID 546	SA-1427.1	Contig115 (8540-9379 p)	57	<p>Identities = 101/275 (36%), Positives = 165/275 (59%), Gaps = 22/275 (8%) gb AAD50462.1 (AF169967) BacA [Flavobacterium johnsoniae]</p> <p>Length = 265</p>
SeqID 547	SA-1429.1	Contig115 (9499-10254 p)	80	<p>Identities = 168/248 (67%), Positives = 205/248 (81%), Gaps = 9/248 (3%) dbj BAA82113.1 (AB022909) negative regulator of genetic competence [Streptococcus mutans]</p> <p>Length = 240</p>
SeqID 548	SA-143.1	Contig138 (88238-89581 p)	40	<p>Identities = 103/460 (22%), Positives = 191/460 (41%), Gaps = 72/460 (15%) pir JF69774 hypothetical protein ydcQ [imported] - Bacillus subtilis dbj BAA19323.1 (AB001488) SIMILAR TO ORF21 OF ENTEROCOCCUS FAECALIS TRANSPOSON TN916, [Bacillus subtilis] emb CAB12293.1 (Z99106) similar to transposon protein [Bacillus subtilis]</p> <p>Length = 480</p>
SeqID 549	SA-1430.1	Contig115 (10400-11416 p)	80	<p>Identities = 267/382 (69%), Positives = 317/382 (82%) dbj BAA82114.1 (AB022909) RgpG [Streptococcus mutans]</p> <p>Length = 388</p>

SeqID 550	SA-1431.1	Contig1115 (11581-12351 p)	77	<p>Identities = 180/250 (72%), Positives = 212/250 (84%) sp P00866 V296_BACSU VEGETATIVE PROTEIN 296 (VEG296) pir JF70019 ABC transporter (ATP-binding protein) homolog yurY - Bacillus subtilis emb CAB15260.1 (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 261</p>
SeqID 551	SA-1432.1	Contig1115 (12388-13650 p)	62	<p>Identities = 174/435 (40%), Positives = 269/435 (61%), Gaps = 15/435 (3%) db BAB07189.1 (AF001518) unknown conserved protein [Bacillus halodurans] Length = 435</p>
SeqID 552	SA-1433.1	Contig1115 (13652-14884 p)	74	<p>Identities = 241/400 (60%), Positives = 308/400 (76%), Gaps = 5/400 (1%) pir JF70019 nifs protein homolog yurW - Bacillus subtilis emb CAB15258.1 (Z99120) similar to Nifs protein homolog [Bacillus subtilis] Length = 406</p>
SeqID 553	SA-1434.1	Contig1115 (14871-15314 p)	58	<p>Identities = 72/139 (51%), Positives = 92/139 (65%) sp O32163 NIFU_BACSU NIFU-LIKE PROTEIN pir JF70019 nitrogen fixation protein nifu homolog yurV - Bacillus subtilis emb CAB15257.1 (Z99120) similar to Nifu protein homolog [Bacillus subtilis] Length = 147</p>
SeqID 554	SA-1435.1	Contig1115 (15414-16832 p)	79	<p>Identities = 315/459 (68%), Positives = 385/459 (83%) pir D70019 conserved hypothetical protein yurU - Bacillus subtilis emb CAB15256.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] Length = 465</p>
SeqID 555	SA-1436.1	Contig1115 (16904-18031 m)	45	<p>Identities = 117/333 (35%), Positives = 187/333 (56%), Gaps = 8/333 (2%) emb CAA60586.1 (X87105) penicillin binding protein 4 [Staphylococcus aureus] emb CAA60582.1 (X87104) penicillin binding protein 4 [Staphylococcus aureus] Length = 431</p>
SeqID 556	SA-1437.2	Contig1115 (18244-19479 m)	71	<p>Identities = 203/415 (48%), Positives = 300/415 (71%), Gaps = 6/415 (1%) emb CAA67776.1 (X99400) D,D-carboxypeptidase [Streptococcus pneumoniae] Length = 413</p>

SeqID 557	SA-1438.2	Contig139 (86184-86444 m)	71	Identities = 61/81 (75%), Positives = 71/81 (87%), Gaps = 1/81 (1%) gbl AAAF80389.1 AF160251_3 (AF160251) ribosomal protein L31 [Listeria innocua] Length = 81
SeqID 558	SA-1439.1	Contig139 (84551-86071 p)	61	Identities = 257/429 (59%), Positives = 312/429 (71%), Gaps = 7/429 (1%) pir T46756 Zn-binding lipoprotein adCA [imported] - Streptococcus pneumoniae (fragment) emb CAA96185.1 (271552) AdcA protein [Streptococcus pneumoniae] Length = 423
SeqID 559	SA-1441.1	Contig138 (87835-88260 p)	No Hits found	
SeqID 560	SA-1440.1	Contig139 (83012-84409 p)	65	Identities = 218/473 (46%), Positives = 310/473 (65%), Gaps = 14/473 (2%) emb CAA86210.1 (Z38063) dipeptidase [Lactobacillus helveticus] Length = 474
SeqID 561	SA-1441.1	Contig139 (82086-82997 p)	82	Identities = 209/303 (68%), Positives = 260/303 (84%) emb CAB96619.1 (AJ400630) hypothetical protein [Streptococcus pneumoniae bacteriophage MM1] emb CAB96622.1 (AJ400631) hypothetical protein [Streptococcus pneumoniae] Length = 303
SeqID 562	SA-1442.2	Contig139 (81115-82089 p)	86	Identities = 254/321 (79%), Positives = 286/321 (88%), Gaps = 1/321 (0%) emb CAB96620.1 (AJ400630) hypothetical protein [Streptococcus pneumoniae bacteriophage MM1] emb CAB96623.1 (AJ400631) hypothetical protein [Streptococcus pneumoniae] Length = 325
SeqID 563	SA-1445.2	Contig139 (80228-81118 p)	68	Identities = 165/291 (56%), Positives = 208/291 (70%), Gaps = 2/291 (0%) sp Q08973 YVCJ_BACSU HYPOTHETICAL 33.9 KD PROTEIN IN CRH-TRXB INTERGENIC REGION pir H70031 conserved hypothetical protein ywcJ - Bacillus subtilis emb CAB08057.1 (Z94043) hypothetical protein [Bacillus subtilis] emb CAB15482.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] Length = 295

SeqID 557	SA-1438.2	Contig139 (86184-86444 m)	71	Identities = 61/81 (75%), Positives = 71/81 (87%), Gaps = 1/81 (1%) gb AAAF80398.1 AF160251.3 (AF160251) ribosomal protein L31 [Listeria innocua] Length = 81
SeqID 558	SA-1439.1	Contig139 (84551-86071 p)	61	Identities = 257/429 (59%), Positives = 312/429 (71%), Gaps = 7/429 (1%) pir T46756 Zn-binding lipoprotein adCA [imported] - Streptococcus pneumoniae (fragment) emb CAA496185.1 (271552) AdCA protein [Streptococcus pneumoniae] Length = 423
SeqID 559	SA-144.1	Contig138 (87835-88260 p)	No Hits found	
SeqID 560	SA-1440.1	Contig139 (83012-84409 p)	65	Identities = 218/473 (46%), Positives = 310/473 (65%), Gaps = 14/473 (2%) emb CAA486210.1 (Z38063) dipeptidase [Lactobacillus helveticus] Length = 474
SeqID 561	SA-1441.1	Contig139 (82086-82997 p)	82	Identities = 209/303 (68%), Positives = 260/303 (84%) emb CAB96619.1 (AJ400630) hypothetical protein [Streptococcus pneumoniae bacteriophage MM1] emb CAB96622.1 (AJ400631) hypothetical protein [Streptococcus pneumoniae] Length = 303
SeqID 562	SA-1442.2	Contig139 (81115-82089 p)	86	Identities = 254/321 (79%), Positives = 286/321 (88%), Gaps = 1/321 (0%) emb CAB96620.1 (AJ400630) hypothetical protein [Streptococcus pneumoniae bacteriophage MM1] emb CAB96623.1 (AJ400631) hypothetical protein [Streptococcus pneumoniae] Length = 325
SeqID 563	SA-1445.2	Contig139 (80228-81118 p)	68	Identities = 165/291 (56%), Positives = 208/291 (70%), Gaps = 2/291 (0%) sp O08973 YVCJ_BACSU HYPOTHETICAL 33.9 KD PROTEIN IN CRH-TRXB INTERGENIC REGION pir H70031 conserved hypothetical protein yycJ - Bacillus subtilis emb CAB08057.1 (Z94043) hypothetical protein [Bacillus subtilis] emb CAB16482.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] Length = 295

SeqID 564	SA-1446.1	Contig139 (79661-80074 m)	36	Identities = 36/134 (26%), Positives = 57/134 (41%), Gaps = 7/134 (5%) emb CAB62728.1 (AL133423) hypothetical protein SC4A7_24c [Streptomyces coelicolor A3(2)] Length = 139
SeqID 565	SA-1447.1	Contig139 (78432-79415 m)	46	Identities = 97/305 (31%), Positives = 160/305 (51%), Gaps = 10/305 (3%) sp P33022 YEIK_ECOLI HYPOTHETICAL 33.7 KD PROTEIN IN NFO-FRUA INTERGENIC REGION. pir A64985 hypothetical 33.7 KD protein in nfo-frua intergenic region - Escherichia coli (strain K-12) gb AA60514.1 (U00007) yeik [Escherichia coli] gb AAC75223.1 (AE000305) orf. hypothetical protein [Escherichia coli K12] prf 2014253BH yeik gene [Escherichia coli] Length = 313
SeqID 566	SA-1448.1	Contig139 (77878-78435 m)	38	Identities = 39/135 (28%), Positives = 72/135 (52%), Gaps = 4/135 (2%) ref NP_053012.1 hypothetical protein [Plasmid pNZ4000] gb AAD40355.1 (AF036485) hypothetical protein [Plasmid pNZ4000] Length = 200
SeqID 567	SA-1449.1	Contig139 (78492-77638 p)	69	Identities = 252/442 (57%), Positives = 316/442 (71%), Gaps = 15/442 (3%) dbj BAB05415.1 (AP001512) asparaginyl-RNA synthetase [Bacillus halodurans] Length = 430
SeqID 568	SA-145.1	Contig138 (87488-87769 p)	No Hits found	
SeqID 569	SA-1450.1	Contig139 (75278-76471 p)	75	Identities = 270/391 (69%), Positives = 314/391 (80%) gbl AAAF12702.1 (AF035157) aspartate aminotransferase [Lactococcus lactis] Length = 393
SeqID 570	SA-1451.1	Contig139 (72727-75192 p)	47	Identities = 145/1927 (7%), Positives = 398/1927 (42%), Gaps = 145/1927 (15%) dbj BAB05410.1 (AP001512) ATP-dependent DNA helicase [Bacillus halodurans] Length = 942
SeqID 571	SA-1453.2	Contig139 (71813-72577 p)	69	Identities = 162/254 (63%), Positives = 188/254 (73%), Gaps = 2/254 (0%) gbl AAC48769.1 (U71200) acetoin reductase [Bos taurus] Length = 257

SeqID 572	SA-1456.1	Contig95 (12824-13120 m)	60	<p>Identities = 53/112 (47%), Positives = 78/112 (69%), Gaps = 1/112 (0%) gblAAC23746.1] (AF052209) competence protein [Streptococcus pneumoniae] Length = 266</p>
SeqID 573	SA-1457.1	Contig95 (10627-12858 p)	29	<p>Identities = 142/468 (30%), Positives = 220/468 (46%), Gaps = 62/468 (13%) pirJF82995 glutamate-cysteine ligase PA5203 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA088588.1 AE004933.4 (AE004933) glutamate-cysteine ligase [Pseudomonas aeruginosa] Length = 527</p>
SeqID 574	SA-1458.1	Contig95 (9882-10556 p)	64	<p>Identities = 107/223 (47%), Positives = 148/223 (65%), Gaps = 7/223 (3%) pirJH81283 helix-turn-helix containing protein Cj1387c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73814.1 (AL135078) helix-turn-helix containing protein [Campylobacter jejuni] Length = 218</p>
SeqID 575	SA-146.1	Contig138 (86863-87177 m)	No Hits found	
SeqID 576	SA-1460.1	Contig95 (8498-9520 m)	77	<p>Identities = 225/341 (65%), Positives = 279/341 (80%) pirJ A43577 regulatory protein pforR - Clostridium perfringens Length = 343</p>
SeqID 577	SA-1462.1	Contig95 (6835-8127 m)	87	<p>Identities = 320/427 (74%), Positives = 378/427 (87%) pirJ A42280 adenylosuccinate synthase (EC 6.3.4.4) purA - Bacillus subtilis dbj BAA05174.1 (D28185) adenylosuccinate synthetase [Bacillus subtilis] emb CAB16079.1 (Z99124) adenylosuccinate synthetase [Bacillus subtilis] Length = 430</p>
SeqID 578	SA-1463.1	Contig95 (6339-6812 p)	No Hits found	
SeqID 579	SA-1465.1	Contig95 (5563-6180 m)	No Hits found	
SeqID 580	SA-1466.1	Contig95 (3956-5395 m)	55	<p>Identities = 184/465 (39%), Positives = 279/465 (59%), Gaps = 25/465 (5%) spj39301 SGAT_ECOLI PUTATIVE TRANSPORT PROTEIN SGAT pirJ D65230 hypothetical 52.9 kD protein in aidB rpsF intergenic region - Escherichia coli (strain K-12) gb AAC77150.1 (AE000491) orf, hypothetical protein [Escherichia coli K12] Length = 484</p>

SeqID 581	SA-1467.1	Contig95 (3650-3928 m)	64	Identities = 42/95 (44%), Positives = 65/95 (68%), Gaps = 1/95 (1%) gblAAG34743.1 AE000033_7 (AE000033) similar to PTS system: EIB [Mycoplasma pneumoniae] Length = 95
SeqID 582	SA-1468.1	Contig95 (3098-3583 m)	58	Identities = 64/150 (42%), Positives = 97/150 (64%), Gaps = 2/150 (1%) spIP39303 PTXA_ECOLI UNKNOWN PENTITOL PHOSPHOTRANSFERASE ENZYME II, A COMPONENT pirJF55230 hypothetical phosphotransferase enzyme II - Escherichia coli (strain K-12) gblAAC77152.1 (AE000491) putative PTS system enzyme II A component [Escherichia coli K12] Length = 154
SeqID 583	SA-1469.1	Contig95 (2320-2985 m)	60	Identities = 108/217 (49%), Positives = 141/217 (64%), Gaps = 3/217 (1%) spIP39304 SGAH_ECOLI PROBABLE HEXULOSE-6-PHOSPHATE SYNTHASE (HUMPS) (D-ARABINO 3-HEXULOSE 6-PHOSPHATE FORMALDEHYDE LYASE) pirJS56421 hypothetical 23.6K protein (aidB-rpsF intergenic region) - Escherichia coli gblAA97092.1 (U14003) ORF_0216 [Escherichia coli] gblAAC77153.1 (AE000491) probable hexulose-6-phosphate synthase [Escherichia coli K12] Length = 216
SeqID 584	SA-147.1	Contig138 (85925-86402 m)	37	Identities = 42/153 (27%), Positives = 71/153 (45%), Gaps = 7/153 (4%) emb CAB76310.1 (AL156060) putative acetyltransferase. [Streptomyces coelicolor A3(2)] Length = 183
SeqID 585	SA-1470.1	Contig95 (1453-2316 m)	68	Identities = 147/285 (51%), Positives = 198/285 (68%), Gaps = 9/285 (3%) spIP39305 SGAU_ECOLI PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (HUMPI) pirJS56422 hypothetical 32K protein (aidB-rpsF intergenic region) - Escherichia coli gblAA97093.1 (U14003) ORF_0284 [Escherichia coli] gblAAC77154.1 (AE000491) putative hexulose-6-phosphate isomerase [Escherichia coli K12] Length = 284

SeqID 586	SA-1471.1	Contig95 (735-1451 m)	73	Identities = 143/229 (62%), Positives = 176/229 (76%), Gaps = 2/229 (0%) gb AAFD45716.1 AF160811_4 (AF160811) L-ribulose 5-phosphate 4-epimerase [Bacillus stearothermophilus] Length = 228
SeqID 587	SA-1472.1	Contig95 (77-724 m)	60	Identities = 124/214 (57%), Positives = 157/214 (72%) sp Q58370TAL_METJA_TRANSALDOLASE-LIKE PROTEIN pir H64419 transaldolase (EC 2.2.1.2) - Methanococcus jannaschii gb AAB98962.1 (U67539) transaldolase [Methanococcus jannaschii] Length = 217
SeqID 588	SA-1473.2	Contig94 (12280-12639 p)	No Hits found	
SeqID 589	SA-1474.1	Contig94 (11451-11573 m)	No Hits found	
SeqID 590	SA-1475.1	Contig94 (10797-11117 m)	No Hits found	
SeqID 591	SA-1477.1	Contig94 (9456-9902 m)	48	Identities = 59/185 (31%), Positives = 96/185 (51%), Gaps = 12/185 (6%) pir A82466 hypothetical protein VCA0380 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96286.1 (AE004374) hypothetical protein [Vibrio cholerae] Length = 201
SeqID 592	SA-1478.1	Contig94 (9817-9236 m)	62	Identities = 49/147 (33%), Positives = 98/147 (66%), Gaps = 2/147 (1%) pir A69849 hypothetical protein yjdf - Bacillus subtilis emb CAB13060.1 (Z99110) yjdf [Bacillus subtilis] Length = 160
SeqID 593	SA-1479.1	Contig94 (8138-8617 m)	58	Identities = 61/152 (40%), Positives = 95/152 (62%) gb AAD50427.1 AF161700.2 (AF161700) ComX1 [Streptococcus pneumoniae] gb AAD50428.1 AF161701.2 (AF161701) ComX2 [Streptococcus pneumoniae] Length = 159
SeqID 594	SA-148.1	Contig138 (85248-85790 m)	46	Identities = 55/175 (31%), Positives = 93/175 (52%), Gaps = 6/175 (3%) sp P05332 YP20_BACLI_HYPOTHETICAL P20 PROTEIN pir S00875 hypothetical protein P20 - Bacillus licheniformis emb CAA30415.1 (X07542) P20 (AA 1-178) [Bacillus licheniformis] Length = 178

SeqID 595	SA-1480.1	Contig94 (7324-8016 m)	41	<p>Identities = 57/226 (25%), Positives = 97/226 (42%), Gaps = 22/226 (9%) ref NP_014926.1 Yor283wp [Saccharomyces cerevisiae] pir S67185 hypothetical protein YOR283w - yeast (Saccharomyces cerevisiae) emb CAA61787.1 (X89633) hypothetical phosphoglycerate mutase [Saccharomyces cerevisiae] emb CAA99510.1 (Z75191) ORF YOR283w [Saccharomyces cerevisiae] Length = 230</p>
SeqID 596	SA-1481.1	Contig94 (6575-7249 m)	50	<p>Identities = 108/169 (63%), Positives = 139/169 (81%) gb AA000280.1 (U78599) putative D,D-carboxypeptidase [Streptococcus mutans] Length = 173</p>
SeqID 597	SA-1482.1	Contig94 (6003-6425 m)	48	<p>Identities = 65/153 (42%), Positives = 94/153 (60%), Gaps = 4/153 (2%) gb AA000279.1 (U78599) putative N-acetyl-muramidase [Streptococcus mutans] Length = 158</p>
SeqID 598	SA-1483.1	Contig94 (4826-5860 m)	80	<p>Identities = 233/344 (67%), Positives = 294/344 (84%) sp O06940 HRCA_STRIMU HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA Length = 344</p>
SeqID 599	SA-1484.1	Contig94 (4251-4784 m)	78	<p>Identities = 129/188 (68%), Positives = 153/188 (80%), Gaps = 2/188 (1%) pir S39341 grpE protein - Lactococcus lactis Length = 190</p>
SeqID 600	SA-1486.1	Contig94 (2241-4070 m)	97	<p>Identities = 609/609 (100%), Positives = 609/609 (100%) sp P95693 DNAK_STRAG DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70) gb AAB39219.1 (U72719) heat shock protein 70 [Streptococcus agalactiae] Length = 609</p>
SeqID 601	SA-1487.1	Contig94 (813-1952 m)	93	<p>Identities = 328/377 (87%), Positives = 356/377 (94%), Gaps = 1/377 (0%) db J BAB16032.1 (AB030809) Streptococcus pneumoniae DnaJ protein homologue [Streptococcus pyogenes] Length = 378</p>
SeqID 602	SA-1488.1	Contig94 (495-827 p)	No Hits found	
SeqID 603	SA-1489.1	Contig94 (1-522 p)	79	<p>Identities = 122/164 (74%), Positives = 138/164 (83%) sp O07211 ISCRK_STRIMU FRUCTOKINASE db J BA02467.1 (D13175) fructokinase [Streptococcus mutans] Length = 293</p>

SeqID 604	SA-149.1	Contig138 (84525-85205 m)	64	<p>Identities = 110/230 (47%), Positives = 154/230 (66%), Gaps = 3/230 (1%) ref NP_012308.1 Yr042cp [Saccharomyces cerevisiae] sp P40586 Y1W2_YEAST HYPOTHETICAL 27.4 KD PROTEIN IN HYR1 3 REGION pir J50347 hypothetical protein Yr042c - yeast (Saccharomyces cerevisiae) emb CAA87001.1 (Z46902) unknown [Saccharomyces cerevisiae] Length = 236</p>
SeqID 605	SA-1490.2	Contig134 (49677-50102 p)	82	<p>Identities = 118/139 (84%), Positives = 129/139 (91%) sp P36254 RL11_STACA 50S RIBOSOMAL PROTEIN L11 pir J53887 ribosomal protein L11 - Staphylococcus carnosus emb CAA53739.1 (X76134) L11 protein [Staphylococcus carnosus] Length = 140</p>
SeqID 606	SA-1491.1	Contig134 (48084-49466 p)	43	<p>Identities = 118/405 (29%), Positives = 199/405 (49%), Gaps = 9/405 (2%) pir JF70705 hypothetical protein RV2333c - Mycobacterium tuberculosis (strain H37RV) emb CAB02058.1 (Z79702) hypothetical protein RV2333c [Mycobacterium tuberculosis] Length = 537</p>
SeqID 607	SA-1492.1	Contig134 (46862-48076 p)	66	<p>Identities = 201/395 (50%), Positives = 274/395 (68%), Gaps = 5/395 (1%) gb AAAF36227.1 AF168363_2 (AF168363) aminoacylase [Lactococcus lactis] Length = 398</p>
SeqID 608	SA-1493.1	Contig134 (45698-46582 m)	40	<p>Identities = 72/259 (27%), Positives = 127/259 (48%), Gaps = 7/259 (2%) ref NP_043632.1 former trsE (rbcR homolog) [Odontella sinensis] sp P49518 YC30_ODOSI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YCF30 pir J57829 probable transcription regulator ycf30 - Odontella sinensis chloroplast emb CAA91684.1 (Z67753) former trsE (rbcR homolog) [Odontella sinensis] Length = 309</p>
SeqID 609	SA-1494.1	Contig134 (45284-45646 m)	No Hits found	

SeqID 604	SA-149.1	Contig138 (84525-85205 m)	64	<p>Identities = 110/230 (47%), Positives = 154/230 (66%), Gaps = 3/230 (1%) ref NP_012308.1 Yr042cp [Saccharomyces cerevisiae] sp P40586 YIW2_YEAST HYPOTHETICAL 27.4 KD PROTEIN IN HYR1 3 REGION pir S50347 hypothetical protein Yr042c - yeast [Saccharomyces cerevisiae] emb CAA87001.1 [Z46902] unknown [Saccharomyces cerevisiae] Length = 236</p>
SeqID 605	SA-1490.2	Contig134 (49877-50102 p)	82	<p>Identities = 118/139 (84%), Positives = 129/139 (91%) sp P36254 RL11_STACA 50S RIBOSOMAL PROTEIN L11 pir S38871 ribosomal protein L11 - Staphylococcus carnosus emb CAA53739.1 [X76134] L11 protein [Staphylococcus carnosus] Length = 140</p>
SeqID 606	SA-1491.1	Contig134 (48084-49466 p)	43	<p>Identities = 118/405 (29%), Positives = 199/405 (49%), Gaps = 9/405 (2%) pir F70705 hypothetical protein Rv2333c - Mycobacterium tuberculosis (strain H37RV) emb CAB02068.1 [Z79702] hypothetical protein Rv2333c [Mycobacterium tuberculosis] Length = 537</p>
SeqID 607	SA-1492.1	Contig134 (46862-48076 p)	66	<p>Identities = 201/395 (50%), Positives = 274/395 (68%), Gaps = 5/395 (1%) gb AAAF36227.1 AF168363_2 (AF168363) aminoacylase [Lactococcus lactis] Length = 398</p>
SeqID 608	SA-1493.1	Contig134 (45698-46582 m)	40	<p>Identities = 72/259 (27%), Positives = 127/259 (48%), Gaps = 7/259 (2%) ref NP_043632.1 former trsE (rbcR homolog) [Odontella sinensis] sp P49518 YC30_ODOS1 HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YCF30 pir J578291 probable transcription regulator ycf30 - Odontella sinensis chloroplast emb CAA91664.1 [Z67753] former trsE (rbcR homolog) [Odontella sinensis] Length = 309</p>
SeqID 609	SA-1494.1	Contig134 (45284-45846 m)	No Hits found	

SeqID 610	SA-1495.1	Contig134 (43540-45255 p)	56	Identities = 203/580 (35%), Positives = 325/580 (56%), Gaps = 50/580 (8%) pir E64556 para-aminobenzoate synthetase - Helicobacter pylori (strain 26695) gb AA070357.1 (AE000547) para-aminobenzoate synthetase (pabB) [Helicobacter pylori 26695] Length = 559
SeqID 611	SA-1498.1	Contig134 (41017-43458 p)	62	Identities = 353/828 (42%), Positives = 511/828 (61%), Gaps = 70/828 (8%) splP21458 SP3E BACSU STAGE III SPORULATION PROTEIN E pir S09411 DNA translocase spolIE - Bacillus subtilis emb CAB13553.1 (Z99112) DNA translocase [Bacillus subtilis] Length = 787
SeqID 612	SA-1499.1	Contig134 (40039-40842 m)	44	Identities = 88/224 (39%), Positives = 123/224 (54%), Gaps = 46/224 (20%) pir T41399 probable cyclophilin-related peptidyl prolyl cis-trans isomerase - (Schizosaccharomyces pombe) emb CAA19257.1 (AL023704) putative Cyclophilin-type peptidyl-prolyl cis-trans isomerase protein [Schizosaccharomyces pombe] Length = 610
SeqID 613	SA-15.1	Contig137 (29069-31870 p)	22	Identities = 152/405 (37%), Positives = 214/405 (52%), Gaps = 26/405 (6%) pir A43607 cell surface antigen SpaA precursor - Streptococcus sobrinus (strain MT3791) dbj BAA14368.1 (D90354) surface protein antigen precursor [Streptococcus sobrinus] Length = 1566
SeqID 614	SA-150.1	Contig138 (83318-84265 p)	No Hits found	
SeqID 615	SA-1500.1	Contig134 (39154-39987 p)	90	Identities = 224/275 (81%), Positives = 255/275 (92%) gb AAD56938.1 AF180520.3 (AF180520) Integral membrane protein MtsC [Streptococcus pyogenes] Length = 284
SeqID 616	SA-1501.1	Contig134 (38436-39152 p)	72	Identities = 143/238 (60%), Positives = 186/238 (78%), Gaps = 22/238 (9%) gb AAD56937.1 AF180520.2 (AF180520) ATP- binding protein MtsB [Streptococcus pyogenes] Length = 241

SeqID 617	SA-1502.2	Contig134 (37339-38265 p)	86	Identities = 240/308 (77%), Positives = 277/308 (89%), Gaps = 1/308 (0%) gb AAD56936.1 AF180520_1 (AF180520) lipoprotein MtsA [Streptococcus pyogenes] Length = 310
SeqID 618	SA-1503.2	Contig108 (5713-10425 m)	66	Identities = 795/1586 (49%), Positives = 1056/1586 (65%), Gaps = 39/1586 (2%) gb AAG09771.1 AF243528_1 (AF243528) cell envelope proteinase [Streptococcus thermophilus] Length = 1585
SeqID 619	SA-1504.1	Contig108 (4794-5480 m)	50	Identities = 87/220 (39%), Positives = 124/220 (55%), Gaps = 4/220 (1%) dbj BAB05663.1 AP001513) two-component response regulator [Bacillus halodurans] Length = 229
SeqID 620	SA-1506.1	Contig108 (3409-4865 m)	40	Identities = 108/379 (28%), Positives = 193/379 (50%), Gaps = 33/379 (8%) pir D70045 two-component sensor histidine kinase homolog yvqB - Bacillus subtilis emb CAB15292.1 (Z99120) similar to two-component sensor histidine kinase [YvqA] [Bacillus subtilis] emb CAA11751.1 (AJ223978) putative sensory protein kinase, YvqB [Bacillus subtilis] Length = 451
SeqID 621	SA-1507.1	Contig108 (2708-3334 m)	33	Identities = 38/144 (26%), Positives = 69/144 (47%), Gaps = 10/144 (6%) ref XP_005848.1 KIAA1074 protein [Homo sapiens] Length = 1709
SeqID 622	SA-1511.1	Contig138 (82830-83321 p)	42	Identities = 40/141 (27%), Positives = 75/141 (52%), Gaps = 3/141 (2%) dbj BAB05334.1 AP001512) RNA polymerase sigma factor Y [Bacillus halodurans] Length = 176
SeqID 623	SA-1511.1	Contig108 (120-2621 p)	78	Identities = 569/835 (68%), Positives = 666/835 (79%), Gaps = 42/835 (5%) sp P38430 SYL_BACSU LEUCYL-TRNA SYNTHETASE (LEUCINE-TRNA LIGASE) (LEURS) pir D99550 leucine-TRNA ligase (EC 6.1.1.4) - Bacillus subtilis gb AAC00259.1 (AF008220) leucine TRNA synthetase [Bacillus subtilis] emb CAB15010.1 (Z99119) leucyl-TRNA synthetase [Bacillus subtilis] Length = 804

SeqID 624	SA-1512.2	Contig138 (776-1330 m)	71	<p>Identities = 107/185 (57%), Positives = 140/185 (74%), Gaps = 3/185 (1%) emb CAB91549.1 (AJ249134) hypothetical protein [Lactococcus lactis] Length = 185</p> <p>Identities = 76/230 (33%), Positives = 118/230 (51%), Gaps = 11/230 (4%) sp P39147 CMF3_BACSU COMF OPERON PROTEIN 3 pir j140389 hypothetical protein F3 - Bacillus subtilis pir jS7621 late competence gene comFC - Bacillus subtilis emb CAA79228.1 (Z18629) F3 [Bacillus subtilis] gb AAC44942.1 (U56901) involved in transformation [Bacillus subtilis] emb CAB15562.1 (Z99122) late competence gene [Bacillus subtilis] Length = 229</p>
SeqID 625	SA-1513.1	Contig138 (1407-2072 m)	51	
SeqID 626	SA-1514.1	Contig138 (2838-3017 p)	No Hits found	<p>Identities = 160/405 (39%), Positives = 228/405 (55%), Gaps = 20/405 (4%) sp P39145 CMF1_BACSU COMF OPERON PROTEIN 1 pir j140387 hypothetical protein F1 - Bacillus subtilis pir jG69602 late competence protein required for DNA uptake comFA - Bacillus subtilis emb CAA79226.1 (Z18629) F1 [Bacillus subtilis] gb AAC44940.1 (U56901) involved in transformation [Bacillus subtilis] emb CAB15564.1 (Z99122) late competence protein [Bacillus subtilis] Length = 463</p>
SeqID 627	SA-1515.1	Contig138 (2072-3361 m)	52	
SeqID 628	SA-1516.1	Contig138 (3417-4061 p)	58	<p>Identities = 96/204 (47%), Positives = 127/204 (62%) dbj BAB07349.1 (AP001519) unknown conserved protein [Bacillus halodurans] Length = 213</p>
SeqID 629	SA-1517.1	Contig138 (4152-5078 p)	88	<p>Identities = 239/306 (78%), Positives = 274/306 (89%) dbj BAA88310.1 (AB028865) O-acetylserine lyase [Streptococcus suis] Length = 308</p>
SeqID 630	SA-1518.1	Contig138 (5230-6324 m)	73	<p>Identities = 199/363 (54%), Positives = 272/363 (74%), Gaps = 2/363 (0%) sp P32816 GLDA_BACST GLYCEROL DEHYDROGENASE (GLDH) pir JQ1474 glycerol dehydrogenase (EC 1.1.1.6) [validated] - Bacillus stearothermophilus gb AA22477.1 (M65289) glycerol dehydrogenase [Bacillus stearothermophilus] Length = 370</p>

SeqID 631	SA-1519.1	Contig138 (6386-7054 m)	57	Identities = 90/214 (42%), Positives = 131/214 (61%), Gaps = 1/214 (0%) emb CAA05516.1 (AJ002527) OrfX [Clostridium beijerinckii] Length = 226
SeqID 632	SA-152.1	Contig138 (81640-82248 p)	42	Identities = 48/182 (26%), Positives = 91/182 (49%), Gaps = 12/182 (6%) pir B70391 transcription regulator TetR/AcrR family - Aquifex aeolicus gb AAC07123.1 (AE000721) transcriptional regulator (TetR/AcrR family) [Aquifex aeolicus] Length = 179
SeqID 633	SA-1520.3	Contig138 (7064-9448 m)	67	Identities = 41/4805 (51%), Positives = 555/805 (68%), Gaps = 14/805 (1%) sp P75793 PFLF_ECOLI PUTATIVE FORMATE ACETYLTRANSFERASE 3 (PYRUVATE FORMATE-LYASE 3) pir JG84819 probable formate C-acetyltransferase (EC 2.3.1.54) - Escherichia coli gb AAC73910.1 (AE000184) putative formate acetyltransferase [Escherichia coli K12] db JBA335511.1 (D90720) Formate acetyltransferase 2 (EC 2.3.1.54) (pyruvate formate-lyase 2) [Escherichia coli] Length = 810
SeqID 634	SA-1521.1	Contig135 (23461-23691 p)	No Hits found	
SeqID 635	SA-1522.1	Contig135 (22356-23378 p)	84	Identities = 259/340 (76%), Positives = 294/340 (86%) gb AAF34406.1 AF164204.1 (AF164204) branched-chain amino acid aminotransferase [Lactococcus lactis subsp. cremoris] gb AAF64593.1 AF169649.1 (AF169649) branched-chain aminotransferase lve [Lactococcus lactis] Length = 340
SeqID 636	SA-1523.1	Contig135 (19784-22243 p)	87	Identities = 640/821 (77%), Positives = 724/821 (87%), Gaps = 5/821 (0%) gb AAD34369.1 AF129764.3 (AF129764) ParC [Streptococcus mitis] Length = 823
SeqID 637	SA-1524.1	Contig135 (17701-19650 p)	94	Identities = 574/649 (88%), Positives = 617/649 (94%), Gaps = 2/649 (0%) emb CAA91550.2 (Z67739) DNA topoisomerase IV [Streptococcus pneumoniae] Length = 647

SeqID 631	SA-1519.1	Contig138 (6386-7054 m)	57	Identities = 90/214 (42%), Positives = 13/1214 (61%), Gaps = 1/214 (0%) emb CAA05516.1 (AJ002527) OrfX [Clostridium beijerinckii] Length = 226
SeqID 632	SA-152.1	Contig138 (81640-82248 p)	42	Identities = 48/182 (26%), Positives = 91/182 (49%), Gaps = 12/182 (6%) pir BT0391 transcription regulator TetR/AcrR family Aquifex aeolicus gb AAC07123.1 (AE000721) transcriptional regulator (TetR/AcrR family) [Aquifex aeolicus] Length = 179
SeqID 633	SA-1520.3	Contig138 (7064-9448 m)	67	Identities = 414/805 (51%), Positives = 555/805 (68%), Gaps = 14/805 (1%) spiP75793 PFLF_ECOLI PUTATIVE FORMATE ACETYLTRANSFERASE 3 (PYRUVATE FORMATE-LYASE 3) pir G64819 probable formate C-acetyltransferase (EC 2.3.1.54) - Escherichia coli gb AAC73910.1 (AE000184) putative formate acetyltransferase [Escherichia coli K12] dbj BAA35511.1 (D90720) Formate acetyltransferase 2 (EC 2.3.1.54) (pyruvate formate-lyase 2), [Escherichia coli] Length = 810
SeqID 634	SA-1521.1	Contig135 (23461-23591 p)	No Hits found	
SeqID 635	SA-1522.1	Contig135 (22356-23378 p)	84	Identities = 259/340 (76%), Positives = 294/340 (86%) gb AAF34406.1 AF164204.1 (AF164204) branched-chain amino acid aminotransferase [Lactococcus lactis subsp. cremoris] gb AAF64593.1 AF169649.1 (AF169649) branched-chain aminotransferase ltvE [Lactococcus lactis] Length = 340
SeqID 636	SA-1523.1	Contig135 (19784-22243 p)	87	Identities = 640/821 (77%), Positives = 724/821 (87%), Gaps = 5/821 (0%) gb AAD34369.1 AF129764.3 (AF129764) ParC [Streptococcus mitis] Length = 823
SeqID 637	SA-1524.1	Contig135 (17701-19650 p)	94	Identities = 574/649 (88%), Positives = 617/649 (94%), Gaps = 2/649 (0%) emb CAA91550.2 (Z67739) DNA topoisomerase IV [Streptococcus pneumoniae] Length = 647

SeqID 638	SA-1525.1	Contig135 (16949-17587 m)	67	<p>Identities = 134/213 (62%), Positives = 169/213 (78%) sp Q54916 PAE_STRPN_HYPOTHETICAL_23.0_KD_PROTEIN IN_PARE_5_REGION (ORF2) emb CAA91549.1 (267739) unidentified [Streptococcus pneumoniae] Length = 213</p>
SeqID 639	SA-1526.1	Contig135 (16230-16883 p)	99	<p>Identities = 217/217 (100%), Positives = 217/217 (100%) sp Q3XDS8 UNG_STRAG_URACIL-DNA_GLYCOSYLASE (UDG) dbj BAA82292.1 (AB028896) Uracil DNA glycosylase [Streptococcus agalactiae] Length = 217</p>
SeqID 640	SA-1527.1	Contig135 (15646-16131 p)	96	<p>Identities = 161/161 (100%), Positives = 161/161 (100%) dbj BAA82291.1 (AB028896) ORF-1 [Streptococcus agalactiae] Length = 161</p>
SeqID 641	SA-1528.1	Contig135 (14291-15532 p)	98	<p>Identities = 413/413 (100%), Positives = 413/413 (100%) dbj BAA82290.1 (AB028896) NeuA [Streptococcus agalactiae] Length = 413</p>
SeqID 642	SA-153.1	Contig138 (80519-81616 p)	30	<p>Identities = 64/187 (34%), Positives = 112/187 (59%), Gaps = 1/187 (0%) pir J136287 probable integral membrane protein - Streptomyces coelicolor emb CAB42664.1 (AL049819) putative integral membrane protein [Streptomyces coelicolor A3(2)] Length = 266</p>
SeqID 643	SA-1530.1	Contig135 (13651-14280 p)	98	<p>Identities = 209/209 (100%), Positives = 209/209 (100%) dbj BAA82289.1 (AB028896) NeuD [Streptococcus agalactiae] Length = 209</p>
SeqID 644	SA-1531.1	Contig135 (12500-13654 p)	96	<p>Identities = 384/384 (100%), Positives = 384/384 (100%) dbj BAA82288.1 (AB028896) NeuC [Streptococcus agalactiae] Length = 384</p>
SeqID 645	SA-1532.1	Contig135 (11398-12423 p)	97	<p>Identities = 341/341 (100%), Positives = 341/341 (100%) dbj BAA33753.1 (AB017355) neuB [Streptococcus agalactiae] dbj BAA82287.1 (AB028896) NeuB [Streptococcus agalactiae] Length = 341</p>

SeqID 646	SA-1533.1	Contig135 (9998-11398 p)	99	<p>Identities = 466/466 (100%), Positives = 466/466 (100%) pir T44650 capsular polysaccharide repeat unit transporter cpsM [imported] - Streptococcus agalactiae dbj BAAC33752.1 (A801735) capsular polysaccharide [Streptococcus agalactiae] dbj BAAC82286.1 (A802896) CpsIA [Streptococcus agalactiae] gb AAD53073.1 (AF163833_13 (AF163833) CpsM [Streptococcus agalactiae] Length = 466</p>
SeqID 647	SA-1535.2	Contig106 (11312-12010 m)	64	<p>Identities = 87/228 (38%), Positives = 150/228 (65%), Gaps = 1/228 (0%) sp P54591 HCG_BACSU HYPOTHETICAL ABC INTERGENIC REGION prf C69822 glycine betaine/L-proline transport homolog yhcG - Bacillus subtilis emb CAA65690.1 (X96983) hypothetical protein [Bacillus subtilis] emb CAB12735.1 (Z99108) similar to glycine betaine/L-proline transport [Bacillus subtilis] Length = 232</p>
SeqID 648	SA-1536.1	Contig106 (10518-11300 m)	37	<p>Identities = 49/208 (23%), Positives = 102/208 (48%), Gaps = 20/208 (9%) gb AAA29909.1 (M74170) ORF 3 [Schistosoma mansoni] Length = 393</p>
SeqID 649	SA-1537.1	Contig106 (9925-10482 p)	40	<p>Identities = 43/174 (24%), Positives = 84/174 (47%), Gaps = 9/174 (5%) prf F64934 hypothetical protein b1750 - Escherichia coli (strain K-12) gb AAC74820.1 (AE000270) orf hypothetical protein [Escherichia coli K12] Length = 252</p>
SeqID 650	SA-1538.1	Contig106 (8523-9152 m)	39	<p>Identities = 63/135 (46%), Positives = 83/135 (60%), Gaps = 6/135 (4%) sp P26840 IMATA_BACSH PROBABLE MACROLIDE ACETYLTRANSFERASE Length = 180</p>
SeqID 651	SA-1539.1	Contig106 (7434-8402 p)	No Hits found	
SeqID 652	SA-1542.1	Contig106 (6238-5555 m)	49	<p>Identities = 37/92 (40%), Positives = 52/92 (56%), Gaps = 10/92 (10%) emb CAA59764.1 (X85757) unknown [Saccharomyces cerevisiae] Length = 133</p>

SeqID 653	SA-1543.1	Contig106 (4507-7299 p)	65	Identities = 410/922 (44%), Positives = 609/922 (65%), Gaps = 22/922 (2%) pir[C69069 cation-transporting P-ATPase Pacl. thermotrophicum gb AA85991.1 (AE000912) cation-transporting P-ATPase Pacl. thermotrophicum Length = 910
SeqID 654	SA-1544.1	Contig106 (3921-4355 p)	67	Identities = 85/132 (64%), Positives = 105/132 (79%) emb CAB46979.1 (AJ243482) CSRA protein [Enterococcus faecalis] Length = 168
SeqID 655	SA-1545.1	Contig106 (3451-3921 p)	46	Identities = 48/152 (31%), Positives = 75/152 (48%), Gaps = 1/152 (0%) dbj BAB05127.1 (AP001511) unknown [Bacillus halodurans] Length = 156
SeqID 656	SA-1546.1	Contig106 (2795-3448 p)	66	Identities = 108/211 (51%), Positives = 149/211 (70%) dbj BAB06554.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 215
SeqID 657	SA-1547.1	Contig106 (26-2689 p)	14	Identities = 76/279 (27%), Positives = 133/279 (47%), Gaps = 4/279 (1%) sp P25146 INLA_LISMO INTERNALIN A PRECURSOR pir JS37387 internalin A precursor - Listeria monocytogenes Length = 800
SeqID 658	SA-155.1	Contig138 (79800-80516 p)	54	Identities = 86/232 (37%), Positives = 137/232 (58%), Gaps = 3/232 (1%) gb AAF50837.1 (AE003568) CG1718 gene product [Drosophila melanogaster] Length = 1713
SeqID 659	SA-1551.2	Contig139 (128987-131698 p)	6	Identities = 41/110 (37%), Positives = 58/110 (50%), Gaps = 4/110 (3%) gb AAD33086.1 (AF071083) fibronectin-binding protein I [Streptococcus pyogenes] Length = 1161
SeqID 660	SA-1552.1	Contig139 (131737-131979 p)	No Hits found	
SeqID 661	SA-1554.1	Contig139 (132099-132542 p)	42	Identities = 58/135 (42%), Positives = 86/135 (62%), Gaps = 2/135 (1%) gb AAC13546.1 (AF019629) putative fibrin-associated protein [Actinomyces naeslundii] Length = 365

SeqID 662	SA-1555.1	Contig139 (132758-133396 p)	19	Identities = 30/96 (31%), Positives = 46/96 (47%), Gaps = 9/96 (9%) gb AAD33086.1 AF071083.1 (AF071083) fibronectin-binding protein [Streptococcus pyogenes] Length = 1161
SeqID 663	SA-1556.1	Contig139 (133726-133872 p)	No Hits found	Identities = 23/67 (34%), Positives = 37/67 (54%), Gaps = 2/67 (2%) gb JAA800100.1 L36660 unknown [Streptococcus pneumoniae] emb CAA84075.1 Z34303 hypothetical protein [Streptococcus pneumoniae] Length = 194
SeqID 664	SA-1558.1	Contig139 (134494-134670 p)	46	Identities = 45/205 (21%), Positives = 93/205 (44%), Gaps = 10/205 (4%) db JBAB04126.1 AP001508 unknown conserved protein in others [Bacillus halodurans] Length = 228
SeqID 665	SA-156.1	Contig138 (78853-79536 p)	38	Identities = 72/279 (25%), Positives = 125/279 (43%), Gaps = 25/279 (8%) db JBA424012.1 AB009635 Fmt [Staphylococcus aureus] Length = 397
SeqID 666	SA-1560.1	Contig139 (135988-136284 p)	No Hits found	Identities = 141/331 (42%), Positives = 201/331 (60%), Gaps = 34/331 (10%) pi G75548 ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1) gb JAAF09790.1 AE001882.8 (AE001882) ABC transporter, ATP-binding protein [Deinococcus radiodurans] Length = 354
SeqID 667	SA-1562.1	Contig139 (136414-137496 p)	31	Identities = 60/271 (22%), Positives = 118/271 (43%), Gaps = 13/271 (4%) emb CAB88837.1 AL353832 putative integral membrane protein. [Streptomyces coelicolor A3(2)] Length = 268
SeqID 668	SA-1563.1	Contig139 (137702-138688 p)	58	
SeqID 669	SA-1564.1	Contig139 (138691-139509 p)	42	

SeqID 670	SA-1555.2	Contig139 (139511-140296 p)	44	Identities = 68/264 (25%), Positives = 123/264 (45%), Gaps = 10/264 (3%) emb CAB88836.1 (AL353832) putative integral membrane transport protein. [Streptomyces coelicolor A3(2)] Length = 295
SeqID 671	SA-1557.3	Contig128 (12896-13207 m)	41	Identities = 25/84 (29%), Positives = 45/84 (52%), Gaps = 6/84 (7%) gb AAD31042.1 AF144646_1 (AF144646) heat shock protein 70 [Crassostrea gigas] Length = 659
SeqID 672	SA-1558.3	Contig128 (13333-14211 p)	67	Identities = 175/280 (62%), Positives = 218/280 (77%), Gaps = 9/280 (3%) sp O07874 RNH3_STRPN RIBONUCLEASE HIII (RNASE HIII) gb AAC45437.1 (U93576) ribonuclease HIII [Streptococcus pneumoniae] Length = 290
SeqID 673	SA-157.1	Contig138 (78521-78832 p)	72	Identities = 67/133 (50%), Positives = 86/133 (64%), Gaps = 16/133 (12%) db BAB04125.1 (AP001508) unknown conserved protein in others [Bacillus halodurans] Length = 174
SeqID 674	SA-1570.1	Contig128 (14227-14820 p)	71	Identities = 120/203 (59%), Positives = 145/203 (71%), Gaps = 9/203 (4%) sp O07344 LEP_STRPN SIGNAL PEPTIDASE I (SPASE I) (LEADER PEPTIDASE I) gb AAB69116.1 (U90721) signal peptidase I [Streptococcus pneumoniae] Length = 204
SeqID 675	SA-1571.2	Contig128 (14949-17369 p)	73	Identities = 454/835 (54%), Positives = 600/835 (71%), Gaps = 37/835 (4%) gb AAK05838.1 AE006404_5 (AE006404) exodeoxyribonuclease V alpha chain (EC 3.1.11.5) [Lactococcus lactis subsp. lactis] Length = 834
SeqID 676	SA-1573.3	Contig128 (17483-17965 p)	42	Identities = 47/173 (27%), Positives = 76/173 (43%), Gaps = 17/173 (9%) emb CAA72923.1 (Y12234) hypothetical protein [Enterococcus faecalis] Length = 169

SeqID 677	SA-1574.1	Contig128 (18036-19055 m)	55	Identities = 136/349 (38%), Positives = 210/349 (59%), Gaps = 14/349 (4%) ptiJ[G82093 DNA-damage-inducible protein P VC2287 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAFP9431.1 (AE004300) DNA-damage-inducible protein P [Vibrio cholerae] Length = 360
SeqID 678	SA-1577.1	Contig128 (19315-21627 p)	95	Identities = 708/770 (91%), Positives = 750/770 (96%) sp Q59934 PFL_STRMU FORMATE ACETYLTRANSFERASE (PYRUVATE FORMATE-LYASE) dbj BAA09085.1 (D50491) Pyruvate formate-lyase [Streptococcus mutans] Length = 775
SeqID 679	SA-1578.1	Contig128 (21728-22102 p)	55	Identities = 53/124 (42%), Positives = 76/124 (60%), Gaps = 2/124 (1%) sp Q46604 FMNB_DESVM FMN-BINDING PROTEIN pdb 1FLMIA Chain A, Dimer Of Fmn-Binding Protein From Desulfovibrio Vulgaris (Miyazaki F) pdb 1FLMIB Chain B, Dimer Of Fmn-Binding Protein From Desulfovibrio Vulgaris (Miyazaki F) pdb 1AXJ Fmn-Binding Protein From Desulfovibrio Vulgaris (Miyazaki F), Nmr, 20 Structures dbj BAA25177.1 (D21804) FMN-binding protein [Desulfovibrio vulgaris] Length = 122
SeqID 680	SA-1579.1	Contig128 (22137-23081 m)	44	Identities = 88/323 (27%), Positives = 142/323 (43%), Gaps = 51/323 (15%) emb CAC16441.1 (AL450165) putative esterase [Streptomyces coelicolor] Length = 353
SeqID 681	SA-1580.1	Contig128 (23063-23818 m)	55	Identities = 92/240 (38%), Positives = 143/240 (59%), Gaps = 11/240 (4%) gb AAD37110.1 (AF112358) C3-degrading proteinase [Streptococcus pneumoniae] Length = 241
SeqID 682	SA-1582.1	Contig128 (23943-24839 p)	21	Identities = 43/180 (23%), Positives = 71/180 (38%), Gaps = 16/180 (8%) dbj BAB07173.1 (AP001518) unknown conserved protein [Bacillus halodurans] Length = 273
SeqID 683	SA-1584.3	Contig128 (24918-25745 m)	77	Identities = 186/290 (64%), Positives = 228/290 (78%), Gaps = 10/290 (3%) gb AAK06146.1 (AE006435) transporter [Lactococcus lactis subsp. lactis] Length = 289

SeqID 684	SA-1585.3	Contig128 (25935-26387 m)	60	<p>Identities = 58/144 (40%), Positives = 92/144 (63%) gb AAK05931.1 AE006413_7 (AE006413) conserved hypothetical protein [Lactococcus lactis] subsp. lactis] Length = 145</p>
SeqID 685	SA-1586.2	Contig128 (26405-27607 m)	48	<p>Identities = 106/401 (26%), Positives = 199/401 (49%), Gaps = 21/401 (5%) pir JB70065 antibiotic resistance protein homolog ywgG - Bacillus subtilis emb CAB05383.1 (Z82987) unknown similar to quinolon resistance protein NorA [Bacillus subtilis] emb CAB15662.1 (Z99122) similar to antibiotic resistance protein [Bacillus subtilis] Length = 396</p>
SeqID 686	SA-1587.2	Contig139 (97176-98552 p)	78	<p>Identities = 280/458 (61%), Positives = 363/458 (79%), Gaps = 3/458 (0%) gb AAD47594.1 AF140784_3 (AF140784) Vexp3 [Streptococcus pneumoniae] Length = 459</p>
SeqID 687	SA-1588.1	Contig139 (96520-97176 p)	76	<p>Identities = 142/207 (68%), Positives = 169/207 (81%) gb AAD47593.1 AF140784_2 (AF140784) Vexp2 [Streptococcus pneumoniae] Length = 215</p>
SeqID 688	SA-1589.1	Contig139 (95233-96510 p)	63	<p>Identities = 165/425 (38%), Positives = 271/425 (62%), Gaps = 4/425 (0%) gb AAD47592.1 AF140784_1 (AF140784) Vexp1 [Streptococcus pneumoniae] Length = 425</p>
SeqID 689	SA-159.1	Contig138 (77622-78329 m)	32	<p>Identities = 44/150 (29%), Positives = 80/150 (53%), Gaps = 14/150 (9%) sp P16396 SUBE_BACSU MINOR EXTRACELLULAR PROTEASE EPR PRECURSOR pir SUBSNMP serine proteinase (EC 3.4.21.-) epr precursor - Bacillus subtilis emb CAA37392.1 (X53307) prepropeptide (AA - 27 to 618) [Bacillus subtilis] gb AA22423.1 (M22407) extracellular protease precursor [Bacillus subtilis] emb CAA51571.1 (X73124) ipa-15r epr [Bacillus subtilis] emb CAB15866.1 (Z99123) extracellular serine protease [Bacillus subtilis] Length = 645</p>
SeqID 690	SA-1590.1	Contig139 (94330-94491 m)	No Hits found	

SeqID 691	SA-1591.1	Contig139 (94053-94157 p)	65	<p>Identities = 40/88 (45%), Positives = 60/88 (67%) ref NP_065294.1 100 pct identical to sp:Y15B_EC01[hypothetical 33.3 kd protein (orfB) of IS150] [Escherichia coli] p[ri]H65154 probable transposase, 33.3K - Escherichia coli insertion sequence IS150 gb AAC76582.1 (AE000433) IS150 putative transposase [Escherichia coli K12] db JBA12587.1 (AP002527) 100 pct identical to sp:Y15B_EC01[hypothetical 33.3 kd protein (orfB) of IS150] [Escherichia coli] Length = 283</p>
SeqID 692	SA-1593.1	Contig139 (93562-93822 p)	50	<p>Identities = 33/76 (43%), Positives = 44/76 (57%), Gaps = 1/76 (1%) ref NP_052792.1 pXO1-96 [Bacillus anthracis] p[ri]H59102 hypothetical protein pXO1-96 - Bacillus anthracis virulence plasmid pXO1 gb AAA74027.1 (U30714) ORFB [Bacillus anthracis] gb AA474029.1 (U30715) ORFB [Bacillus anthracis] gb AAD32400.1 AAD32400 (AF065404) pXO1-96 [Bacillus anthracis] Length = 274</p>
SeqID 693	SA-1594.1	Contig139 (93367-93540 p)	37	<p>Identities = 29/59 (49%), Positives = 39/59 (65%) gb AAB00677.1 (L40841) transposase [Enterococcus faecium] Length = 310</p>
SeqID 694	SA-1595.1	Contig139 (92774-93178 p)	36	<p>Identities = 28/116 (24%), Positives = 59/116 (50%), Gaps = 6/116 (5%) sp Q48585 Y13A_LACJO INSERTION ELEMENT IS1223 HYPOTHETICAL 20.7 KD PROTEIN (ORFA) gb AAA56999.1 (U08558) ORFA, putative Helix-Turn-Helix motif from amino acid 21 through 42 and from amino acid 78 through 99 [Lactobacillus johnsonii] Length = 177</p>
SeqID 695	SA-1596.1	Contig139 (91891-92511 m)	67	<p>Identities = 115/194 (59%), Positives = 139/194 (71%), Gaps = 11/194 (5%) p[ri]T13289 probable integrase - Streptococcus phage phi-O1205 gb AAC79517.1 (U89874) ORF-1 [Streptococcus thermophilus temperate bacteriophage O1205] Length = 359</p>

SeqID 696	SA-1597.1	Contig139 (91399-91746 p)	78	<p>Identities = 110/115 (95%), Positives = 112/115 (96%) sp O3403 JRL19_STRTR_50S_RIBOSOMAL_PROTEIN_L19 gb AAC01534.1 (U89973) ribosomal protein L19 [Streptococcus thermophilus] Length = 115</p>
SeqID 697	SA-1598.1	Contig139 (89623-90819 p)	51	<p>Identities = 131/393 (33%), Positives = 206/393 (52%), Gaps = 20/393 (5%) pir J744296 hypothetical protein [imported] - Bacillus halodurans dbj BA75315.1 (AB011836) similar to Bordetella paraperuensis transposase for insertion sequence element (27 - identity) [Bacillus halodurans] dbj BA04382.1 (AP001509) unknown conserved protein in others [Bacillus halodurans] Length = 424</p>
SeqID 698	SA-1599.1	Contig139 (89355-89630 p)	52	<p>Identities = 24/89 (26%), Positives = 50/89 (55%), Gaps = 2/89 (2%) pir G71950 hypothetical protein hpo276 - Helicobacter pylori (strain J99) gb AA05887.1 (AE01465) putative [Helicobacter pylori J99] Length = 100</p>
SeqID 699	SA-16.1	Contig137 (28276-28605 m)	41	<p>Identities = 35/103 (33%), Positives = 46/103 (43%), Gaps = 14/103 (13%) gb AAC02237.1 (U72957) merozoite surface protein 2 [Plasmodium falciparum] Length = 176</p>
SeqID 700	SA-160.2	Contig138 (76196-77368 m)	71	<p>Identities = 236/387 (60%), Positives = 281/387 (71%), Gaps = 10/387 (2%) gb AA05433.1 (AE006366) N- acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) [Lactococcus lactis subsp. lactis] Length = 382</p>
SeqID 701	SA-1601.1	Contig139 (88835-89278 p)	55	<p>Identities = 63/146 (43%), Positives = 87/146 (59%), Gaps = 17/146 (0%) sp O34559 FLAW_BACSU PROBABLE FLAVODOXIN 2, pir E9886 flavodoxin homolog ykuP [similarity] Bacillus subtilis emb CAA10879.1 (AJ222587) YkuP protein [Bacillus subtilis] emb CAB13290.1 (Z39111) similar to sulfite reductase [Bacillus subtilis] Length = 178</p>

SeqID 702	SA-1602.1	Contig139 (87754-88776 p)	51	Identities = 123/343 (35%), Positives = 175/343 (50%), Gaps = 26/343 (7%) pir T35340 probable adenosine deaminase - Streptomyces coelicolor emb CAB42949.1 (A049863) putative adenosine deaminase [Streptomyces coelicolor A3(2)] Length = 359
SeqID 703	SA-1603.2	Contig139 (86553-87488 m)	66	Identities = 144/306 (47%), Positives = 209/306 (68%), Gaps = 4/306 (1%) pir F69999 conserved hypothetical protein YtiJ - Bacillus subtilis gb AAC00337.1 (AF008220) YtiJ [Bacillus subtilis] emb CAB14885.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 313
SeqID 704	SA-1604.1	Contig90 (12596-12865 m)	76	Identities = 67/89 (75%), Positives = 76/89 (85%) sp O31587 R14B_BACSU 30S RIBOSOMAL PROTEIN S14-2 pir F69835 ribosomal protein S14 homolog yhzA - Bacillus subtilis emb CAB12716.1 (Z99108) similar to ribosomal protein S14 [Bacillus subtilis] Length = 89
SeqID 705	SA-1605.2	Contig90 (11209-12234 p)	58	Identities = 139/339 (41%), Positives = 201/339 (59%), Gaps = 4/339 (1%) refNP_047071.1 L4171.5 [Leishmania major] pir T02833 threonine aldolase L4171.5 [imported] - Leishmania major (strain Friedlin) gb AAC24656.1 (AE001274) L4171.5 [Leishmania major] Length = 359
SeqID 706	SA-1606.2	Contig90 (10079-11089 p)	81	Identities = 244/343 (71%), Positives = 280/343 (81%), Gaps = 7/343 (2%) gb AAK04393.1 AE006266.12 (AE006266) O-sialoglycoprotein endopeptidase [Lactococcus lactis subsp. lactis] Length = 346
SeqID 707	SA-1607.1	Contig90 (9557-10003 p)	48	Identities = 44/141 (31%), Positives = 73/141 (51%), Gaps = 8/141 (5%) pir B70351 ribosomal-protein-alanine acetyltransferase - Aquifex aeolicus gb AAC06803.1 (AE000696) ribosomal-protein-alanine acetyltransferase [Aquifex aeolicus] Length = 154

SeqID 708	SA-1608.1	Contig90 (8905-9594 p)	54	Identities = 94/182 (51%), Positives = 127/182 (69%), Gaps = 6/182 (3%) emb[CAB76861.1] (Y17797) hypothetical protein [Enterococcus faecalis] Length = 204
SeqID 709	SA-1609.1	Contig90 (8493-8723 m)	55	Identities = 30/67 (44%), Positives = 45/67 (66%), Gaps = 7/67 (10%) dbj[BAB06380.1] (AP001516) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 69
SeqID 710	SA-1612.2	Contig136 (90788-91228 m)	47	Identities = 37/142 (26%), Positives = 71/142 (49%), Gaps = 77/142 (4%) pir[B70057 transcription regulator MarR family homolog ywHa - Bacillus subtilis emb[CAB02511.1] (Z80360) Unknown, similar to regulatory proteins [Bacillus subtilis] emb[CAB15782.1] (Z99123) similar to transcriptional regulator (MarR family) [Bacillus subtilis] Length = 139
SeqID 711	SA-1610.1	Contig90 (6760-8439 m)	77	Identities = 351/550 (63%), Positives = 442/550 (79%) dbj[BAB06381.1] (AP001516) unknown conserved protein [Bacillus halodurans] Length = 555
SeqID 712	SA-1611.1	Contig90 (6089-6598 p)	38	Identities = 45/119 (37%), Positives = 67/119 (55%), Gaps = 4/119 (3%) emb[CAB6624.1] (X97985) ORF1 [Staphylococcus aureus] Length = 255
SeqID 713	SA-1612.1	Contig90 (4595-5941 p)	89	Identities = 390/449 (86%), Positives = 406/449 (89%), Gaps = 1/449 (0%) gb AAAC4800.1 (U61271) glutamine synthetase type 1 [Streptococcus agalactiae] Length = 449
SeqID 714	SA-1613.1	Contig90 (4190-4561 p)	69	Identities = 59/123 (47%), Positives = 89/123 (71%), Gaps = 5/123 (4%) sp P19083 GLNR_BACCE REGULATORY PROTEIN - GLNR pir J10076 hypothetical 15K protein (glnA 5 region) - Bacillus cereus dbj BAA00402.1 (D00513) ORF129 [Bacillus cereus] Length = 129
SeqID 715	SA-1614.1	Contig90 (3628-4110 p)	33	Identities = 35/146 (23%), Positives = 64/146 (42%), Gaps = 7/146 (4%) dbj BAB04661.1 (AP001510) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 360

SeqID 716	SA-1615.1	Contig90 (2945-3355 m)	56	<p>Identities = 61/134 (45%), Positives = 78/134 (57%), Gaps = 5/134 (3%) refNP_009839.1 Ycr013cp [Saccharomyces cerevisiae] sp P25614 YCQ3_YEAST VERY HYPOTHETICAL 22.8 KD PROTEIN IN PGK1-POL4 INTERGENIC REGION pir I519423 probable membrane protein YCR013c - yeast (Saccharomyces cerevisiae) emb CAA42330.1 (X59720) YCR013c, len:215 [Saccharomyces cerevisiae] Length = 215</p>
SeqID 717	SA-1616.1	Contig90 (2112-3308 p)	75	<p>Identities = 254/398 (63%), Positives = 303/398 (75%), Gaps = 2/398 (0%) sp Q8ZSC4 PGK_STAAU PHOSPHOGLYCERATE KINASE emb CAB38646.1 (AJ133520) phosphoglycerate kinase [Staphylococcus aureus] Length = 396</p>
SeqID 718	SA-1617.2	Contig90 (1108-1977 p)	81	<p>Identities = 182/291 (62%), Positives = 237/291 (80%), Gaps = 7/291 (2%) emb CAA73175.1 (Y12602) acid phosphatase [Streptococcus equisimilis] Length = 285</p>
SeqID 719	SA-1619.1	Contig108 (18754-19293 m)	62	<p>Identities = 89/146 (60%), Positives = 113/146 (76%), Gaps = 1/146 (0%) gb AAAF08325.1 U78969_2 (U78969) Flar [Streptococcus pyogenes] Length = 172</p>
SeqID 720	SA-162.1	Contig136 (88924-90741 m)	52	<p>Identities = 216/543 (39%), Positives = 322/543 (58%), Gaps = 25/543 (4%) emb CA569751.1 (AL137187) putative ABC transporter [Streptomyces coelicolor A3(2)] Length = 577</p>
SeqID 721	SA-1620.1	Contig108 (17468-18553 m)	43	<p>Identities = 94/307 (30%), Positives = 157/307 (50%), Gaps = 21/307 (6%) pir I372378 glycerol dehydrogenase - Thermotoga maritima (strain MSB8) gb AAD35508.1 AE001721.7 (AE001721) glycerol dehydrogenase [Thermotoga maritima] Length = 364</p>
SeqID 722	SA-1621.1	Contig108 (16596-17303 p)	23	<p>Identities = 38/98 (38%), Positives = 59/98 (59%) emb CAC01354.1 (AL390975) putative integral membrane protein [Streptomyces coelicolor A3(2)] Length = 198</p>

SeqID 723	SA-1622.1	Contig108 (14405-16249 p)	69	Identities = 301/610 (49%), Positives = 437/610 (71%), Gaps = 9/610 (1%) dbj BAB05348.1 (AP001512) unknown conserved protein [Bacillus halodurans] Length = 618
SeqID 724	SA-1623.1	Contig108 (12108-14360 p)	68	Identities = 397/751 (52%), Positives = 519/751 (68%), Gaps = 14/751 (1%) dbj BAB04157.1 (AP001508) homocysteine methyl transferase [Bacillus halodurans] Length = 756
SeqID 725	SA-1624.1	Contig108 (11622-11753 p)	No Hits found	Identities = 86/225 (38%), Positives = 142/225 (62%), Gaps = 1/225 (0%) gb AAK05711.1 AE006391_10 (AE006391) amino acid permease [Lactococcus lactis subsp. lactis] Length = 235
SeqID 726	SA-1625.2	Contig108 (10745-11440 p)	60	
SeqID 727	SA-1626.1	Contig87 (8382-8996 m)	No Hits found	
SeqID 728	SA-1627.1	Contig87 (7700-8284 m)	No Hits found	
SeqID 729	SA-1628.1	Contig87 (7137-7703 m)	No Hits found	
SeqID 730	SA-1629.1	Contig87 (4483-7137 m)	74	Identities = 544/880 (61%), Positives = 676/880 (76%), Gaps = 11/880 (1%) pi T SYBSVS valine-tRNA ligase (EC 6.1.1.9) - Bacillus stearothermophilus Length = 880
SeqID 731	SA-163.1	Contig136 (87180-88934 m)	55	Identities = 228/526 (43%), Positives = 331/526 (62%), Gaps = 2/526 (0%) emb CAB69752.1 (AL137187) putative ABC transporter [Streptomyces coelicolor A3(2)] Length = 642
SeqID 732	SA-1630.1	Contig87 (3318-4247 p)	34	Identities = 57/231 (24%), Positives = 109/231 (46%), Gaps = 10/231 (4%) pi T T35598 hypothetical protein SC6G9.01c - Streptomyces coelicolor (fragment) emb CAB45592.1 (AL079356) hypothetical protein [Streptomyces coelicolor] Length = 409
SeqID 733	SA-1632.1	Contig87 (1942-2862 m)	43	Identities = 100/306 (32%), Positives = 152/306 (48%), Gaps = 3/306 (0%) pi T T50594 probable oxidoreductase [imported] - Streptomyces coelicolor emb CAB61731.1 (AL133220) putative oxidoreductase. [Streptomyces coelicolor A3(2)] Length = 351

SeqID 734	SA-1634.1	Contig87 (879-1781 m)	44	<p>Identities = 70/284 (24%), Positives = 135/284 (46%), Gaps = 8/284 (2%) refNP_053049.1 hypothetical protein [Plasmid pNZ4000] gb AAD040365.1 (AF036485) hypothetical protein [Plasmid pNZ4000] Length = 302</p>
SeqID 735	SA-1635.1	Contig87 (3-611 m)	23	<p>Identities = 38/107 (35%), Positives = 59/107 (54%), Gaps = 6/107 (5%) sp P37507 YQAQ_BACSU HYPOTHETICAL 13.9 KD PROTEIN IN COTF-TETB INTERGENIC REGION. pir IS66000 yyaQ protein - Bacillus subtilis db BA005206.1 (D26185) unknown [Bacillus subtilis] emb CAB16112.1 (Z99124) yyaQ [Bacillus subtilis] Length = 118</p>
SeqID 736	SA-1636.2	Contig124 (24911-26119 m)	73	<p>Identities = 234/384 (60%), Positives = 300/384 (77%), Gaps = 2/384 (0%) sp P42602 YGJU_ECOLI HYPOTHETICAL SYMPORTER YGJU pir F65097 hypothetical 43.5 kD protein in elgC-exuT intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_o414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] Length = 414</p>
SeqID 737	SA-1638.1	Contig124 (24194-24742 m)	61	<p>Identities = 109/182 (59%), Positives = 141/182 (76%) emb CAB59830.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 182</p>
SeqID 738	SA-164.1	Contig136 (86448-87072 m)	51	<p>Identities = 67/182 (36%), Positives = 111/182 (60%), Gaps = 4/182 (2%) db BAB05604.1 (AP001513) unknown conserved protein [Bacillus halodurans] Length = 251</p>
SeqID 739	SA-1640.2	Contig124 (22501-24177 m)	44	<p>Identities = 150/481 (31%), Positives = 247/481 (51%), Gaps = 15/481 (3%) pir H69858 cation ABC transporter (ATP-binding protein) homolog ykoD - Bacillus subtilis emb CAA05601.1 (AJ002571) YkoD [Bacillus subtilis] emb CAB13179.1 (Z99110) similar to cation ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 490</p>

SeqID 734	SA-1634.1	Contig87 (879-1781 m)	44	<p>Identities = 70/284 (24%), Positives = 135/284 (46%), Gaps = 8/284 (2%) ref NP_053049.1 hypothetical protein [Plasmid pNZ4000] gb AAD40365.1 (AF036485) hypothetical protein [Plasmid pNZ4000] Length = 302</p>
SeqID 735	SA-1635.1	Contig87 (3-611 m)	23	<p>Identities = 38/107 (35%), Positives = 59/107 (54%), Gaps = 6/107 (5%) sp P37507 YQAQ_BACSU HYPOTHETICAL 13.9 KD PROTEIN IN COTF-TETB INTERGENIC REGION pr S66000 yyaQ protein - Bacillus subtilis db JBA05206.1 (D26185) unknown [Bacillus subtilis] emb CAB16112.1 (Z99124) yyaQ [Bacillus subtilis] Length = 118</p>
SeqID 736	SA-1636.2	Contig124 (24911-26119 m)	73	<p>Identities = 234/384 (60%), Positives = 300/384 (77%), Gaps = 2/384 (0%) sp P42602 YGJU_ECOLI HYPOTHETICAL SYMPORTER YGJU pr JF65097 hypothetical 43.5 kD protein in elgC-exuT intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_o414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] Length = 414</p>
SeqID 737	SA-1638.1	Contig124 (24194-24742 m)	61	<p>Identities = 109/182 (59%), Positives = 141/182 (76%) emb CAB59830.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 182</p>
SeqID 738	SA-164.1	Contig136 (86446-87072 m)	51	<p>Identities = 67/182 (36%), Positives = 111/182 (60%), Gaps = 4/182 (2%) db JBA05604.1 (AP001513) unknown conserved protein [Bacillus halodurans] Length = 251</p>
SeqID 739	SA-1640.2	Contig124 (22501-24177 m)	44	<p>Identities = 150/481 (31%), Positives = 247/481 (51%), Gaps = 15/481 (3%) pr JH69858 cation ABC transporter (ATP-binding protein) homolog ykoD - Bacillus subtilis emb CAA05601.1 (AJ002571) YkoD [Bacillus subtilis] emb CAB13179.1 (Z99110) similar to cation ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 490</p>

SeqID 740	SA-164.1.2	Contig124 (21678-22508 m)	25	Identities = 46/134 (34%), Positives = 74/134 (54%), Gaps = 3/134 (2%) pirJF75200 hypothetical protein PAB22261 - <i>Pyrococcus abyssi</i> (strain Orsay) emb CAB49053.1 (AJ249283) hypothetical protein [Pyrococcus abyssi] Length = 248
SeqID 741	SA-1642.1	Contig124 (20872-21643 p)	49	Identities = 70/183 (38%), Positives = 113/183 (61%), Gaps = 2/183 (1%) gb AAC46144.1 (AF001974) putative TriA [Thermoanaerobacter ethanolicus] Length = 195
SeqID 742	SA-1643.1	Contig124 (19568-20959 p)	55	Identities = 170/461 (36%), Positives = 263/461 (56%), Gaps = 28/461 (6%) pirJG53610 ntpJ protein - <i>Enterococcus hirae</i> Length = 448
SeqID 743	SA-1644.1	Contig124 (18852-19565 p)	70	Identities = 132/240 (55%), Positives = 171/240 (71%), Gaps = 4/240 (1%) sp P25813 GIDB_BACSU GLUCOSE INHIBITED DIVISION PROTEIN B pir JBVBSGB glucose-inhibited division protein gidB - <i>Bacillus subtilis</i> emb CAA44405.1 (X62539) homologous to E.coli gidB [Bacillus subtilis] db BAA05230.1 (D26185) unknown [Bacillus subtilis] emb CAB16137.1 (Z299124) glucose-inhibited division protein [Bacillus subtilis] Length = 239
SeqID 744	SA-1645.1	Contig124 (18170-18724 m)	78	Identities = 124/182 (68%), Positives = 152/182 (83%) gb AAG23700.1 (AF017421) LemA-like protein [Streptococcus gordonii] Length = 189
SeqID 745	SA-1646.1	Contig124 (17259-18149 m)	85	Identities = 220/297 (74%), Positives = 261/297 (87%), Gaps = 1/297 (0%) sp O30795 HTPX_STRGC PROBABLE PROTEINASE HTPX HOMOLOG pir J748855 probable heat shock protein HtpX [imported] - <i>Streptococcus gordonii</i> gb AA870525.1 (AF017421) putative heat shock protein HtpX [Streptococcus gordonii] Length = 297
SeqID 746	SA-1647.1	Contig124 (16621-17154 m)	70	Identities = 92/174 (52%), Positives = 133/174 (75%), Gaps = 3/174 (1%) gb AAG32547.1 (U12643) YfN-like hypothetical protein [Streptococcus gordonii] Length = 176

SeqID 747	SA-1648.1	Contig124 (15697-16386 m)	91	Identities = 193/229 (84%), Positives = 211/229 (91%), Gaps = 1/229 (0%) gb AAC64935.1 (AF082668) CsrR [Streptococcus pyogenes] Length = 228
SeqID 748	SA-1649.2	Contig124 (14202-15707 m)	72	Identities = 248/501 (49%), Positives = 364/501 (72%), Gaps = 4/501 (0%) gb AAC64936.1 (AF082668) CsrS [Streptococcus pyogenes] Length = 500
SeqID 749	SA-165.1	Contig136 (85759-86465 m)	58	Identities = 84/226 (37%), Positives = 138/226 (60%), Gaps = 9/226 (3%) dbj BAB04091.1 (AF001508) two-component response regulator [Bacillus halodurans] Length = 222
SeqID 750	SA-1650.2	Contig134 (63460-63936 p)	41	Identities = 49/136 (36%), Positives = 69/136 (50%), Gaps = 8/136 (5%) pir G75571 MutT/nudix family protein - Deinococcus radiodurans (strain R1) gb AAF09597.1 AE001864_3 (AE001864) MutT/nudix family protein [Deinococcus radiodurans] Length = 350
SeqID 751	SA-1651.1	Contig134 (64258-65064 p)	47	Identities = 70/254 (27%), Positives = 127/254 (49%), Gaps = 2/254 (0%) pir G83412 hypothetical protein PA1860 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05249.1 AE004612_3 (AE004612) hypothetical protein [Pseudomonas aeruginosa] Length = 275
SeqID 752	SA-1653.1	Contig134 (65459-65986 p)	84	Identities = 140/164 (85%), Positives = 157/164 (95%) gb AAC38046.1 (AF000954) No definition line found [Streptococcus mutans] Length = 164
SeqID 753	SA-1654.1	Contig134 (65937-66335 p)	90	Identities = 109/133 (81%), Positives = 122/133 (90%), Gaps = 2/133 (1%) pir A36933 diacylglycerol kinase homolog - Streptococcus mutans Length = 137
SeqID 754	SA-1655.1	Contig134 (66332-67276 p)	83	Identities = 273/299 (91%), Positives = 290/299 (96%) gb AAD41632.1 AF072811_1 (AF072811) GTPase Era [Streptococcus pneumoniae] Length = 299
SeqID 755	SA-1656.1	Contig134 (67495-67914 p)	No Hits found	
SeqID 756	SA-1657.1	Contig134 (68290-68625 p)	No Hits found	

SeqID 757	SA-1658.1	Contig134 (68686-68698 p)	52	Identities = 31/87 (35%), Positives = 48/87 (54%), Gaps = 1/87 (1%) embjCAC03528.1 [Auj276410] BlyP protein [Streptococcus pneumoniae] Length = 229
SeqID 758	SA-1659.1	Contig134 (69387-69447 p)	No Hits found	
SeqID 759	SA-166.1	Contig136 (84529-85758 m)	35	Identities = 76/315 (24%), Positives = 149/315 (47%), Gaps = 33/315 (10%) gb AA77919.1 (AF039062) putative histidine protein kinase [Lactococcus lactis] Length = 414
SeqID 760	SA-1660.1	Contig134 (69841-71433 m)	10	Identities = 36/119 (30%), Positives = 57/119 (47%), Gaps = 15/119 (12%) pir S74641 hypothetical protein sil1681 - Synchocystis sp. (strain PCC 6803) dbj BAA16793.1 (D90900) hypothetical protein [Synchocystis sp.] Length = 507
SeqID 761	SA-1662.1	Contig134 (71635-72498 p)	48	Identities = 71/273 (26%), Positives = 140/273 (51%), Gaps = 16/273 (5%) sp P493330 RGG_STRGC RGG PROTEIN pir A41898 positive regulator of glucosyltransferase and Spp phenotype rgg - Streptococcus gordonii gb AA26988.1 (M89776) rgg [Streptococcus gordonii] Length = 297
SeqID 762	SA-1663.1	Contig134 (72647-73488 p)	77	Identities = 182/271 (67%), Positives = 217/271 (79%) sp P56045 FPG_STRMU FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) dbj BAA05066.1 (D26071) formamidopyrimidine-DNA glycosylase [Streptococcus mutans] Length = 273
SeqID 763	SA-1665.1	Contig134 (73444-74052 p)	52	Identities = 80/189 (42%), Positives = 113/189 (59%), Gaps = 1/189 (0%) sp O34932 YTAG_BACSU HYPOTHETICAL 22.0 KD PROTEIN IN GAPB-MUTM INTERGENIC REGION pir A69988 conserved hypothetical protein ytaG - Bacillus subtilis gb AAC00353.1 (AF008220) YtaG [Bacillus subtilis] embj CAB14868.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 197

SeqID 764	SA-1669.1	Contig134 (74176-74877 p)	51	Identities = 68/247 (27%), Positives = 126/247 (50%), Gaps = 17/247 (6%) pir E69771 ABC transporter (ATP-binding protein) homolog ydbJ - Bacillus subtilis dbj BAA19286.1 (AB001488) PROBABLE TRANSPORT ATP BINDING PROTEIN. [Bacillus subtilis] emb CAB12256.1 (Z99106) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 308
SeqID 765	SA-1669.1	Contig134 (74855-76513 p)	No Hits found	
SeqID 766	SA-167.1	Contig136 (83535-84413 m)	74	Identities = 183/290 (63%), Positives = 223/290 (76%) gb AAG02450.1 AF290097_1 (AF290097) mevalonate kinase [Streptococcus pyogenes] Length = 292
SeqID 767	SA-1671.2	Contig134 (76757-77878 p)	77	Identities = 230/396 (58%), Positives = 315/396 (79%) emb CAA07482.1 (AJ007367) multi-drug resistance efflux pump [Streptococcus pneumoniae] Length = 399
SeqID 768	SA-1673.2	Contig133 (6150-7757 m)	87	Identities = 413/535 (77%), Positives = 476/535 (88%), Gaps = 1/535 (0%) sp Q5905 DEXB_STREQ GLUCAN 1,6-ALPHA-GLUCOSIDASE (DEXTRAN GLUCOSIDASE) (EXO-1,6-ALPHA-GLUCOSIDASE) (GLUCODEXTRANASE) pir S39970 glukan 1,6-alpha-glucosidase (EC 3.2.1.70) - Streptococcus equisimilis emb CAA51348.1 (X72832) glukan 1,6-alpha-glucosidase [Streptococcus equisimilis] pir Z009358A glukan 1,6-alpha-glucosidase [Streptococcus equisimilis] Length = 537
SeqID 769	SA-1674.1	Contig133 (5067-6062 m)	91	Identities = 267/331 (80%), Positives = 306/331 (91%) sp P96995 GALE_STRMU UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) pir JC5313 UDP-glucose 4-epimerase (EC 5.1.3.2) - Streptococcus mutans gb AAB49738.1 (U21942) UDP-galactose 4-epimerase [Streptococcus mutans] Length = 333

SeqID 770	SA-1675.1	Contig133 (4366-5046 p)	58	Identities = 71/223 (31%), Positives = 139/223 (61%), Gaps = 7/223 (3%) dbj BA08470.1 (AP001516) two-component response regulator [Bacillus halodurans] Length = 230
SeqID 771	SA-1676.1	Contig133 (2946-4364 p)	47	Identities = 132/461 (28%), Positives = 245/461 (52%), Gaps = 7/461 (1%) pir A70009 two-component sensor histidine kinase homolog ynfL - Bacillus subtilis emb CAB07946.1 (Z93937) unknown [Bacillus subtilis] emb CAB15141.1 (Z99120) similar to two-component sensor histidine kinase [YnfM] [Bacillus subtilis] Length = 533
SeqID 772	SA-1677.1	Contig133 (1347-2684 m)	82	Identities = 323/428 (76%), Positives = 375/428 (88%) gb AAB18291.1 (U35658) L-malate permease [Streptococcus bovis] Length = 441
SeqID 773	SA-1678.2	Contig133 (628-1212 p)	22	Identities = 36/70 (51%), Positives = 44/70 (62%) pir B72732 hypothetical protein APE0395 - Aeropyrum pernix (strain K1) dbj BAA79350.1 (AP000059) 127aa long hypothetical protein [Aeropyrum pernix] Length = 127
SeqID 774	SA-1679.2	Contig133 (159-1322 m)	83	Identities = 285/386 (73%), Positives = 332/386 (85%), Gaps = 1/386 (0%) gb AAB07709.1 (U35659) malic enzyme [Streptococcus bovis] Length = 389
SeqID 775	SA-168.1	Contig136 (82609-83553 m)	80	Identities = 220/312 (70%), Positives = 254/312 (84%) gb AAG02456.1 AF290099_2 (AF290099) mevalonate diphosphate decarboxylase [Streptococcus pneumoniae] Length = 317
SeqID 776	SA-1680.2	Contig96 (2340-2804 p)	59	Identities = 74/146 (50%), Positives = 103/146 (69%), Gaps = 3/146 (2%) gb AAK04739.1 AE006297_2 (AE006297) transcriptional regulator CtsR [Lactococcus lactis subsp. lactis] Length = 151
SeqID 777	SA-1681.2	Contig96 (2801-5248 p)	69	Identities = 404/831 (48%), Positives = 567/831 (67%), Gaps = 52/831 (6%) gb AAK04740.1 AE006297_3 (AE006297) ATP-dependent protease ATP-binding subunit [Lactococcus lactis subsp. lactis] Length = 816

SeqID 778	SA-1682.1	Contig96 (5468-5959 m)	50	Identities = 53/156 (33%), Positives = 84/156 (52%) gb AAAF15587.1 AF187951.1 (AF187951) promotes resistance to glutamine synthetase inhibitors [Activation-tagging vector pSKI015] Length = 183
SeqID 779	SA-1683.1	Contig96 (5973-6614 m)	85	Identities = 179/213 (84%), Positives = 197/213 (92%) gb AAC97156.1 (U49397) unknown [Streptococcus pyogenes] Length = 213
SeqID 780	SA-1685.1	Contig96 (6735-7712 m)	93	Identities = 282/325 (86%), Positives = 306/325 (93%) gb AAC97155.1 (U49397) unknown [Streptococcus pyogenes] Length = 325
SeqID 781	SA-1686.1	Contig96 (7696-8571 m)	84	Identities = 224/271 (82%), Positives = 247/271 (90%) sp Q3ZB49HSLQ_STRPY_33_KDA_CHAPERONIN (HEAT SHOCK PROTEIN 33 HOMOLOG) (HSP33) gb AAC97154.1 (U49397) unknown [Streptococcus pyogenes] Length = 277
SeqID 782	SA-1687.1	Contig98 (8711-9967 m)	34	Identities = 64/350 (18%), Positives = 146/350 (41%), Gaps = 7/350 (2%) gb AAB93480.1 (AF019377) tellurite resistance protein [Rhodobacter sphaeroides] Length = 396
SeqID 783	SA-1689.2	Contig96 (9964-10782 m)	37	Identities = 56/238 (23%), Positives = 105/238 (43%), Gaps = 25/238 (10%) emb CAB39037.2 (AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] Length = 1946
SeqID 784	SA-169.1	Contig136 (81624-82616 m)	70	Identities = 170/330 (51%), Positives = 233/330 (70%), Gaps = 1/330 (0%) gb AAAG02457.1 AF290009.3 (AF290009) phosphomevalonate kinase [Streptococcus pneumoniae] Length = 336
SeqID 785	SA-1690.2	Contig96 (10906-11172 m)	55	Identities = 35/76 (46%), Positives = 49/76 (64%) gb AAK03132.1 (AE006146) unknown [Pasteurella multocida] Length = 757
SeqID 786	SA-1694.1	Contig83 (3183-4526 m)	37	Identities = 143/211 (67%), Positives = 170/211 (79%), Gaps = 3/211 (1%) gb AAD00288.1 (U78607) putative secreted protein [Streptococcus mutans] Length = 211
SeqID 787	SA-1695.1	Contig83 (2091-3071 m)	78	Identities = 209/312 (66%), Positives = 266/312 (84%), Gaps = 3/312 (0%) gb AAAG62181.1 (M92842) prs [Listeria monocytogenes] Length = 318

SeqID 788	SA-1696.1	Contig83 (808-1986 m)	74	Identities = 261/391 (66%), Positives = 323/391 (81%) gb AAAF06954.1 AF146529.1 (AF146529) aromatic amino acid aminotransferase [Lactococcus lactis subsp. cremoris] Length = 391
SeqID 789	SA-1697.1	Contig83 (57-318 m)	47	Identities = 81/242 (33%), Positives = 124/242 (50%), Gaps = 3/242 (1%) db JBA05088.1 (AF001511) unknown conserved protein [Bacillus halodurans] Length = 254
SeqID 790	SA-1698.2	Contig124 (4176-4679 m)	49	Identities = 70/150 (46%), Positives = 100/150 (66%), Gaps = 2/150 (1%) gb AAK06154.1 AE006436.3 (AE006436) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 164
SeqID 791	SA-1699.1	Contig124 (4765-6096 m)	70	Identities = 237/432 (54%), Positives = 315/432 (72%), Gaps = 3/432 (0%) sp P40778 MURC_BACSU UDP-N- ACETYLMURAMATE--ALANINE LIGASE (UDP-N- ACETYLMURAMATE--L-ALANINE SYNTHETASE) p I C68682 UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) murC - Bacillus subtilis gb AAC00294.1 (AF008220) putative UDP-N-acetylmuramate-alanine ligase [Bacillus subtilis] emb CAB14957.1 (Z99119) UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis] Length = 432
SeqID 792	SA-17.1	Contig137 (28295-29017 p)	49	Identities = 82/270 (30%), Positives = 124/270 (45%), Gaps = 34/270 (12%) p I S45091 hypothetical protein Iota - Streptococcus pyogenes plasmid pDB101. p I S68125 hypothetical protein Iota - Streptococcus pyogenes plasmid pSM19035 emb CAA47097.1 (X68468) orf Iota [Streptococcus pyogenes] Length = 268
SeqID 793	SA-170.1	Contig136 (80632-81627 m)	58	Identities = 127/331 (38%), Positives = 195/331 (58%), Gaps = 9/331 (2%) db JBA07793.1 (AB037668) hypothetical protein [Streptomyces sp. CL190] Length = 363
SeqID 794	SA-1700.1	Contig124 (6106-6896 m)	No Hits found	
SeqID 795	SA-1702.1	Contig124 (6888-9886 m)	38	Identities = 280/678 (38%), Positives = 405/678 (59%), Gaps = 21/678 (3%) emb CAA67095.1 (X98455) SNF [Bacillus cereus] Length = 1064

SeqID 796	SA-1704.1	Contig124 (10142-11452 m)	92	Identities = 377/436 (86%), Positives = 414/436 (94%) dbj BA48823.1 (AB016077) phosphoglycerate dehydrogenase [Streptococcus mutans] Length = 436
SeqID 797	SA-1705.1	Contig124 (11500-12402 m)	63	Identities = 105/313 (33%), Positives = 191/313 (60%), Gaps = 17/313 (5%) sp P05567 DUAL_BACSU PRIMOSOMAL PROTEIN DUAL prj JQBS44 primosome component (helicase loader) dnal - Bacillus subtilis emb CAA28633.1 (X04963) ORF 311 (AA 1-311) [Bacillus subtilis] emb CAA9605.1 (Z75208) replication protein [Bacillus subtilis] gb AAC00359.1 (AF082220) Dnal [Bacillus subtilis] emb CAB14656.1 (Z99118) helicase loader [Bacillus subtilis] Length = 311
SeqID 798	SA-1706.2	Contig124 (12399-13574 m)	52	Identities = 125/388 (32%), Positives = 207/388 (53%), Gaps = 14/388 (3%) gb AAK04849.1 AE006308.9 (AE006308) replication protein DnaB [Lactococcus lactis subsp. lactis] Length = 391
SeqID 799	SA-1707.2	Contig124 (13574-14053 m)	72	Identities = 100/150 (66%), Positives = 119/150 (78%), Gaps = 2/150 (1%) gb AAK04848.1 AE006308.8 (AE006308) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 148
SeqID 800	SA-171.1	Contig136 (80346-80564 m)	No Hits found	
SeqID 801	SA-1710.1	Contig98 (11651-12985 m)	No Hits found	
SeqID 802	SA-1711.1	Contig98 (10742-11626 p)	42	Identities = 97/251 (38%), Positives = 147/251 (57%), Gaps = 15/251 (5%) sp P54604 YHCT_BACSU HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INTERGENIC REGION prj JH69823 conserved hypothetical protein yncT - Bacillus subtilis emb CAA65704.1 (X96983) hypothetical protein [Bacillus subtilis] emb CAB12749.1 (Z99108) similar to hypothetical proteins [Bacillus subtilis] Length = 302
SeqID 803	SA-1712.1	Contig98 (8377-10698 m)	71	Identities = 424/773 (54%), Positives = 555/773 (70%), Gaps = 47/773 (6%) gb AAAF04735.1 AF101780.1 (AF101780) penicillin-binding protein 2a [Streptococcus pneumoniae] Length = 731

SeqID 804	SA-1714.1	Contig98 (7967-8140 m)	No Hits found	
SeqID 805	SA-1715.2	Contig98 (5728-6195 p)	49	Identities = 54/136 (39%), Positives = 77/136 (56%), Gaps = 19/136 (13%) pir JQ0138 hypothetical 18.2K protein - Pseudomonas aeruginosa Length = 202
SeqID 806	SA-1716.2	Contig98 (5724-7655 m)	22	Identities = 96/302 (31%), Positives = 143/302 (46%), Gaps = 37/302 (12%) gb AB71985.1 (U73163) Milk protein [Streptococcus equi] Length = 374
SeqID 807	SA-1718.2	Contig102 (7846-9225 p)	54	Identities = 147/473 (31%), Positives = 256/473 (54%), Gaps = 34/473 (7%) pir D69159 methyl coenzyme M reductase system, component A2 homolog - Methanobacterium thermocautotrophicum (strain Delta H) gb AAB84980.1 (AE000829) methyl coenzyme M reductase system, component A2 homolog [Methanothermobacter thermocautotrophicus] Length = 480
SeqID 808	SA-1719.1	Contig102 (7122-7853 p)	36	Identities = 49/192 (25%), Positives = 89/192 (45%), Gaps = 6/192 (3%) pir C69159 conserved hypothetical protein MTH453 - Methanobacterium thermocautotrophicum (strain Delta H) gb AAB84959.1 (AE000829) conserved protein [Methanobacterium thermocautotrophicum] Length = 252
SeqID 809	SA-172.1	Contig136 (79446-80300 p)	48	Identities = 96/291 (29%), Positives = 151/291 (51%), Gaps = 28/291 (9%) db BAB10885.1 (AB010693) gene_id:K2TC13.21-pir T04769--strong similarity to unknown protein [Arabidopsis thaliana] Length = 325
SeqID 810	SA-1720.1	Contig102 (6544-7140 p)	No Hits found	
SeqID 811	SA-1722.1	Contig102 (6129-6533 p)	42	Identities = 38/153 (24%), Positives = 69/153 (43%), Gaps = 1/153 (0%) emb CAC17502.1 (AL450432) conserved hypothetical protein [Streptomyces coelicolor] Length = 677
SeqID 812	SA-1723.1	Contig102 (5905-6087 p)	No Hits found	

SeqID 813	SA-1724.1	Contig102 (5475-5918 p)	62	<p>Identities = 77/221 (34%), Positives = 114/221 (50%), Gaps = 47/221 (21%) pirI30345 lrp5 protein - <i>Yersinia enterocolitica</i> embICAA73130.1 (Y12527) lrp5 protein [Yersinia enterocolitica] Length = 525</p> <p>Identities = 111/270 (41%), Positives = 165/270 (61%), Gaps = 22/270 (8%) spIP40871IDBE_BACSU.2.3- DIHYDROXYBENZOATE-AMP LIGASE [DIHYDROXYBENZOIC ACID-ACTIVATING ENZYME] pirID9815 2.3-dihydroxybenzoate-[carrier protein] ligase (EC 6.2.1.-) dhbE - <i>Bacillus subtilis</i> gbAAC44632.1 (U28444) 2.3-dihydroxybenzoate-AMP ligase [Bacillus subtilis] embICAB15188.1 (Z99120) 2,3-dihydroxybenzoate-AMP ligase (enterobactin synthetase component E) [Bacillus subtilis] Length = 539</p>
SeqID 814	SA-1725.1	Contig102 (4535-5375 p)	59	
SeqID 815	SA-1726.1	Contig102 (3969-4343 p)	48	<p>Identities = 43/113 (38%), Positives = 64/113 (56%), Gaps = 1/113 (0%) pirIE71058 hypothetical protein PH1163 - <i>Pyrococcus horikoshii</i> dbjIBAA30283.1 (AP000005) 148aa long hypothetical protein [Pyrococcus horikoshii] Length = 148</p> <p>Identities = 78/151 (51%), Positives = 108/151 (70%) dbjIBAB05053.1 (AP001511) late competence operon required for DNA binding and uptake [Bacillus halodurans] Length = 188</p>
SeqID 816	SA-1728.1	Contig102 (3469-3921 p)	67	
SeqID 817	SA-1729.1	Contig102 (2390-3457 p)	68	<p>Identities = 183/352 (51%), Positives = 258/352 (72%), Gaps = 3/352 (0%) embICAA70068.1 (Y08842) aminopeptidase P [Lactococcus lactis] Length = 352</p>
SeqID 818	SA-173.1	Contig136 (78431-79545 p)	51	<p>Identities = 83/308 (26%), Positives = 160/308 (51%), Gaps = 12/308 (3%) pirIF59795 conserved hypothetical protein yefQ - <i>Bacillus subtilis</i> embICAB12492.1 (Z99107) similar to hypothetical proteins [Bacillus subtilis] Length = 303</p>
SeqID 819	SA-1730.1	Contig102 (1574-2290 p)	No Hits found	

SeqID 820	SA-1731.1	Contig102 (43-1572 p)	58	Identities = 198/481 (41%), Positives = 300/481 (62%), Gaps = 24/481 (4%) pirJF69763 multidrug resistance protein homolog ynfB - <i>Bacillus subtilis</i> dbj BA00916.1 (D50453) homolog of multidrug resistance protein B, <i>EmrB</i> , of <i>E. coli</i> [Bacillus subtilis] emb CAB12192.1 (Z99106) similar to multidrug resistance protein [Bacillus subtilis] Length = 472
SeqID 821	SA-1732.1	Contig130 (71572-71979 p)	67	Identities = 73/135 (54%), Positives = 94/135 (69%), Gaps = 5/135 (3%) gb AA098856.1 (AF043542) nucleoside diphosphate kinase [Gallus gallus] Length = 153
SeqID 822	SA-1734.1	Contig130 (70987-71262 p)	No Hits found	
SeqID 823	SA-1736.1	Contig130 (69998-70358 p)	No Hits found	
SeqID 824	SA-1737.1	Contig130 (69290-69665 p)	No Hits found	
SeqID 825	SA-1738.1	Contig130 (68962-69303 p)	54	Identities = 44/104 (42%), Positives = 63/104 (60%), Gaps = 2/104 (1%) pirJF81982 hypothetical protein NMA0629 [imported] - <i>Neisseria meningitidis</i> (group A strain Z2491) emb CAB83918.1 (AL162753) hypothetical protein NMA0629 [Neisseria meningitidis] Length = 108
SeqID 826	SA-1739.1	Contig136 (68096-68965 p)	41	Identities = 71/224 (31%), Positives = 123/224 (54%) pirJG81982 hypothetical protein NMA0630 [imported] - <i>Neisseria meningitidis</i> (group A strain Z2491) emb CAB83919.1 (AL162753) hypothetical protein NMA0630 [Neisseria meningitidis] Length = 304
SeqID 827	SA-174.1	Contig136 (77700-78344 p)	58	Identities = 79/204 (38%), Positives = 132/204 (63%), Gaps = 4/204 (1%) snpP64176 HLV3_BACCE HEMOLYSIN III (HLV-III) pir S59667 hemolysin III - <i>Bacillus cereus</i> emb CAA58877.1 (X84058) novel hemolytic factor [Bacillus cereus] Length = 219

SeqID 828	SA-1740.2	Contig130 (63931-68094 p)	21	Identities = 170/765 (22%), Positives = 303/765 (39%), Gaps = 90/765 (11%) pir F81299 hypothetical protein Cj1523c [imported] -Campylobacter jejuni (strain NCTC 11168) emb CAB73943.1 (AL139078) hypothetical protein Cj1523c [Campylobacter jejuni] Length = 984
SeqID 829	SA-1741.2	Contig133 (58296-58787 p)	32	Identities = 35/109 (32%), Positives = 62/109 (56%), Gaps = 1/109 (0%) pir T35305 probable acetyltransferase - Streptomyces coelicolor emb CAB51273.1 (AL086872) putative acetyltransferase [Streptomyces coelicolor A3(2)] Length = 169
SeqID 830	SA-1742.1	Contig133 (58780-60048 p)	72	Identities = 248/417 (59%), Positives = 315/417 (75%), Gaps = 4/417 (0%) pir D69981 conserved hypothetical protein yrnN - Bacillus subtilis emb CAB14895.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] emb CAB14712.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 421
SeqID 831	SA-1744.1	Contig133 (60591-60896 m)	No Hits found	
SeqID 832	SA-1745.1	Contig133 (60880-61281 m)	No Hits found	
SeqID 833	SA-1746.1	Contig133 (61269-62477 m)	No Hits found	
SeqID 834	SA-1747.1	Contig133 (62478-62811 m)	No Hits found	
SeqID 835	SA-1748.1	Contig133 (62938-63327 m)	30	Identities = 26/79 (32%), Positives = 47/79 (59%), Gaps = 1/79 (1%) pir T13289 probable integrase - Streptococcus phage phi-O1205 gb AAC79517.1 (U88974) ORF1 [Streptococcus thermophilus temperate bacteriophage O1205] Length = 359
SeqID 836	SA-1749.1	Contig133 (63625-63741 m)	No Hits found	
SeqID 837	SA-175.1	Contig136 (77246-76995 p)	No Hits found	
SeqID 838	SA-1750.1	Contig133 (63820-64088 m)	No Hits found	

SeqID 839	SA-1751.1	Contig133 (64228-64722 p)	27	Identities = 28/80 (35%), Positives = 49/80 (61%) pirID69888 transcription regulator phage-related homolog yobd - <i>Bacillus subtilis</i> gblAAB84427.1 (AF027868) transcription regulator [Bacillus subtilis] embICAB13777.1 (Z99114) similar to transcriptional regulator (phage-related) (Xre family) [Bacillus subtilis] Length = 112
SeqID 840	SA-1753.2	Contig103 (9236-10060 p)	64	Identities = 138/268 (51%), Positives = 166/268 (68%), Gaps = 2/268 (0%) gblAAK04909.1(AE006314.7 (AE006314) conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 269
SeqID 841	SA-1754.1	Contig103 (8439-9236 p)	54	Identities = 91/264 (34%), Positives = 146/264 (54%), Gaps = 4/264 (1%) spIP75809 YBUI_ECOLI PROTEIN YBUI Length = 271
SeqID 842	SA-1755.1	Contig103 (4809-8348 p)	61	Identities = 458/1193 (38%), Positives = 728/1193 (60%), Gaps = 27/1193 (2%) spIP51834 SMC_BACSU CHROMOSOME PARTITION PROTEIN SMC pirIG69708 chromosome segregation SMC protein - <i>Bacillus subtilis</i> embICAB13467.1 (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis] Length = 1186
SeqID 843	SA-1756.1	Contig103 (4115-4801 p)	63	Identities = 115/231 (49%), Positives = 155/231 (66%), Gaps = 1/231 (0%) spIP51833 RNC_BACSU RIBONUCLEASE III (RNASE III) pirIB69693 rbonuclease III (EC 3.1.26.3) - <i>Bacillus subtilis</i> embICAB13466.1 (Z99112) rbonuclease III [Bacillus subtilis] Length = 249
SeqID 844	SA-1757.1	Contig103 (3571-3939 p)	54	Identities = 50/114 (43%), Positives = 72/114 (62%) embICAB12789.1 (AJ279090) hypothetical protein [Staphylococcus carnosus] Length = 129
SeqID 845	SA-1758.1	Contig103 (2759-3568 p)	90	Identities = 223/269 (82%), Positives = 246/269 (90%) embICAB65453.1 (AJ012051) Vck protein [Streptococcus pyogenes] Length = 270
SeqID 846	SA-1759.1	Contig103 (1406-2755 p)	86	Identities = 335/443 (75%), Positives = 392/443 (87%) embICAB65452.1 (AJ012051) Vck protein [Streptococcus pyogenes] Length = 452

SeqID 839	SA-1751.1	Contig133 (64228-64722 p)	27	Identities = 28/80 (35%), Positives = 49/80 (61%) p[ir]D9898 transcription regulator phage-related homolog yobD - <i>Bacillus subtilis</i> gblAAB84427.1 (AF027868) transcription regulator [<i>Bacillus subtilis</i>] emb CAB13777.1 (Z99114) similar to transcriptional regulator (phage-related) (Xre family) [<i>Bacillus subtilis</i>] Length = 112
SeqID 840	SA-1753.2	Contig103 (9236-10060 p)	64	Identities = 138/288 (51%), Positives = 189/268 (68%), Gaps = 2/268 (0%) gblAAK04909.1AE06314.7 (AE06314) conserved hypothetical protein [<i>Lactococcus lactis</i> subsp. <i>lactis</i>] Length = 269
SeqID 841	SA-1754.1	Contig103 (8439-9236 p)	54	Identities = 51/264 (34%), Positives = 145/264 (54%), Gaps = 4/264 (1%) sp P75809 YB_J_ECOLI PROTEIN YB_J Length = 271
SeqID 842	SA-1755.1	Contig103 (4809-8348 p)	61	Identities = 458/1193 (38%), Positives = 728/1193 (60%), Gaps = 27/1193 (2%) sp P51834 SMC_BACSU CHROMOSOME PARTITION PROTEIN SMC p[ir]G9708 chromosome segregation SMC protein - <i>Bacillus subtilis</i> emb CAB13467.1 (Z99112) chromosome segregation SMC protein homolog [<i>Bacillus subtilis</i>] Length = 1186
SeqID 843	SA-1756.1	Contig103 (4115-4801 p)	63	Identities = 115/231 (49%), Positives = 155/231 (66%), Gaps = 1/231 (0%) sp P51833 RNC_BACSU RIBONUCLEASE III (RNASE III) p[ir]B99693 ribonuclease III (EC 3.1.26.3) - <i>Bacillus subtilis</i> emb CAB13466.1 (Z99112) ribonuclease III [<i>Bacillus subtilis</i>] Length = 249
SeqID 844	SA-1757.1	Contig103 (3571-3939 p)	54	Identities = 50/114 (43%), Positives = 72/114 (62%) emb CAC12789.1 (AJ279090) hypothetical protein [<i>Staphylococcus carnosus</i>] Length = 129
SeqID 845	SA-1758.1	Contig103 (2755-3568 p)	90	Identities = 23/269 (82%), Positives = 246/269 (90%) emb CAB65453.1 (AJ012051) Vck protein [<i>Streptococcus pyogenes</i>] Length = 270
SeqID 846	SA-1759.1	Contig103 (1406-2755 p)	86	Identities = 335/443 (75%), Positives = 392/443 (87%) emb CAB65452.1 (AJ012051) Vck protein [<i>Streptococcus pyogenes</i>] Length = 452

SeqID 847	SA-1761.1	Contig136 (75871-77154 p)	77	Identities = 266/421 (63%), Positives = 344/421 (81%), Gaps = 3/421 (0%) gblAAC02454.1(AF290098) HMG-CoA reductase [Streptococcus pneumoniae] Length = 424 Identities = 205/237 (86%), Positives = 222/237 (93%) emb CAB66461.1(AJ012051) VioR protein [Streptococcus pyogenes] Length = 239
SeqID 848	SA-1760.1	Contig103 (703-1413 p)	93	
SeqID 849	SA-1761.1	Contig103 (15-215 p)	No Hits found	
SeqID 850	SA-1762.2	Contig118 (26352-25687 p)	57	Identities = 33/110 (30%), Positives = 65/110 (59%) gblAAC62417.1(AF084104) hypothetical protein [Bacillus firmus] Length = 118
SeqID 851	SA-1763.1	Contig118 (24102-25268 p)	73	Identities = 227/390 (58%), Positives = 284/390 (72%), Gaps = 2/390 (0%) dbj BA05375.1(AP001512) chorismate synthase [Bacillus halodurans] Length = 390
SeqID 852	SA-1764.1	Contig118 (23034-24101 p)	55	Identities = 137/351 (39%), Positives = 199/351 (56%), Gaps = 4/351 (1%) sp P73997 AROB_SYNY3 3-DEHYDROQUINATE SYNTHASE pir IS75507 3-dehydroquinolate synthase - Synecocystis sp. (strain PCC 6803) dbj BA18086.1(D90911) 3-dehydroquinolate synthase [Synecocystis sp.] Length = 361
SeqID 853	SA-1765.1	Contig118 (22263-22840 p)	53	Identities = 70/233 (30%), Positives = 127/233 (54%), Gaps = 12/233 (5%) sp P35146 AROD_BACSU 3-DEHYDROQUINATE DEHYDRATASE (3-DEHYDROQUINASE) (TYPE 1DHQASE) pir IS45563 3-dehydroquinolate dehydratase (EC 4.2.1.10) aroC - Bacillus subtilis gbl AA67501.1(L09228) dehydroquinolate dehydratase [Bacillus subtilis] emb CAB14240.1(Z99116) 3-dehydroquinolate dehydratase [Bacillus subtilis] Length = 255

SeqID 854	SA-1766.1	Contig118 (21106-22263 p)	59	<p>Identities = 161/396 (40%), Positives = 234/396 (59%), Gaps = 11/396 (2%) spIP39687[YWBD_BACSU HYPOTHETICAL 44.4 KD PROTEIN IN EPR-GALK INTERGENIC REGION. pir IS39674 ywbd protein - Bacillus subtilis emb CAA51575.1 (X73124) ipa-19d [Bacillus subtilis] emb CAB15862.1 (Z99123) alternate gene name: ipa-19d-similar to hypothetical proteins [Bacillus subtilis] Length = 396</p>
SeqID 855	SA-1767.1	Contig118 (18827-20971 m)	57	<p>Identities = 298/682 (43%), Positives = 417/682 (60%), Gaps = 33/682 (4%) pir D59815 conserved hypothetical protein ynfI - Bacillus subtilis dbj BAZ0116.1 (D86418) YnfI [Bacillus subtilis] emb CAB12545.1 (Z99107) alternate gene name: ynfP-similar to hypothetical proteins [Bacillus subtilis] Length = 682</p>
SeqID 856	SA-1768.2	Contig118 (18227-16586 p)	91	<p>Identities = 101/119 (84%), Positives = 110/119 (91%) gb AAK05940.1(AE006414.6 (AE006414) 50S ribosomal protein L20 [Lactococcus lactis subsp. lactis] Length = 119</p>
SeqID 857	SA-1769.2	Contig118 (15777-15974 m)	44	<p>Identities = 36/85 (55%), Positives = 49/85 (75%), Gaps = 2/85 (3%) gb AAK05803.1(AE006401.4 (AE006401) ferredoxin [Lactococcus lactis subsp. lactis] Length = 67</p>
SeqID 858	SA-177.1	Contig136 (74670-75869 p)	72	<p>Identities = 261/365 (67%), Positives = 325/365 (83%) gb AAG02448.1(AF290096.1 (AF290096) HMGC-CoA synthase [Streptococcus pyogenes] Length = 391</p>
SeqID 859	SA-1770.1	Contig118 (15299-15790 p)	40	<p>Identities = 44/135 (32%), Positives = 66/135 (48%), Gaps = 10/135 (7%) spIP36920[EBSA_ENTFA PORE FORMING PROTEIN EBSA. pir IA48939 ebsa protein - Enterococcus faecalis gb AAC35851.1 (L23802) pore-forming peptide [Enterococcus faecalis] Length = 153</p>

SeqID 860	SA-1771.1	Contig118 (14050-15270 p)	81	<p>Identities = 274/406 (67%), Positives = 334/406 (81%), Gaps = 4/406 (0%) spjP42020 PEPT_LACLC PEPTIDASE T (AMINOTRIPEPTIDASE) (TRIPEPTIDASE) gb AA020627.1 (L27596) tripeptidase [Lactococcus lactis] Length = 413</p>
SeqID 861	SA-1772.1	Contig118 (12280-13914 p)	54	<p>Identities = 178/545 (32%), Positives = 302/545 (54%), Gaps = 26/545 (4%) pjljG6992 spore cortex protein homolog Ygp - Bacillus subtilis gb AAC00276.1 (AF002220) Ygp [Bacillus subtilis] emb CAB14983.1 (Z98119) similar to spore cortex protein [Bacillus subtilis] Length = 544</p>
SeqID 862	SA-1773.1	Contig118 (10702-12096 m)	47	<p>Identities = 153/468 (32%), Positives = 237/468 (49%), Gaps = 23/468 (4%) dbj BAB06290.1 (AP001515) UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate ligase [Bacillus halodurans] Length = 486</p>
SeqID 863	SA-1774.2	Contig118 (9753-10547 m)	68	<p>Identities = 141/259 (54%), Positives = 193/259 (74%) gb AAD33527.2 AF132117.4 (AF132117) FhuA [Staphylococcus aureus] gb AAF58153.1 AF251216.1 (AF251216) FhuC [Staphylococcus aureus] Length = 265</p>
SeqID 864	SA-1775.2	Contig118 (8797-8729 m)	55	<p>Identities = 95/301 (31%), Positives = 178/301 (58%), Gaps = 11/301 (3%) dbj BAB07609.1 (AP001520) ferrichrome ABC transporter (ferrichrome-binding protein) [Bacillus halodurans] Length = 308</p>
SeqID 865	SA-1776.1	Contig118 (7758-8781 m)	56	<p>Identities = 117/313 (37%), Positives = 195/313 (61%), Gaps = 3/313 (0%) gb AAD33526.3 AF132117.3 (AF132117) ferrichrome transport permease [Staphylococcus aureus] gb AAF58154.1 AF251216.2 (AF251216) FhuB [Staphylococcus aureus] Length = 341</p>
SeqID 866	SA-1778.1	Contig118 (6758-7759 m)	61	<p>Identities = 122/334 (36%), Positives = 210/334 (62%), Gaps = 3/334 (0%) gb AAD33524.3 AF132117.1 (AF132117) ferrichrome transport permease [Staphylococcus aureus] gb AAF58155.1 AF251216.3 (AF251216) FhuG [Staphylococcus aureus] Length = 338</p>

SeqID 867	SA-1779.2	Contig118 (6075-6728 p)	50	Identities = 89/233 (38%), Positives = 128/233 (54%), Gaps = 23/233 (9%) gb AA05909.1 AE06411_4 (AE06411) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 265
SeqID 868	SA-178.1	Contig136 (73704-74543 m)	83	Identities = 215/280 (76%), Positives = 244/280 (86%), Gaps = 2/280 (0%) sp P19368 TYSY_LACLA THYMIDYLATE SYNTHASE (TS) (TSASE) pir A43797 thymidylate synthase (EC 2.1.1.45) - Lactococcus lactis subsp. lactis gb AA025221.1 (M33770) thymidylate synthase (EC 2.1.1.45) [Lactococcus lactis] Length = 279
SeqID 869	SA-1780.2	Contig138 (28940-29971 m)	53	Identities = 137/350 (39%), Positives = 211/350 (60%), Gaps = 3/350 (0%) emb CAB54584.1 (AJ006400) histidine kinase [Streptococcus pneumoniae] Length = 365
SeqID 870	SA-1781.1	Contig138 (30022-30762 m)	51	Identities = 73/239 (30%), Positives = 127/239 (52%), Gaps = 4/239 (1%) emb CAB69806.1 (AJ243712) YVFS protein [Bacillus cereus] Length = 239
SeqID 871	SA-1783.1	Contig138 (30749-31645 m)	42	Identities = 83/216 (38%), Positives = 136/216 (62%), Gaps = 1/216 (0%) gb AA021390.1 AF302051_4 (AF302051) ABC transporter ATP binding subunit [Bacillus licheniformis] Length = 289
SeqID 872	SA-1784.1	Contig138 (31774-33384 m)	74	Identities = 303/533 (56%), Positives = 401/533 (74%), Gaps = 15/533 (2%) gb AA034762.1 AF228345_1 (AF228345) unknown [Listeria monocytogenes] Length = 520
SeqID 873	SA-1785.1	Contig138 (33573-34055 p)	89	Identities = 129/160 (80%), Positives = 149/160 (92%) gb AA028749.1 AF295118_1 (AF295118) LuxS [Streptococcus pyogenes] Length = 170
SeqID 874	SA-1787.1	Contig138 (34280-35743 m)	30	Identities = 71/398 (17%), Positives = 152/398 (37%), Gaps = 16/398 (4%) gb AAD16120.1 (AF094508) dentin phosphoryn [Homo sapiens] Length = 788

SeqID 875	SA-1788.1	Contig138 (35756-36910 m)	70	Identities = 204/383 (53%), Positives = 276/383 (71%), Gaps = 3/383 (0%) spIP50840YPCB_BACSU HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSORS prjIF69941 conserved hypothetical protein ypsC - Bacillus subtilis gb AAB38473.1 (L47838) putative [Bacillus subtilis] emb CAB14134.1 (Z99115) similar to hypothetical proteins [Bacillus subtilis] Length = 385
SeqID 876	SA-179.1	Contig136 (73130-73624 m)	62	Identities = 83/166 (50%), Positives = 121/166 (72%), Gaps = 1/166 (0%) gb AAC33872.1 (AF055727) dithyolate reductase [Streptococcus pneumoniae] Length = 168
SeqID 877	SA-1791.2	Contig138 (37380-37724 m)	57	Identities = 46/102 (45%), Positives = 69/102 (67%), Gaps = 14/102 (13%) spIP50839YPSB_BACSU HYPOTHETICAL 11.6 KD PROTEIN IN COTD-KDUD INTERGENIC REGION prjIF69941 hypothetical protein ypsB - Bacillus subtilis gb AAB38472.1 (L47838) putative [Bacillus subtilis] emb CAB14135.1 (Z99115) ypsB [Bacillus subtilis] Length = 98
SeqID 878	SA-1792.1	Contig86 (6483-7529 m)	57	Identities = 131/350 (37%), Positives = 200/350 (56%), Gaps = 14/350 (4%) spIP42977IPAPS_BACSU POLY(A) POLYMERASE (PAP) prjIB69672 poly(A) polymerase papS - Bacillus subtilis gb AAB38446.1 (L47708) poly(A) polymerase [Bacillus subtilis] emb CAB14161.1 (Z99115) poly(A) polymerase [Bacillus subtilis] Length = 357
SeqID 879	SA-1793.1	Contig86 (4604-6472 m)	63	Identities = 259/625 (43%), Positives = 397/625 (63%), Gaps = 11/625 (1%) prjIA69814 ABC transporter (ATP-binding protein) homolog ymrK - Bacillus subtilis dbj BAA20107.1 (D86418) YmrK [Bacillus subtilis] emb CAB12556.1 (Z99107) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] emb CAB12556.1 (Z99108) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 629

SeqID 880	SA-1794.1	Contig86 (4134-4807 m)	57	Identities = 56/161 (34%), Positives = 92/161 (56%), Gaps = 8/161 (4%) sp P39337 JGM_ECOLI_HYPOTHETICAL_18.6_KDA PROTEIN IN ARG-VALS INTERGENIC REGION Length = 167
SeqID 881	SA-1795.1	Contig86 (2328-4087 m)	58	Identities = 227/565 (40%), Positives = 342/565 (60%), Gaps = 1/565 (0%) emb CAB69751.1 (AL137187) putative ABC transporter [Streptomyces coelicolor A3(2)] Length = 577
SeqID 882	SA-1796.1	Contig86 (654-2245 m)	65	Identities = 270/611 (44%), Positives = 391/611 (63%), Gaps = 31/611 (5%) emb CAB69752.1 (AL137187) putative ABC transporter [Streptomyces coelicolor A3(2)] Length = 642
SeqID 883	SA-1797.1	Contig86 (4-513 p)	69	Identities = 78/167 (46%), Positives = 118/167 (69%), Gaps = 1/167 (0%) pir J433141 hypothetical protein (gtd 3 region) - Streptococcus mutans Length = 169
SeqID 884	SA-1798.3	Contig93 (7851-8347 p)	65	Identities = 250/500 (50%), Positives = 329/500 (65%), Gaps = 4/500 (0%) sp P23865 MALD_STRPN+ALPHA-GLUCANOTRANSFERASE (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) gb AA28923.1 (J01796) amylomaltase [Streptococcus pneumoniae] Length = 505
SeqID 885	SA-1799.3	Contig93 (9359-11623 p)	59	Identities = 297/776 (38%), Positives = 452/776 (57%), Gaps = 41/776 (5%) sp P39123 PHSG_BACSU GLYCOGEN PHOSPHORYLASE pir S36628 glycogen phosphorylase (EC 2.4.1.1) - Bacillus subtilis pir S40052 glycogen phosphorylase (EC 2.4.1.1) g P - Bacillus subtilis emb CAA81044.1 (Z25795) Glycogen Phosphorylase [Bacillus subtilis] gb AAC00218.1 (AF008220) glycogen phosphorylase [Bacillus subtilis] emb CAB15072.1 (Z39119) glycogen phosphorylase [Bacillus subtilis] Length = 798

SeqID 886	SA-18.1	Contig137 (25957-28218 p)	35	<p>Identities = 178/715 (24%), Positives = 273/715 (37%), Gaps = 117/715 (16%) pir G41882.130K surface exclusion protein [Sec10 precursor - Enterococcus faecalis plasmid pCF10 gb AAA65947.1] (M64978) surface exclusion protein [Plasmid pCF10] Length = 891</p>
SeqID 887	SA-1801.2	Contig139 (45477-45692 p)	75	<p>Identities = 28/76 (36%), Positives = 55/76 (71%), Gaps = 4/76 (5%) pir E83139 exodeoxyribonuclease VII small subunit PA4042 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA07428.1 AE004821_2 (AE004821) exodeoxyribonuclease VII small subunit [Pseudomonas aeruginosa] Length = 80</p>
SeqID 888	SA-1802.1	Contig139 (44159-45499 p)	63	<p>Identities = 194/446 (43%), Positives = 284/446 (63%), Gaps = 10/446 (2%) sp P54521 EX7L_BACSU PUTATIVE EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EXONUCLEASE VII LARGE SUBUNIT) pir G69960 exodeoxyribonuclease VII (large subunit) homolog yqjB - Bacillus subtilis dbj BAA12573.1 (D84432) YqjB [Bacillus subtilis] emb CAB14361.1 (Z89116) similar to exodeoxyribonuclease VII (large subunit) [Bacillus subtilis] Length = 448</p>
SeqID 889	SA-1803.1	Contig139 (43197-44033 p)	67	<p>Identities = 149/277 (53%), Positives = 191/277 (68%) sp P96050 FOL_STRTTR HYPOTHETICAL 29.9 KD PROTEIN IN FOLD-PBP2B INTERGENIC REGION (ORF1091) gb AAC44613.1 (U58210) orf1091 [Streptococcus thermophilus] Length = 278</p>
SeqID 890	SA-1804.1	Contig139 (42346-43200 p)	83	<p>Identities = 209/282 (74%), Positives = 249/282 (87%) sp P96050 FOLD_STRTTR FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE] gb AAC44612.1 (U58210) tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus] Length = 284</p>

SeqID 891	SA-1806.1	Contig139 (40513-42207 p)	60	Identities = 238/548 (43%), Positives = 343/548 (62%), Gaps = 14/548 (2%) doiJBAB04828.1 (AF001510) phosphomannomutase [Bacillus nadorans] Length = 578
SeqID 892	SA-1807.2	Contig139 (39492-40226 p)	78	Identities = 153/239 (64%), Positives = 193/239 (80%) refINP_069514.1 glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus] pirlj1489334 glutamine transport protein glnQ - Archaeoglobus fulgidus gb/AAB0561.1 (AE001058) glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus] Length = 242
SeqID 893	SA-1808.2	Contig139 (38801-39499 p)	55	Identities = 92/209 (44%), Positives = 129/209 (61%), Gaps = 10/209 (4%) refINP_069070.1 glutamine ABC transporter, permealase protein (glnP) [Archaeoglobus fulgidus] pirlj1489278 glutamine ABC transporter, permealase protein (glnP) homolog - Archaeoglobus fulgidus gb/AAB91000.1 (AE001090) glutamine ABC transporter, permealase protein (glnP) [Archaeoglobus fulgidus] Length = 224
SeqID 894	SA-1809.2	Contig98 (8855-9556 m)	68	Identities = 150/231 (64%), Positives = 178/231 (76%), Gaps = 1/231 (0%) spIQ9ZHA7IDCOP_STRPN OROTIDINE 5 - PHOSPHATE DECARBOXYLASE (OMP DECARBOXYLASE) (OMPDCASE) gb/AAC95452.1 (AF068902) orotidine-5 - decarboxylase PyrF [Streptococcus pneumoniae] Length = 233
SeqID 895	SA-181.1	Contig136 (71686-72912 m)	85	Identities = 306/395 (77%), Positives = 357/395 (89%), Gaps = 1/395 (0%) gb/AAC63738.1 (AF236863) protease ClpX [Lactococcus lactis] Length = 411
SeqID 896	SA-1810.1	Contig98 (8213-8842 m)	84	Identities = 152/208 (73%), Positives = 180/208 (86%) gb/AAC95453.1 (AF068902) orotate phosphoribosyltransferase PyrE [Streptococcus pneumoniae] Length = 210

SeqID 897	SA-1812.1	Contig89 (6909-8201 m)	57	Identities = 176/422 (41%), Positives = 255/422 (59%), Gaps = 9/422 (1%) sp O68990 PYRC_AQUAE DIHYDROOROTASE (DHOASE) p pf C70370 dihydroorotase - Aquifex aeolicus gb AAC06948.1 (AE000708) dihydroorotase [Aquifex aeolicus] Length = 422
SeqID 898	SA-1813.1	Contig89 (5821-6744 m)	80	Identities = 197/303 (65%), Positives = 250/303 (82%) gb AAF72727.1 (AF264709) aspartate transcarbamoylase [Enterococcus faecalis] Length = 308
SeqID 899	SA-1814.1	Contig89 (4731-5807 m)	82	Identities = 242/355 (68%), Positives = 305/355 (85%) emb CAB89872.1 (AJ132624) carbamoyl phosphate synthetase small subunit [Lactococcus lactis] Length = 357
SeqID 900	SA-1815.1	Contig89 (1518-4700 m)	84	Identities = 771/1082 (72%), Positives = 900/1082 (84%), Gaps = 5/1082 (0%) emb CAA03928.1 (AJ000109) carbamoylphosphate synthetase [Lactococcus lactis] Length = 1054
SeqID 901	SA-1816.1	Contig89 (1068-1391 m)	No Hits found	
SeqID 902	SA-1817.2	Contig89 (289-1071 m)	22	Identities = 39/130 (30%), Positives = 59/130 (45%), Gaps = 26/130 (20%) p pf T38271 conserved hypothetical protein SPAC23C4.16c - fission yeast (Schizosaccharomyces pombe) emb CAB16887.1 (Z99753) conserved hypothetical protein [Schizosaccharomyces pombe] Length = 424
SeqID 903	SA-1818.2	Contig91 (6891-7685 p)	68	Identities = 166/266 (62%), Positives = 207/266 (77%), Gaps = 2/266 (0%) gb AAK03380.1 (AE006360) glutamate racemase (EC 5.1.1.3) [Lactococcus lactis subsp. lactis] Length = 271
SeqID 904	SA-1819.1	Contig91 (7682-8656 p)	38	Identities = 96/189 (50%), Positives = 130/189 (67%), Gaps = 1/189 (0%) p pf C99986 conserved hypothetical protein ysnA - Bacillus subtilis emb CAA99555.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14796.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 198

SeqID 905	SA-182.1	Contig136 (71079-71675 m)	80	Identities = 141/193 (73%), Positives = 165/193 (85%) gb AA63739.1 AF236863.3 (AF236863) hypothetical GTP-binding protein [Lactococcus lactis] Length = 195
SeqID 906	SA-1820.1	Contig91 (8638-9159 p)	53	Identities = 55/169 (32%), Positives = 96/169 (56%), Gaps = 1/169 (0%) db JAB05785.1 (AP001517) unknown conserved protein [Bacillus halodurans] Length = 169
SeqID 907	SA-1821.1	Contig91 (9156-9629 p)	44	Identities = 37/136 (27%), Positives = 73/136 (53%), Gaps = 1/136 (0%) db JAB05201.1 (AP001512) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 146
SeqID 908	SA-1822.1	Contig91 (9748-10359 p)	43	Identities = 66/271 (24%), Positives = 116/271 (42%), Gaps = 35/271 (12%) db JAB05248.1 (AP001512) integrase/recombinase [Bacillus halodurans] Length = 299
SeqID 909	SA-1823.1	Contig91 (10398-10685 p)	70	Identities = 52/106 (49%), Positives = 78/106 (73%) pir JAB3244 conserved hypothetical protein PA3198 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA06586.1 AE004744.1 (AE004744) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 250
SeqID 910	SA-1824.1	Contig91 (10786-11070 p)	49	Identities = 39/138 (28%), Positives = 65/138 (46%), Gaps = 14/138 (10%) sp P35154 YIPUG_BACSU HYPOTHETICAL 29.6 KD PROTEIN IN RIBT-DACB INTERGENIC REGION (ORFX7) pir J54549 conserved hypothetical protein ypuG - Bacillus subtilis gb AA487487.1 (L09228) ORFX7 [Bacillus subtilis] emb CA614254.1 (Z299116) similar to hypothetical proteins [Bacillus subtilis] Length = 251
SeqID 911	SA-1825.1	Contig91 (11067-11651 p)	52	Identities = 75/180 (41%), Positives = 107/180 (58%), Gaps = 10/180 (5%) db JAB05230.1 (AP001512) unknown conserved protein [Bacillus halodurans] Length = 197
SeqID 912	SA-1826.1	Contig91 (11641-12363 p)	67	Identities = 130/239 (54%), Positives = 175/239 (72%), Gaps = 2/239 (0%) db JAB05295.1 (AP001512) pseudouridy/ate synthase [Bacillus halodurans] Length = 242

SeqID 913	SA-1827.1	Contig91 (12363-12614 p)	66	Identities = 43/75 (57%), Positives = 57/75 (75%), Gaps = 1/75 (1%) pirI[G72251 conserved hypothetical protein - Thermoboga maritima strain MS88] gb AAD36530.1 AE001797_10 (AE001797) conserved hypothetical protein [Thermoboga maritima] Length = 81
SeqID 914	SA-1828.1	Contig91 (12762-12881 p)	No Hits found	Identities = 44/172 (25%), Positives = 80/172 (45%), Gaps = 27/172 (15%) gb AAG09669.1 AF248037.4 (AF248037) unknown [Streptococcus agalactiae] Length = 174
SeqID 915	SA-183.1	Contig136 (70469-71098 p)	36	Identities = 165/480 (34%), Positives = 261/480 (54%), Gaps = 10/480 (2%) ref NP_069873.1 TRK potassium uptake system protein (trkH) [Archaeoglobus fulgidus] pir G69364 TRK potassium uptake system protein (trkH) homolog - Archaeoglobus fulgidus gb AAB90400.1 (AE001046) TRK potassium uptake system protein (trkH) [Archaeoglobus fulgidus] Length = 478
SeqID 916	SA-1830.1	Contig91 (12638-14077 m)	53	Identities = 136/446 (30%), Positives = 238/446 (52%), Gaps = 12/446 (2%) ref NP_069872.1 TRK potassium uptake system protein (trkA-2) [Archaeoglobus fulgidus] sp Q29420 TRKA_ARCFU TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKA HOMOLOG pir G69354 TRK potassium uptake system protein (trkA-2) homolog - Archaeoglobus fulgidus gb AAB90401.1 (AE001046) TRK potassium uptake system protein (trkA-2) [Archaeoglobus fulgidus] Length = 435
SeqID 917	SA-1832.1	Contig91 (14082-15431 m)	52	Identities = 91/289 (31%), Positives = 146/289 (50%), Gaps = 14/289 (4%) sp P12055 STR_STAAU STREPTOMYCIN RESISTANCE PROTEIN pir S00936 str protein - Staphylococcus aureus plasmid pS194 emb CAA29839.1 (X08627) ORF (str) [Staphylococcus aureus] Length = 282
SeqID 918	SA-1834.1	Contig85 (10632-11486 p)	50	
SeqID 919	SA-1835.1	Contig85 (9974-10453 p)	No Hits found	
SeqID 920	SA-1836.1	Contig85 (8870-9625 p)	No Hits found	

SeqID 921	SA-1837.1	Contig85 (8753-9031 p)	45	Identities = 31/103 (30%), Positives = 57/103 (55%), Gaps = 4/103 (3%) pir G575166 hypothetical protein PAB0331 - Pyrococcus abyssi (strain Orsary) emb CA849414.1 (AJ246284) hypothetical protein [Pyrococcus abyssi] Length = 114
SeqID 922	SA-1838.1	Contig85 (7686-8174 p)	26	Identities = 32/110 (29%), Positives = 54/110 (49%), Gaps = 4/110 (3%) ref NP_057431.1 putative N-acetyltransferase Camello 2 [Homo sapiens] gb AA722299.1 AF18571_1 (AF18571) putative N-acetyltransferase Camello 2 [Homo sapiens] Length = 227
SeqID 923	SA-1839.1	Contig85 (6726-7517 p)	35	Identities = 42/188 (22%), Positives = 94/188 (49%), Gaps = 4/188 (2%) pir B70082 hypothetical protein yxIG - Bacillus subtilis db BA411738.1 (D83026) hypothetical [Bacillus subtilis] emb CA816891.1 (Z99123) yxIG [Bacillus subtilis] = 259 Length = 259
SeqID 924	SA-1840.1	Contig85 (5857-6759 p)	58	Identities = 105/301 (34%), Positives = 176/301 (57%), Gaps = 11/301 (3%) sp P54592 YHCH_BACSU HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN 2 IN GLPD-CSPB INTERGENIC REGION pir D89822 ABC transporter (ATP- binding protein) homolog yncH - Bacillus subtilis emb CAA65691.1 (X96983) hypothetical protein [Bacillus subtilis] emb CAB12736.1 (Z99108) similar to ABC transporter (ATP- binding protein) [Bacillus subtilis] Length = 305
SeqID 925	SA-1841.1	Contig85 (4576-5652 p)	19	Identities = 39/134 (29%), Positives = 71/134 (52%), Gaps = 16/134 (11%) gb AB71491.1 (U53767) ORF6 [Bacillus pumilus] Length = 211
SeqID 926	SA-1842.1	Contig85 (3704-4327 p)	50	Identities = 50/186 (26%), Positives = 105/186 (55%), Gaps = 5/186 (2%) pir S32217 hypothetical protein 2 - Bacillus megaterium emb CAA79986.1 (Z21972) ORF2 [Bacillus megaterium] Length = 216

SeqID 927	SA-1843.1	Contig85 (3203-3499 m)	58	Identities = 53/96 (55%), Positives = 70/96 (72%) p[rlC70033 hypothetical protein yvdc - Bacillus subtilis emb CAB15470.1 (Z99121) yvdc [Bacillus subtilis] Length = 106
SeqID 928	SA-1844.1	Contig85 (2626-3186 m)	62	Identities = 83/186 (44%), Positives = 117/186 (62%) dbj BAB06803.1 (AP001517) unknown conserved protein [Bacillus halodurans] Length = 187
SeqID 929	SA-1845.1	Contig85 (1458-2333 m)	21	Identities = 40/132 (30%), Positives = 63/132 (47%), Gaps = 8/132 (6%) p[rlE59787 hypothetical protein ydL - Bacillus subtilis dbj BAA19725.1 (D88802) transmembrane [Bacillus subtilis] emb CAB12420.1 (Z99107) ydL [Bacillus subtilis] Length = 244
SeqID 930	SA-1846.1	Contig85 (999-1301 p)	47	Identities = 39/92 (41%), Positives = 53/92 (57%), Gaps = 1/92 (1%) sp P54510 YQHL_BACSU HYPOTHETICAL 14.6 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION p[rlC59959 glpE protein homolog yqHl - Bacillus subtilis dbj BAA12549.1 (D84432) YqHl [Bacillus subtilis] emb CAB14385.1 (Z99116) similar to hypothetical proteins [Bacillus subtilis] Length = 126
SeqID 931	SA-1847.1	Contig85 (59-826 p)	96	Identities = 252/255 (98%), Positives = 252/255 (98%) emb CAA51283.1 (X72764) cAMP factor [Streptococcus agalactiae] Length = 255
SeqID 932	SA-1849.1	Contig88 (13289-14137 p)	54	Identities = 94/276 (34%), Positives = 154/276 (55%), Gaps = 2/276 (0%) dbj BAB07346.1 (AP001519) unknown conserved protein [Bacillus halodurans] Length = 283
SeqID 933	SA-1851.1	Contig136 (69874-70248 m)	No Hits found	
SeqID 934	SA-1850.1	Contig88 (12909-13289 p)	No Hits found	
SeqID 935	SA-1851.1	Contig88 (12304-12837 p)	No Hits found	
SeqID 936	SA-1852.1	Contig88 (11759-12253 p)	61	Identities = 65/165 (39%), Positives = 102/165 (61%), Gaps = 5/165 (3%) gb AAFG6143.1 (U81488) TceEorf2 [Lactococcus lactis subsp. cremoris] Length = 171

SeqID 937	SA-1853.1	Contig88 (10706-11140 m)	37	Identities = 42/134 (31%), Positives = 55/134 (40%), Gaps = 18/134 (13%) dbj BA049921.1 (AP001306) contains similarity to cell wall-plasma membrane linker protein-gene_id:MK23.5 [Arabidopsis thaliana] Length = 1480
SeqID 938	SA-1855.1	Contig88 (9608-11570 p)	66	Identities = 320/660 (48%), Positives = 439/660 (66%), Gaps = 48/660 (6%) dbj BA04547.1 (AP001510) PTS system: fructose-specific enzyme II _B component [Bacillus halodurans] Length = 625
SeqID 939	SA-1858.1	Contig88 (8698-9609 p)	61	Identities = 146/303 (48%), Positives = 197/303 (64%) sp Q31714 KIPF_BACSU_1- PHOSPHOFRUCTOKINASE (FRUCTOSE 1-PHOSPHATE KINASE) pir A69627 fructose 1-phosphate kinase fruB - Bacillus subtilis emb CAB13312.1 (Z89111) fructose-1-phosphate kinase [Bacillus subtilis] gb AAC24914.1 (AF012285) fructose-1-phosphate kinase [Bacillus subtilis] Length = 303
SeqID 940	SA-1859.1	Contig88 (7958-8701 p)	53	Identities = 96/248 (38%), Positives = 148/248 (58%), Gaps = 1/248 (0%) dbj BA04545.1 (AP001510) transcriptional repressor [Bacillus halodurans] Length = 251
SeqID 941	SA-186.1	Contig136 (59056-59623 m)	No Hits found	
SeqID 942	SA-1860.1	Contig88 (6592-7827 p)	68	Identities = 216/410 (52%), Positives = 284/410 (68%) emb CAB89121.1 (AJ277485) beta-lactam resistance factor [Streptococcus pneumoniae] Length = 410
SeqID 943	SA-1861.1	Contig88 (4808-6449 p)	21	Identities = 93/183 (50%), Positives = 116/183 (62%), Gaps = 9/183 (4%) pir C60328 hypothetical protein 2 (sr 5' region) - Streptococcus mutans (strain OMZ175, serotype f) Length = 179
SeqID 944	SA-1862.1	Contig88 (3679-4602 p)	48	Identities = 85/301 (28%), Positives = 150/301 (49%), Gaps = 7/301 (2%) pir H75119 probable 2-dehydropanoate 2-reductase (EC 1.1.1.169) PAB0512 - Pyrococcus abyssi (strain Orsay) emb CAB49673.1 (AJ248285) PROBABLE 2-DEHYDRO-PANTOATE 2-REDUCTASE (EC 1.1.1.169) [Pyrococcus abyssi] Length = 300

SeqID 945	SA-1863.1	Contig88 (3120-3626 m)	No Hits found	
SeqID 946	SA-1866.2	Contig129 (15399-16343 m)	54	Identities = 111/300 (37%), Positives = 175/300 (58%), Gaps = 4/300 (1%) sp P37517 CCPB_BACSU CATABOLITE CONTROL PROTEIN B. pil S66011 transcription regulator homolog yiaG - Bacillus subtilis dbj BA005217.1 (D26185) LACI family of transcriptional repressor (probable) [Bacillus subtilis] emb CAB16124.1 (Z99124) similar to transcriptional regulator (LacI family) [Bacillus subtilis] Length = 311
SeqID 947	SA-1867.1	Contig129 (14405-15340 p)	31	Identities = 63/218 (28%), Positives = 107/218 (48%), Gaps = 3/218 (1%) gb AAB17013.1 (L38252) esterase [Acholeobacter woffii] Length = 303
SeqID 948	SA-1868.1	Contig129 (13444-14127 m)	90	Identities = 228/228 (100%), Positives = 228/228 (100%) emb CAA72897.1 (Y12224) hypothetical protein [Streptococcus agalactiae] Length = 228
SeqID 949	SA-1869.1	Contig129 (12353-13390 m)	95	Identities = 343/345 (99%), Positives = 343/345 (99%) emb CAA72898.1 (Y12224) hypothetical protein [Streptococcus agalactiae] Length = 345
SeqID 950	SA-1870.1	Contig129 (11665-12273 m)	97	Identities = 202/202 (100%), Positives = 202/202 (100%) sp O54086 SODM_STRAG SUPEROXIDE DISMUTASE [MN-FE] Length = 202
SeqID 951	SA-1871.1	Contig129 (10476-11327 m)	63	Identities = 118/275 (42%), Positives = 183/275 (65%) dbj BAA11696.1 (D83026) LicT antiterminator [Bacillus subtilis] emb CAB15944.1 (Z99124) transcriptional antiterminator [BglI family] [Bacillus subtilis] Length = 277

SeqID 952	SA-1872.2	Contig129 (8615-10483 m)	55	<p>Identities = 225/594 (37%), Positives = 351/594 (58%), Gaps = 11/594 (1%) sp P40739 PTBA_BACSU PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IABC COMPONENT (EIA3C-BGL) (BETA-GLUCOSIDES-PERMEASE IABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EII-BGL) pif 40406 beta-glucoside permease - Bacillus subtilis emb CAA84286.1 (Z34526) beta-glucoside permease [Bacillus subtilis] Length = 609</p>
SeqID 953	SA-1874.1	Contig115 (24509-25441 p)	77	<p>Identities = 195/308 (63%), Positives = 245/308 (79%), Gaps = 4/308 (1%) sp P24137 OPPF_BACSU OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPF pif E38447 oligopeptide transport ATP-binding protein oppF - Bacillus subtilis gb AA462592.1 (M57688) sporulation protein [Bacillus subtilis] Length = 306</p>
SeqID 954	SA-1875.1	Contig115 (23463-24509 p)	80	<p>Identities = 230/342 (67%), Positives = 283/342 (82%), Gaps = 2/342 (0%) gb AAAF73093.1 AF103793_4 (AF103793) ATPase OppD [Listeria monocytogenes] Length = 358</p>
SeqID 955	SA-1876.1	Contig115 (22419-23450 p)	63	<p>Identities = 157/325 (48%), Positives = 219/325 (67%), Gaps = 4/325 (1%) gb AAAF73092.1 AF103793_3 (AF103793) transmembrane protein OppC [Listeria monocytogenes] Length = 344</p>
SeqID 956	SA-1878.1	Contig115 (21495-22409 p)	69	<p>Identities = 147/304 (48%), Positives = 221/304 (72%), Gaps = 1/304 (0%) gb AAAF73091.1 AF103793_2 (AF103793) transmembrane protein OppB [Listeria monocytogenes] Length = 309</p>
SeqID 957	SA-1879.2	Contig115 (19721-21376 p)	74	<p>Identities = 352/512 (68%), Positives = 416/512 (80%), Gaps = 2/512 (0%) gb AAO17885.1 (AF100466) hyaluronate-associated protein precursor [Streptococcus equi] Length = 522</p>

SeqID 958	SA-188.1	Contig136 (67560-68948 m)	74	Identities = 278/454 (61%), Positives = 351/454 (77%), Gaps = 3/454 (0%) p[1]A69751 histidine permease homolog ybgF - Bacillus subtilis embiCAB12034.1 (Z99105) similar to histidine permease [Bacillus subtilis] dbjBAA33138.1 (AB006424) ybgF [Bacillus subtilis] Length = 470
SeqID 959	SA-188.1.2	Contig132 (48543-48848 p)	78	Identities = 89/101 (88%), Positives = 94/101 (92%) spQ9WVWb[R]L24_STRPN 50S RIBOSOMAL PROTEIN L24 gb AAD33257.1(AF126059_B (AF126059) Rpl24 [Streptococcus pneumoniae] gb AAD33276.1 (AF126060) Rpl24 [Streptococcus pneumoniae] gb AAD33285.1 (AF126061) Rpl24 [Streptococcus pneumoniae] Length = 101
SeqID 960	SA-1882.2	Contig132 (48872-49414 p)	90	Identities = 157/180 (87%), Positives = 172/180 (95%) gb AAK06185.1(AE006437_15 (AE006437) 50S ribosomal protein L5 [Lactococcus lactis subsp. lactis] Length = 180
SeqID 961	SA-1883.1	Contig132 (49772-50170 p)	86	Identities = 100/132 (75%), Positives = 116/132 (87%) spP12879[IR]S8_BACSU 30S RIBOSOMAL PROTEIN S8 (BS8) gb AAB06813.1 (L47971) ribosomal protein S8 [Bacillus subtilis] Length = 132
SeqID 962	SA-1884.1	Contig132 (50280-50816 p)	72	Identities = 110/178 (61%), Positives = 134/178 (74%) sp P02391[RL6_BACST 50S RIBOSOMAL PROTEIN L6 (BL10) Length = 178
SeqID 963	SA-1885.1	Contig132 (50817-51273 p)	78	Identities = 86/120 (71%), Positives = 97/120 (80%), Gaps = 2/120 (1%) sp P46899[RL18_BACSU 50S RIBOSOMAL PROTEIN L18 gb AAB06815.1 (L47971) ribosomal protein L18 [Bacillus subtilis] Length = 120
SeqID 964	SA-1886.1	Contig132 (51292-51786 p)	81	Identities = 119/158 (75%), Positives = 139/158 (87%) sp P02357[IR]S5_BACST 30S RIBOSOMAL PROTEIN S5 (BS5) p[1]R3BS5F ribosomal protein S5 - Bacillus stearothermophilus gb AAA22699.1 (M57621) ribosomal protein S5 [Bacillus stearothermophilus] Length = 166
SeqID 965	SA-1887.1	Contig132 (51534-51890 m)	No Hits found	

SeqID 966	SA-1888.1	Contig132 (51801-51980 p)	67	<p>Identities = 40/58 (68%), Positives = 46/58 (78%) sp O06444 RL30_STAAU 50S RIBOSOMAL PROTEIN L30 gb AAB54020.1 (U96620) ribosomal protein L30 [Staphylococcus aureus] Length = 59</p>
SeqID 967	SA-1891.1	Contig132 (52105-52545 p)	84	<p>Identities = 116/146 (79%), Positives = 128/146 (87%) sp O06445 RL15_STAAU 50S RIBOSOMAL PROTEIN L15 gb AAB54021.1 (U96620) ribosomal protein L15 [Staphylococcus aureus] Length = 146</p>
SeqID 968	SA-1892.1	Contig132 (52566-53870 p)	82	<p>Identities = 292/433 (67%), Positives = 361/433 (82%), Gaps = 2/433 (0%) sp P27148 SECY_LACLA PREPROTEIN TRANSLOCASE SECY SUBUNIT p I S17985 preprotein translocase secY - Lactococcus lactis subsp. lactis emb CAA41939.1 (X59250) SecY protein [Lactococcus lactis] p I 1715214A secY gene [Lactococcus lactis] Length = 439</p>
SeqID 969	SA-1893.1	Contig132 (53965-54603 p)	77	<p>Identities = 146/214 (68%), Positives = 170/214 (79%), Gaps = 6/214 (2%) sp P27143 KAD_LACLA ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) p I S17987 adenylate kinase (EC 2.7.4.3) - Lactococcus lactis subsp. lactis p I B44812 adenylate kinase (EC 2.7.4.3) - Lactococcus lactis emb CAA41940.1 (X59250) adenylate kinase [Lactococcus lactis] Length = 215</p>

SeqID 970	SA-1894.2	Contig132 (28026-29129 p)	23	<p>Identities = 51/213 (23%), Positives = 89/213 (40%), Gaps = 32/213 (15%) pri T19214 UDP-glucose-glycoprotein glucosyltransferase (EC 2.4.1.-) precursor F26H9.8 - <i>Caenorhabditis elegans</i> emb CAB03874.1 (Z81467) predicted using GeneFinder~Similarity to <i>Drosophila</i> UDP-glucose-glycoprotein glucosyltransferase (TR-Q09332), contains similarity to Pfam domain: PF01501 (Glycosyl transferase family 8). Score=-22.6; E-value=4.8e-06; N=1-cDNA EST yk250b10.3 co> emb CAB04207.1 (Z81516) predicted using GeneFinder~Similarity to <i>Drosophila</i> UDP-glucose-glycoprotein glucosyltransferase (TR-Q09332), contains similarity to Pfam domain: PF01501 (Glycosyl transferase family 8). Score=-22.6; E-value=4.8e-06; N=1-cDNA EST yk250b10.3 co> Length = 1377</p>
SeqID 971	SA-1897.1	Contig132 (29215-30513 p)	83	<p>Identities = 324/433 (74%), Positives = 367/433 (83%) dbj BAB04344.1 (AP01509) adenylosuccinate lyase [<i>Bacillus halodurans</i>] Length = 433</p>
SeqID 972	SA-1898.1	Contig132 (30700-31569 p)	No Hits found	
SeqID 973	SA-1899.1	Contig132 (31858-32856 p)	74	<p>Identities = 186/322 (60%), Positives = 254/322 (78%) sp O32055 RUVB_BACSU HOLLIDAY JUNCTION DNA HELICASE RUVB emb CAB75331.1 (Y15896) RuvB protein [<i>Bacillus subtilis</i>] Length = 334</p>
SeqID 974	SA-190.1	Contig136 (66611-67555 m)	53	<p>Identities = 140/305 (45%), Positives = 191/305 (61%), Gaps = 6/305 (1%) sp Q47690 MMUM_ECOLI HOMOCYSTEINE S-METHYLTRANSFERASE (S-METHYLMETHIONINE:HOMOCYSTEINE METHYLTRANSFERASE) pri E54751 probable membrane protein yegD - <i>Escherichia coli</i> gp AA08682.1 (U70214) similar to <i>S. cerevisiae</i> YLL062c [<i>Escherichia coli</i>] gp AAC73364.1 (AE000134) putative enzyme [<i>Escherichia coli</i> K12] Length = 310</p>

SeqID 975	SA-1900.3	Contig132 (33008-33445 p)	61	<p>Identities = 76/141 (53%), Positives = 100/141 (70%), Gaps = 4/141 (2%) gblAAK06300.1(AE006449.6 (AE006449) protein-tyrosine phosphatase (EC 3.1.3.48) [Lactococcus subsp. lactis] Length = 145</p>
SeqID 976	SA-1901.2	Contig106 (12011-12379 m)	62	<p>Identities = 51/116 (43%), Positives = 79/116 (67%) dbjBAA83965.1 (AB024564) YHCF [Bacillus halodurans] family [Bacillus halodurans] Length = 126</p>
SeqID 977	SA-1902.2	Contig106 (12524-15628 p)	78	<p>Identities = 64/1036 (62%), Positives = 814/1036 (78%), Gaps = 4/1036 (0%) gblAAF98350.1 (AF280766) DNA polymerase III alpha subunit [Streptococcus pyogenes] Length = 1034</p>
SeqID 978	SA-1904.1	Contig106 (15709-16731 p)	88	<p>Identities = 270/337 (80%), Positives = 302/337 (89%), Gaps = 1/337 (0%) gblAAF25803.1(AF172173.1 (AF172173) phosphofructokinase [Streptococcus thermophilus] Length = 339</p>
SeqID 979	SA-1906.1	Contig106 (16780-18282 p)	89	<p>Identities = 413/500 (82%), Positives = 452/500 (99%) gblAAF25804.1(AF172173.2 (AF172173) pyruvate kinase [Streptococcus thermophilus] Length = 500</p>
SeqID 980	SA-1908.2	Contig106 (18453-19010 p)	48	<p>Identities = 62/185 (33%), Positives = 97/185 (51%), Gaps = 12/185 (6%) spjP72365(LEP_STAAU SIGNAL PEPTIDASE IB (SPASE IB) (LEADER PEPTIDASE IB) gblAAC44435.1 (U65000) type-I signal peptidase SpsB [Staphylococcus aureus] Length = 191</p>
SeqID 981	SA-1909.2	Contig133 (13473-13898 m)	78	<p>Identities = 92/141 (65%), Positives = 115/141 (81%) spP23494(LACA_LACA GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT pirjA39778 galactose-6-phosphate isomerase (EC 5.3.1.-) component Laca - Lactococcus lactis gblAAA25168.1 (M65190) lacA [Lactococcus lactis] gblAAA25177.1 (M60447) galactose 6-P isomerase [Lactococcus lactis] Length = 141</p>

SeqID 982	SA-191.2	Contig136 (64409-66517 p)	72	<p>Identities = 437/589 (74%), Positives = 513/589 (86%), Gaps = 5/589 (0%) gb AA08910.1 (L34877) Clp-like ATP-dependent protease binding subunit [Bos taurus] Length = 589</p> <p>Identities = 138/171 (80%), Positives = 157/171 (91%) sp P23495 LACB_LACLA GALACTOSE-6-PHOSPHATE ISOMERASE LACB SUBUNIT pir J39778 galactose-6-phosphate isomerase (EC 5.3.1.-) component LacB - Lactococcus lactis gb AA25178.1 (M65190) lacB [Lactococcus lactis] gb AA25178.1 (M60447) galactose 6-P isomerase [Lactococcus lactis] Length = 171</p>
SeqID 983	SA-1910.1	Contig133 (12937-13452 m)	86	<p>Identities = 192/310 (61%), Positives = 236/310 (75%) sp P23391 LACC_LACLA TAGATOSE-6-PHOSPHATE KINASE (PHOSPHOTAGATOKINASE) pir J39778 tagatose-6-phosphate kinase (EC 2.7.1.-) LacC - Lactococcus lactis gb AA25170.1 (M65190) lacC [Lactococcus lactis] gb AA25178.1 (M60447) tagatose 6-P kinase [Lactococcus lactis] Length = 310</p>
SeqID 984	SA-1911.1	Contig133 (11994-12926 m)	72	<p>Identities = 253/325 (77%), Positives = 295/325 (89%) sp P28593 LACD_LACLA TAGATOSE 1,6-DIPHOSPHATE ALDOLASE (TAGATOSE-BISPHOSPHATE ALDOLASE) (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE) pir J39778 LacD tagatose-1,6-diphosphate aldolase - Lactococcus lactis gb AA25171.1 (M65190) lacD [Lactococcus lactis] gb AA25180.1 (M60447) tagatose 1,6-dip aldolase [Lactococcus lactis] Length = 325</p>
SeqID 985	SA-1912.1	Contig133 (11015-11992 m)	89	<p>Identities = 173/298 (58%), Positives = 219/298 (73%) sp P23406 LAXP_LACLA LACX PROTEIN, PLASMIID pir J23696 lacx protein - Lactococcus lactis gb AA25184.1 (M60447) ORF [Lactococcus lactis] Length = 299</p>
SeqID 986	SA-1913.1	Contig133 (10065-10961 m)	66	

SeqID 987	SA-1915.1	Contig133 (9119-9970 m)	47	<p>Identities = 101/278 (36%), Positives = 160/278 (57%), Gaps = 1/278 (0%) spIQ54087.LRPR_STRFQ LEUCINE RICH PROTEIN pir J59972 leucine-rich protein - Streptococcus equisimilis emb CAA51350.1 (X72832) leucine rich protein [Streptococcus equisimilis] pir J20093588 Leu-rich protein [Streptococcus equisimilis] Length = 282</p>
SeqID 988	SA-1916.2	Contig133 (7885-9018 m)	90	<p>Identities = 320/377 (84%), Positives = 359/377 (94%) sp Q00752 MSMK_STRMU MULTIPLE SUGAR-BINDING TRANSPORT ATP-BINDING PROTEIN MSMK pir E2400 ABC- type transport system ATP-binding protein msmk [validated] - Streptococcus mutans gp AA426938.1 (M77351) ATP-binding protein [Streptococcus mutans] Length = 377</p>
SeqID 989	SA-1918.2	Contig82 (6068-7264 p)	91	<p>Identities = 342/399 (85%), Positives = 378/399 (94%) emb CAC21180.1 (AJ251799) putative phosphotransferase [Streptococcus thermophilus] Length = 403</p>
SeqID 990	SA-1919.1	Contig82 (5330-6001 p)	57	<p>Identities = 99/199 (49%), Positives = 140/199 (69%), Gaps = 1/199 (0%) sp P43048 DEOC_MYCHO DEOXYRIBOSE- PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE) pir J542197 deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma hominis (SGC3) pir J572522 deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma hominis (SGC3) emb CAA81846.1 (Z27121) deoxyribose aldolase [Mycoplasma hominis] Length = 217</p>
SeqID 991	SA-1921.1	Contig82 (4098-5300 p)	62	<p>Identities = 160/405 (39%), Positives = 256/405 (62%), Gaps = 8/405 (1%) db JBA05165.1 (AP001512) nucleoside transporter [Bacillus halodurans] Length = 406</p>

SeqID 992	SA-1922.1	Contig82 (3298-4077 p)	63	<p>Identities = 145/246 (58%), Positives = 171/246 (68%) sp O3390 UDP_TREPA URIDINE PHOSPHORYLASE (UDRPASE) p I F71251 probable uridine phosphorylase (udp) - syphilis spirochete gb AAC65977.1 (AE001270) uridine phosphorylase (udp) [Treponema pallidum] Length = 258</p> <p>Identities = 50/171 (29%), Positives = 86/171 (50%), Gaps = 17/171 (9%) db JBAB06113.1 (AP001515) transcriptional regulator (GntR family) [Bacillus halodurans] Length = 242</p>
SeqID 993	SA-1923.1	Contig82 (2403-3140 m)	33	
SeqID 994	SA-1924.1	Contig82 (2094-2402 m)	No Hits found	
SeqID 995	SA-1925.1	Contig82 (803-1717 m)	45	<p>Identities = 84/314 (26%), Positives = 140/314 (43%), Gaps = 28/314 (8%) p I S55315 mucin (clone PGM-2A) - pig p I 47141 gastric mucin (clone PGM-2A) - pig (fragment) gb AAC46526.1 (U10281) gastric mucin [Sus scrofa] Length = 528</p> <p>Identities = 47/1539 (87%), Positives = 512/539 (94%), Gaps = 1/539 (0%) gb AAD23455.1 (AF117741) chaperonin GroEL [Streptococcus pneumoniae] Length = 540</p>
SeqID 997	SA-1927.1	Contig82 (3-344 m)	No Hits found	
SeqID 998	SA-1928.1	Contig82 (16-276 p)	81	<p>Identities = 52/91 (57%), Positives = 75/91 (82%), Gaps = 1/91 (1%) gb AAD23454.1 (AF117741) co-chaperonin GroES [Streptococcus pneumoniae] Length = 94</p>
SeqID 999	SA-1929.2	Contig84 (8598-9638 m)	63	<p>Identities = 191/454 (42%), Positives = 289/454 (63%), Gaps = 17/454 (3%) db JBAB04579.1 (AP001510) BH0860-unknown conserved protein [Bacillus halodurans] Length = 458</p>

SeqID 1000	SA-193.2	Contig136 (63475-63975 m)	64	<p>Identities = 96/164 (58%), Positives = 125/164 (75%), Gaps = 1/164 (0%) spIP429232RL10_BACSU 50S RIBOSOMAL PROTEIN L10 (BL5) (COLD ACCLIMATIZATION PROTEIN) (CAP) (VEGETATIVE PROTEIN 300) (VEG300) pIRID69695 ribosomal protein L10 (BL5) rpJ - Bacillus subtilis clj[BAA08940.1] (D50303) Ribosomal Protein L10 [Bacillus subtilis] emb[CAB11880.1] (Z99104) ribosomal protein L10 (BL5) [Bacillus subtilis] Length = 166</p>
SeqID 1001	SA-1930.1	Contig84 (7772-8539 p)	44	<p>Identities = 72/213 (33%), Positives = 115/213 (53%), Gaps = 11/213 (5%) pIRJC70361 conserved hypothetical protein aq_701 - Aquifex aeolicus gb AAC06891.1 (AE000703) hypothetical protein [Aquifex aeolicus] Length = 413</p>
SeqID 1002	SA-1931.1	Contig84 (5832-7613 m)	73	<p>Identities = 344/578 (59%), Positives = 445/578 (76%) spIP14951IUVRC_BACSU EXCINUCLEASE ABC SUBUNIT C pIRJ437192 excinuclease ABC, chain C - Bacillus subtilis gb AA87316.1 (J03294) deoxyribodipyrimidine photolyase [Bacillus subtilis] emb[CAB99578.1] (Z75208) deoxyribodipyrimidine photolyase [Bacillus subtilis] emb[CAB14809.1] (Z99118) excinuclease ABC (subunit C) [Bacillus subtilis] Length = 596</p>
SeqID 1003	SA-1932.2	Contig84 (3955-5790 p)	45	<p>Identities = 151/585 (25%), Positives = 281/585 (47%), Gaps = 31/585 (5%) gb AAK06095.1 AE006429.13 (AE006429) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 617</p>
SeqID 1004	SA-1933.2	Contig84 (3237-3839 m)	65	<p>Identities = 94/203 (46%), Positives = 134/203 (65%), Gaps = 3/203 (1%) gb AAK04278.1 AE006255.8 (AE006255) oxidoreductase [Lactococcus lactis subsp. lactis] Length = 203</p>
SeqID 1005	SA-1934.2	Contig84 (1784-3190 m)	77	<p>Identities = 311/474 (65%), Positives = 369/474 (77%), Gaps = 11/474 (2%) gb AAC45369.1 (U78036) dipeptidase [Lactococcus lactis] Length = 472</p>

SeqID 1006	SA-1935.1	Contig84 (1103-1887 m)	76	Identities = 125/192 (65%), Positives = 163/192 (84%). Gaps = 1/192 (0%) sp O66222 Y22A_HAEN HYPOTHETICAL PROTEIN H1020.2 gb AAC21888.1 (U32707) H. influenzae predicted coding region H10220.2 [Haemophilus influenzae Rd] Length = 214
SeqID 1007	SA-1937.1	Contig84 (354-1088 m)	39	Identities = 70/244 (28%), Positives = 103/244 (41%), Gaps = 3/244 (12%) pf J72330 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb AAD35886.1 AE001748.2 (AE001748) conserved hypothetical protein [Thermotoga maritima] Length = 233
SeqID 1008	SA-1939.1	Contig84 (3-185 m)	40	Identities = 27/63 (42%), Positives = 36/63 (56%) pf T31110 extracellular matrix binding protein - Abiotrophia defectiva (fragment) gb AAD03320.1 (AF067776) extracellular matrix binding protein [Abiotrophia defectiva] Length = 2055
SeqID 1009	SA-194.1	Contig 136 (63046-63411 m)	73	Identities = 83/123 (67%), Positives = 96/123 (77%), Gaps = 2/123 (1%) sp P02394 RL7_BACSU 50S RIBOSOMAL PROTEIN L7/L12 (BL9) (A TYPE) (VEGETATIVE PROTEIN 341) (VEG341) pf J5589 ribosomal protein L7/L12 - Bacillus subtilis emb CAB11861.1 (Z59104) ribosomal protein L12 (BL9) [Bacillus subtilis] Length = 123
SeqID 1010	SA-1940.1	Contig103 (17991-18413 p)	85	Identities = 112/141 (79%), Positives = 124/141 (87%) sp Q9ZA56 HPRK_STRMU HPR(SER) KINASE/PHOSPHATASE pf T11568 probable HPr kinase (EC 2.7.1.-) - Streptococcus mutans gb AAC80172.1 (U75480) putative HPr(Ser) Kinase [Streptococcus mutans] Length = 311
SeqID 1011	SA-1941.1	Contig103 (17560-17875 p)	No Hits found	

SeqID 1012	SA-1942.1	Contig103 (17500-17763 p)	38	Identities = 21/63 (33%), Positives = 36/63 (56%), Gaps = 2/63 (3%) prfJ[E70043] hypothetical protein yJc - Bacillus subtilis gb AAAC67275.1 (AF017113) yJc [Bacillus subtilis] emb CAB15516.1 (Z99121) yJc [Bacillus subtilis] emb CAB15528.1 (Z99122) yJc [Bacillus subtilis] Length = 65
SeqID 1013	SA-1943.1	Contig103 (16961-17419 p)	57	Identities = 63/146 (43%), Positives = 92/146 (62%), Gaps = 5/146 (3%) dbj BA00855.1 (AB031213) YdcK [Bacillus halodurans] dbj BA04251.1 (AP001508) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 151
SeqID 1014	SA-1944.1	Contig103 (14838-16998 p)	67	Identities = 37/9729 (51%), Positives = 515/729 (69%), Gaps = 25/729 (3%) dbj BA04250.1 (AP001508) unknown conserved protein [Bacillus halodurans] Length = 728
SeqID 1015	SA-1945.1	Contig103 (13888-14731 p)	61	Identities = 164/300 (54%), Positives = 217/300 (71%), Gaps = 1/300 (0%) gb AA094650.1 (U96107) N5, N10-methylenetetrahydromethanopterin reductase homolog [Staphylococcus carnosus] Length = 301
SeqID 1016	SA-1946.1	Contig103 (13427-13555 m)	No Hits found	
SeqID 1017	SA-1948.1	Contig103 (12519-13334 m)	64	Identities = 141/283 (49%), Positives = 196/283 (69%), Gaps = 3/283 (1%) prfJ[E89758] hypothetical protein ycgR - Bacillus subtilis dbj BA008959.1 (D50453) homologue of unidentified protein of E. coli [Bacillus subtilis] emb CAB12119.1 (Z99105) ycgR [Bacillus subtilis] Length = 284
SeqID 1018	SA-195.1	Contig136 (62894-63439 p)	45	Identities = 38/157 (24%), Positives = 82/157 (52%), Gaps = 6/157 (3%) prfJ[T39903] serine-rich protein - fission yeast (Schizosaccharomyces pombe) emb CA22127.1 (AL033534) hypothetical serine-rich secreted protein [Schizosaccharomyces pombe] Length = 534
SeqID 1019	SA-1950.1	Contig103 (12179-12337 p)	No Hits found	

SeqID 1020	SA-1951.1	Contig103 (11707-12519 m)	55	<p>Identities = 101/290 (34%), Positives = 160/290 (54%), Gaps = 25/290 (8%) <i>prlD69759</i> hypothetical protein <i>yggQ</i> - <i>Bacillus subtilis</i> <i>dbjBA008958.1</i> (D50453) <i>yggQ</i> [<i>Bacillus subtilis</i>] <i>embICAB12118.1</i> (Z99105) <i>yggQ</i> [<i>Bacillus subtilis</i>] Length = 285</p>
SeqID 1021	SA-1952.2	Contig103 (10060-11670 p)	61	<p>Identities = 239/537 (44%), Positives = 330/537 (60%), Gaps = 79/537 (14%) <i>gblAAK04911.1</i> (AE006314) cell division protein <i>FtsY</i> [<i>Lactococcus lactis</i> subsp. <i>lactis</i>] Length = 459</p>
SeqID 1022	SA-1953.1	Contig111 (18352-19497 m)	77	<p>Identities = 231/381 (60%), Positives = 300/381 (78%), Gaps = 4/381 (1%) <i>gblAAAF91339.1</i> (AF249729) <i>ATPase OpuCA</i> [<i>Listeria monocytogenes</i>] Length = 397</p>
SeqID 1023	SA-1954.1	Contig111 (17717-18352 m)	74	<p>Identities = 122/212 (57%), Positives = 162/212 (75%) <i>gblAAAF91340.1</i> (AF249729) <i>ATPase OpuCB</i> [<i>Listeria monocytogenes</i>] Length = 218</p>
SeqID 1024	SA-1955.1	Contig111 (16788-17714 m)	62	<p>Identities = 166/303 (54%), Positives = 222/303 (72%), Gaps = 1/303 (0%) <i>spIO32243</i> <i>OPOC_BACSU GLYCINE BETAINICARNITINECHOLINE-BINDING PROTEIN PRECURSOR</i> (OSMOPROTECTANT-BINDING PROTEIN) <i>pirI659670</i> glycine betaine/carnitine/choline ABC transporter (osmoprotect) <i>opuCC</i> - <i>Bacillus subtilis</i> <i>embICAB15386.1</i> (Z99121) glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein) [<i>Bacillus subtilis</i>] Length = 303</p>
SeqID 1025	SA-1956.1	Contig111 (16137-16778 m)	82	<p>Identities = 135/213 (63%), Positives = 179/213 (83%) <i>gblAAAF91342.1</i> (AF249729) <i>ATPase OpuCD</i> [<i>Listeria monocytogenes</i>] Length = 223</p>

SeqID 1026	SA-1957.1	Contig111 (14894-15880 p)	50	Identities = 85/335 (25%), Positives = 171/335 (50%), Gaps = 15/335 (4%) pir JH72265 hypothetical protein TM1336 - Thermotoga maritima (strain MS88) gb AA036408.1 AE001788_3 (AE001788) permease, putative [Thermotoga maritima] Length = 390
SeqID 1027	SA-1958.1	Contig111 (13949-14821 p)	49	Identities = 75/279 (26%), Positives = 144/279 (50%) sp P43330 RGG_STRCG RGG PROTEIN pir J441898 positive regulator of glucosyltransferase and Spp phenotype rgg - Streptococcus gordonii gb AA026968.1 (M89776) rgg [Streptococcus gordonii] Length = 297
SeqID 1028	SA-1959.1	Contig111 (12837-13118 p)	No Hits found	
SeqID 1029	SA-196.1	Contig136 (62632-62808 m)	No Hits found	
SeqID 1030	SA-1960.1	Contig111 (12417-12803 p)	No Hits found	
SeqID 1031	SA-1961.1	Contig111 (12013-12432 p)	No Hits found	
SeqID 1032	SA-1962.2	Contig111 (11221-11808 p)	24	Identities = 32/126 (25%), Positives = 52/126 (40%), Gaps = 20/126 (15%) pir F71614 chromatinic RING finger DRING protein homolog PF00440c - malaria parasite (Plasmodium falciparum) gb AAC71877.1 (AE001395) chromatinic RING finger protein, DRING ortholog [Plasmodium falciparum] Length = 568
SeqID 1033	SA-1963.2	Contig111 (10793-11221 p)	37	Identities = 33/113 (29%), Positives = 53/113 (46%), Gaps = 19/113 (16%) pir E71619 RAD2 endonuclease PF0265c - malaria parasite (Plasmodium falciparum) gb AAC71842.1 (AE001383) RAD2 endonuclease [Plasmodium falciparum] Length = 1516
SeqID 1034	SA-1966.1	Contig136 (26286-28304 m)	43	Identities = 155/698 (22%), Positives = 293/698 (41%), Gaps = 157/698 (22%) pir F70175 rep helicase, single-stranded DNA- dependent ATPase (rep) homolog - Lyme disease spirochete gb AAC66967.1 (AE001162) rep helicase, single- stranded DNA-dependent ATPase (rep) [Borrelia burgdorferi] Length = 659

SeqID 1035	SA-1967.1	Contig136 (25592-25951 m)	55	Identities = 61/118 (51%), Positives = 79/118 (66%), Gaps = 1/118 (0%) gb AAC98436.1 (L29324) unknown [Streptococcus pneumoniae] Length = 118
SeqID 1036	SA-1968.1	Contig136 (25217-25582 m)	76	Identities = 72/121 (59%), Positives = 95/121 (78%) gb AAC98435.1 (L29324) unknown [Streptococcus pneumoniae] Length = 121
SeqID 1037	SA-1969.1	Contig136 (23353-25230 m)	49	Identities = 241/416 (57%), Positives = 312/416 (74%), Gaps = 4/416 (0%) gb AAC98434.1 (L29324) relaxase [Streptococcus pneumoniae] Length = 431
SeqID 1038	SA-197.1	Contig136 (61820-62635 m)	81	Identities = 195/268 (72%), Positives = 233/268 (86%), Gaps = 1/268 (0%) gb AAD41248.1 (AF106927.1) (AF106927) unknown [Streptococcus suis] Length = 272
SeqID 1039	SA-1971.2	Contig136 (22443-23198 m)	77	Identities = 146/250 (58%), Positives = 197/250 (78%) sp P26422 LACR_STRMU LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR pir B43258 regulatory protein lacR - Streptococcus mutans gb AA26903.1 (M80797) lactose repressor [Streptococcus mutans] Length = 251
SeqID 1040	SA-1973.3	Contig117 (6819-7409 m)	54	Identities = 78/193 (40%), Positives = 111/193 (57%), Gaps = 14/193 (7%) gb AAK04415.1 (AE006268.1) (AE006268) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 191
SeqID 1041	SA-1974.2	Contig117 (5976-6734 p)	No Hits found	
SeqID 1042	SA-1975.2	Contig117 (5755-5973 p)	59	Identities = 28/60 (46%), Positives = 45/60 (74%) pir G75183 probable repressor protein PAB7155 - Pyrococcus abyssi (strain Orsay) emb CA84550.1 (AJ248284) repressor protein, putative [Pyrococcus abyssi] Length = 73
SeqID 1043	SA-1976.2	Contig117 (5390-5713 p)	No Hits found	

SeqID 1044	SA-1977.1	Contig117 (4126-4944 p)	42	<p>Identities = 70/258 (27%), Positives = 122/258 (47%), Gaps = 14/258 (5%) snpP27129REAL_ECOLI_LIPOPOLYSACCHARIDE 1,2-GLUCOSYLTRANSFERASE [EC 2.4.1.58] - glucosyltransferase I [EC 2.4.1.58] - gblAAB18603.1 U00039 UDP-D- glucose (galactosyl)lipopolysaccharide glucosyltransferase [Escherichia coli] gblAAC76650.1 AE000440 UDP-D- glucose (galactosyl)lipopolysaccharide glucosyltransferase [Escherichia coli K12] Length = 338</p>
SeqID 1045	SA-1978.1	Contig117 (3322-4038 p)	56	<p>Identities = 84/242 (34%), Positives = 147/242 (60%), Gaps = 16/242 (6%) dbjBAB07774.1 AP001520 unknown conserved protein [Bacillus halodurans] Length = 236</p>
SeqID 1046	SA-198.1	Contig136 (61161-61589 m)	71	<p>Identities = 90/141 (63%), Positives = 102/141 (71%) gblAAC98422.1 L29323 methyl transferase [Streptococcus pneumoniae] Length = 172</p>
SeqID 1047	SA-1982.1	Contig117 (622-3240 p)	70	<p>Identities = 482/885 (54%), Positives = 618/885 (69%), Gaps = 27/885 (3%) dbjBAB04986.1 AP001511 alanyl-RNA synthetase [Bacillus halodurans] Length = 879</p>
SeqID 1048	SA-1983.1	Contig117 (121-606 p)	42	<p>Identities = 43/144 (29%), Positives = 75/144 (51%), Gaps = 2/144 (1%) pir G70079 hypothetical protein yxiI - Bacillus subtilis dbjBAA11710.1 D83026 hypothetical [Bacillus subtilis] emb CAB16920.1 Z99123 yxiI [Bacillus subtilis] Length = 162</p>
SeqID 1049	SA-1985.2	Contig128 (12351-12893 m)	55	<p>Identities = 60/175 (34%), Positives = 103/175 (58%), Gaps = 6/175 (3%) gblAA05744.1 AE006395.4 AE006395 HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 186</p>

SeqID 1050	SA-1986.1	Contig128 (9927-12275 m)	58	<p>Identities = 321/790 (40%), Positives = 466/790 (58%), Gaps = 18/790 (2%) spIP94545[MUS2_BACSU MUTS2 PROTEIN pir D59985 DNA mismatch repair protein homolog y8D - Bacillus subtilis emb CA95659.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14818.1 (Z95118) similar to DNA mismatch repair protein [Bacillus subtilis] Length = 785</p>
SeqID 1051	SA-1987.1	Contig128 (9423-9770 m)	42	<p>Identities = 42/143 (29%), Positives = 71/143 (49%), Gaps = 71/143 (43%) spIQ57819 Y374_METJA HYPOTHETICAL PROTEIN MJ0374 pir F6346 hypothetical protein MJ0374 - Methanococcus jannaschii gb AAB89363.1 (U67490) lipoprotein B (lppB) [Methanococcus jannaschii] Length = 330</p>
SeqID 1052	SA-1988.1	Contig128 (9028-9360 m)	60	<p>Identities = 64/100 (64%), Positives = 78/100 (78%), Gaps = 1/100 (1%) emb CAB40815.2 (AJ133006) thiodoxin [Listeria monocytogenes] Length = 103</p>
SeqID 1053	SA-1989.1	Contig128 (8385-8682 p)	25	<p>Identities = 27/67 (40%), Positives = 51/67 (75%) pir I40868 hypothetical protein 3 nanH region - Clostridium perfringens emb CAA60798.1 (X87369) ORF3 [Clostridium perfringens] Length = 265</p>
SeqID 1054	SA-199.1	Contig136 (60382-61734 m)	85	<p>Identities = 322/448 (71%), Positives = 386/448 (85%), Gaps = 3/448 (0%) gb AAC98421.1 (L29323) methyl transferase [Streptococcus pneumoniae] Length = 452</p>
SeqID 1055	SA-1990.2	Contig128 (7088-8212 p)	58	<p>Identities = 169/388 (43%), Positives = 224/388 (57%), Gaps = 26/388 (6%) gb AAK04939.1 AE06318_2 (AE06318) A/G- specific adenine glycosylase (EC 3.2.2.1) [Lactococcus lactis subsp. lactis] Length = 387</p>
SeqID 1056	SA-1992.1	Contig128 (47161-47817 m)	19	<p>Identities = 31/105 (29%), Positives = 51/105 (48%), Gaps = 4/105 (3%) emb CAB95931.1 (AL359989) galactose-1- phosphate uridylyltransferase [Streptomyces coelicolor A3(2)] Length = 353</p>

SeqID 1057	SA-1993.1	Contig128 (45990-47117 p)	65	Identities = 186/410 (45%), Positives = 259/410 (62%), Gaps = 27/410 (6%) dbjBAB06996.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 422
SeqID 1058	SA-1994.1	Contig128 (45274-45810 m)	44	Identities = 51/173 (29%), Positives = 87/173 (49%), Gaps = 20/173 (11%) emb CAA73267.1 (Y12736) orfX [Lactococcus lactis subsp. cremoris] Length = 200
SeqID 1059	SA-1995.1	Contig128 (44643-45251 m)	24	Identities = 29/87 (33%), Positives = 51/87 (58%), Gaps = 1/87 (1%) dbjBAB06137.1 (AP001515) DNA polymerase III (alpha subunit) [Bacillus halodurans] Length = 1433
SeqID 1060	SA-1996.1	Contig128 (43791-44516 m)	29	Identities = 46/141 (32%), Positives = 71/141 (49%), Gaps = 11/141 (7%) sp P32184 TIPA_STRCO TRANSCRIPTIONAL ACTIVATOR TIPA, pir S35354 tpaA protein - Streptomyces lividans, pir T36339 transcription regulator - Streptomyces coelicolor, gb AAB27737.1 (S94314) TipA-AS-thioesteron-specific recognition protein (TipA-transcriptional activator, TipAS=transcriptional activation modulator) [Streptomyces lividans, Peptide, 253 aa] emb CAB42766.1 (AL049841) transcriptional regulator [Streptomyces coelicolor A3(2)] Length = 253
SeqID 1061	SA-1997.1	Contig128 (42531-43721 p)	63	Identities = 166/397 (41%), Positives = 255/397 (63%), Gaps = 14/397 (3%) pir H64571 cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) - Helicobacter pylori (strain 26695) gb AAD07482.1 (AE000557) cyclopropane fatty acid synthase (cfa) [Helicobacter pylori 26695] Length = 389

SeqID 1062	SA-1998.1	Contig128 (42071-42370 p)	44	Identities = 44/97 (45%), Positives = 60/97 (61%) sp P24281 YAAK_BACSU HYPOTHETICAL 11.8 KD PROTEIN IN DNAAZ-REC INTERGENIC REGION. pir S13787 conserved hypothetical protein yaak - Bacillus subtilis. emb CAA34878.1 (X17014) ORF-107 [Bacillus subtilis] obj BAA05236.1 (D26185) unknown [Bacillus subtilis] emb CAB11796.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 107
SeqID 1063	SA-1999.1	Contig128 (41421-41759 m)	No Hits found	
SeqID 1064	SA-2.1	Contig137 (42467-42724 p)	No Hits found	
SeqID 1065	SA-20.1	Contig137 (24860-25942 p)	20	Identities = 37/161 (22%), Positives = 75/161 (45%), Gaps = 8/161 (4%) pir S45089 hypothetical protein eta - Streptococcus pyogenes plasmid pDB101 pir S88123 hypothetical protein eta - Streptococcus pyogenes plasmid pMD101 emb CAA47095.1 (X68468) orf eta [Streptococcus pyogenes] Length = 231
SeqID 1066	SA-200.1	Contig136 (59952-60398 m)	59	Identities = 69/143 (48%), Positives = 97/143 (67%), Gaps = 3/143 (2%) gb AAC98423.1 (L29323) unknown [Streptococcus pneumoniae] Length = 149
SeqID 1067	SA-2000.1	Contig128 (40742-41188 m)	No Hits found	
SeqID 1068	SA-2004.1	Contig128 (151-2997 m)	82	Identities = 640/941 (68%), Positives = 784/941 (83%), Gaps = 3/941 (0%) sp Q34863 UVRA_BACSU EXCINUCLEASE ABC SUBUNIT A. pir F69729 excinuclease ABC chain A - Bacillus subtilis. gb AAC67271.1 (AF017113) excinuclease ABC subunit A [Bacillus subtilis] emb CAB15533.1 (Z99122) excinuclease ABC (subunit A) [Bacillus subtilis] Length = 957
SeqID 1069	SA-2005.1	Contig128 (3111-3782 m)	No Hits found	
SeqID 1070	SA-2006.1	Contig128 (3807-4751 m)	50	Identities = 108/295 (36%), Positives = 174/295 (58%), Gaps = 4/295 (1%) pir J75272 probable transport protein - Deinococcus radiodurans (strain R1) gb AAAF12002.1 AE002075.6 (AE002075) transport protein, putative [Deinococcus radiodurans] Length = 312

SeqID 1071	SA-2007.1	Contig128 (4921-5160 m)	73	Identities = 52/79 (65%), Positives = 64/79 (80%) pir[S66013 ribosomal protein S18 (rpsR) - Bacillus subtilis dbj BA05219.1 (226185) ribosomal protein S18 [Bacillus subtilis] emb CAB16126.1 (239124) ribosomal protein S18 [Bacillus subtilis] Length = 81
SeqID 1072	SA-2008.2	Contig128 (5205-5696 m)	90	Identities = 136/163 (83%), Positives = 149/163 (90%) gb AAAF98351.1 (AF280767) single strand binding protein [Streptococcus pyogenes] Length = 163
SeqID 1073	SA-2009.2	Contig128 (5708-5995 m)	78	Identities = 72/96 (75%), Positives = 81/96 (84%), Gaps = 1/96 (1%) gb AAK06289.1 (AE006448.7) (AE006448) 30S ribosomal protein S6 [Lactococcus lactis subsp. lactis] Length = 97
SeqID 1074	SA-2010.1	Contig113 (25825-26142 p)	64	Identities = 52/83 (55%), Positives = 68/93 (72%) gb AAC14608.1 (U95840) transmembrane protein Tmp5 [Lactococcus lactis] Length = 273
SeqID 1075	SA-2012.1	Contig113 (25470-25775 m)	No Hits found	
SeqID 1076	SA-2013.1	Contig113 (22823-23569 m)	40	Identities = 92/204 (45%), Positives = 101/204 (49%), Gaps = 1/204 (0%) pir JH72504 hypothetical protein APE2014 - Aeropyrum pernix (strain K1) dbj BA081024.1 (AP0000063) 280aa long hypothetical protein [Aeropyrum pernix] Length = 280
SeqID 1077	SA-2014.1	Contig113 (22538-22783 m)	No Hits found	
SeqID 1078	SA-2015.2	Contig113 (22413-24389 p)	85	Identities = 490/652 (75%), Positives = 561/652 (85%), Gaps = 5/652 (0%) gb AAC16243.2 (AF061748) cell division protein FtsH [Streptococcus pneumoniae] Length = 652

SeqID 1079	SA-2017.2	Contig113 (21848-22390 p)	81	<p>identities = 121/179 (67%), Positives = 152/179 (84%), Gaps = 1/179 (0%) sp Q02522 HPRT_LACLA HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (HGPRT) pr IS0100 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - Lactococcus lactis emb CAA48876.1 (X68123) hypoxanthine guanine phosphoribosyltransferase [Lactococcus lactis] emb CAA47404.1 (X67015) hypoxanthine phosphoribosyltransferase [Lactococcus lactis] gb AAK04118.1 AE006241_7 (AE006241) hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) [Lactococcus lactis subsp. lactis] pr J190538 A hypoxanthine guanine phosphoribosyltransferase [Lactococcus lactis] Length = 183</p>
SeqID 1080	SA-2018.2	Contig113 (20569-21843 p)	53	<p>identities = 142/418 (33%), Positives = 230/418 (54%), Gaps = 21/418 (5%) gb AAK04117.1 AE006241_6 (AE006241) cell cycle protein MesJ [Lactococcus lactis subsp. lactis] Length = 423</p>
SeqID 1081	SA-2019.2	Contig113 (19401-20567 p)	26	<p>identities = 77/284 (27%), Positives = 117/284 (41%), Gaps = 54/284 (19%) pr J1714238 A beta lactamase mutant S-3P [Staphylococcus aureus] Length = 281</p>
SeqID 1082	SA-202.1	Contig136 (59573-59959 m)	No Hits found	
SeqID 1083	SA-2022.2	Contig93 (6702-7730 p)	68	<p>identities = 159/334 (47%), Positives = 236/334 (70%), Gaps = 15/334 (4%) gb AAK05774.1 AE006398_5 (AE006398) transcriptional regulator [Lactococcus lactis subsp. lactis] Length = 324</p>
SeqID 1084	SA-2024.1	Contig93 (5199-6446 m)	42	<p>identities = 121/418 (28%), Positives = 190/418 (44%), Gaps = 43/418 (10%) sp P29850 MALX_STRPN MALTOSE/MALTODEXTRIN-BINDING PROTEIN PRECURSOR pr J32568 malX protein - Streptococcus pneumoniae gb AAZ6925.1 (L08611) MalX [Streptococcus pneumoniae] Length = 423</p>

SeqID 1085	SA-2025.1	Contig93 (3731-5071 m)	56	Identities = 174/428 (40%), Positives = 263/428 (60%), Gaps = 21/428 (4%) prjIS33815 malF protein homolog cymF - Klebsiella oxytoca embICA60005.1 [X86014] cymF [Klebsiella oxytoca] Length = 427
SeqID 1086	SA-2026.1	Contig93 (2896-3731 m)	61	Identities = 109/269 (40%), Positives = 171/269 (63%), Gaps = 5/269 (1%) prjIS33816 malG protein homolog cymG - Klebsiella oxytoca embICA60006.1 [X86014] cymG [Klebsiella oxytoca] Length = 277
SeqID 1087	SA-2028.1	Contig93 (1192-2574 m)	69	Identities = 259/485 (53%), Positives = 353/485 (72%), Gaps = 9/485 (1%) spJP94408YCLF_BACSU HYPOTHETICAL 53.3 KD PROTEIN IN SPP-GERKA INTERGENIC REGION prjIC89762 di-tripeptide ABC transporter (membrane pr) homolog ycf - Bacillus subtilis dbjBAA09000.1 [D50453] homologue of Di-tripeptide transporter Dip of L. lactis [Bacillus subtilis] embICAB12175.1 [Z99106] similar to di-tripeptide ABC transporter (membrane protein) [Bacillus subtilis] Length = 492
SeqID 1088	SA-2029.1	Contig93 (663-1147 p)	40	Identities = 37/114 (32%), Positives = 66/114 (57%), Gaps = 10/114 (8%) dbjBAB07289.1 [AP001519] mutator MutT protein [Bacillus halodurans] Length = 159
SeqID 1089	SA-203.1	Contig136 (59343-59546 m)	No Hits found	
SeqID 1090	SA-2030.1	Contig93 (411-599 p)	No Hits found	
SeqID 1091	SA-2031.1	Contig93 (20-400 p)	52	Identities = 41/117 (35%), Positives = 67/117 (57%) gbIAAF51315.1 [U96168] unknown [Streptococcus cristatus] Length = 442
SeqID 1092	SA-2033.2	Contig123 (38766-39380 p)	52	Identities = 73/188 (38%), Positives = 108/188 (56%), Gaps = 11/188 (5%) dbjBAA21095.1 [D68438] reph [Lactobacillus acidophilus] Length = 193
SeqID 1093	SA-2034.1	Contig123 (37952-38569 p)	No Hits found	
SeqID 1094	SA-2035.2	Contig123 (36936-37967 p)	22	Identities = 50/196 (25%), Positives = 89/196 (42%), Gaps = 12/196 (6%) gbIAAB60012.1 [U05422] ORF21 [Enterococcus faecalis] prjIJ114402D ORF 21 [Enterococcus faecalis] Length = 461

SeqID 1095	SA-2037.2	Contig123 (36547-36867 p)	No Hits found	
SeqID 1096	SA-2038.1	Contig123 (36896-36345 p)	No Hits found	
SeqID 1097	SA-2040.1	Contig123 (34160-35575 p)	No Hits found	
SeqID 1098	SA-2041.2	Contig123 (33771-34109 p)	60	Identities = 50/110 (45%), Positives = 76/110 (68%) ref NP_054018.1 CadX [Staphylococcus lugdunensis] gb AAAB16271.1 U74623 CadX [Staphylococcus lugdunensis] Length = 115
SeqID 1099	SA-2042.2	Contig123 (33133-33759 p)	97	Identities = 198/209 (94%), Positives = 203/209 (96%) prf E1967 cadmium resistance protein NMA0496 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB83789.1 (AL162753) cadmium resistance protein [Neisseria meningitidis Z2491] Length = 213
SeqID 1100	SA-2045.2	Contig132 (41522-42709 p)	59	Identities = 171/393 (43%), Positives = 256/393 (64%), Gaps = 2/393 (0%) gb AAK06200.1 AE006438.14 (AE006438) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 400
SeqID 1101	SA-2047.1	Contig132 (39834-41324 p)	51	Identities = 186/500 (37%), Positives = 258/500 (51%), Gaps = 67/500 (13%) emb CAB95221.1 (AL359773) possible threonine synthase [Leishmania major] Length = 576
SeqID 1102	SA-2048.1	Contig132 (36697-39713 p)	76	Identities = 238/340 (70%), Positives = 276/340 (81%), Gaps = 2/340 (0%) prf H81186 alcohol dehydrogenase, propanol- preferring NMB0546 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF40975.1 (AE002410) alcohol dehydrogenase, propanol-preferring [Neisseria meningitidis MC58] Length = 348
SeqID 1103	SA-205.1	Contig136 (58759-59349 m)	No Hits found	
SeqID 1104	SA-2050.2	Contig132 (36876-38518 p)	84	Identities = 65/873 (75%), Positives = 760/873 (86%), Gaps = 2/873 (0%) gb AAK03537.1 (AE005181) Adh2 [Pasteurella multocida] Length = 875
SeqID 1105	SA-2051.1	Contig129 (2-493 m)	58	Identities = 68/155 (43%), Positives = 98/155 (62%) gb AAAF13747.1 AF117351.4 (AF117351) unknown [Zymomonas mobilis] Length = 236

SeqID 1106	SA-2052.1	Contig129 (646-1674 p)	80	<p>Identities = 227/341 (66%), Positives = 278/341 (80%) sp Q32054 IQUEA_BACSU S-ADENOSYLMETHIONINE:TRNA RIBOSYLTRANSFERASE-ISOMERASE [QUEUOSINE BIOSYNTHESIS PROTEIN QUEA] p rlj A69688 S- adenosylmethionine-tRNA ribosyltransferase-isomerase [EC 5.4.99.-] queA [similarity] - Bacillus subtilis emb CAB14732.1 (Z99118) S-adenosylmethionine tRNA ribosyltransferase [Bacillus subtilis] emb CAB75332.1 (Y15896) QueA protein [Bacillus subtilis] Length = 342</p>
SeqID 1107	SA-2053.1	Contig129 (1761-2198 p)	54	<p>Identities = 56/145 (38%), Positives = 86/145 (59%), Gaps = 2/145 (1%) emb CAA73494.1 (Y13052) ORF145 [Staphylococcus sciuri] Length = 145</p>
SeqID 1108	SA-2054.1	Contig129 (2253-3317 m)	No Hits found	
SeqID 1109	SA-2056.1	Contig129 (3418-4874 m)	74	<p>Identities = 232/416 (55%), Positives = 314/416 (74%), Gaps = 3/416 (0%) sp Q57483 Y092_HAEIN HYPOTHETICAL PROTEIN HI0092 p rlj D64142 hypothetical protein HI0092 - Haemophilus influenzae (strain Rd KW20) gb AAAC21770.1 (U32694) H. influenzae predicted coding region HI0092 [Haemophilus influenzae Rd] Length = 419</p>
SeqID 1110	SA-2059.2	Contig129 (4699-5841 m)	59	<p>Identities = 177/367 (48%), Positives = 235/367 (63%), Gaps = 2/367 (0%) gb AAG58254.1 AE005541.6 (AE005541) ori, hypothetical protein [Escherichia coli O157:H7] Length = 367</p>
SeqID 1111	SA-206.1	Contig136 (58190-58678 m)	No Hits found	
SeqID 1112	SA-2060.1	Contig129 (6008-7102 p)	50	<p>Identities = 94/370 (25%), Positives = 184/370 (49%), Gaps = 13/370 (3%) db JBA0805450.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 371</p>
SeqID 1113	SA-2061.2	Contig129 (7171-8598 m)	80	<p>Identities = 334/475 (70%), Positives = 392/475 (82%), Gaps = 8/475 (1%) gb JAAF89979.1 AF206272.5 (AF206272) beta- glucosidase [Streptococcus mutans] Length = 479</p>

SeqID 1114	SA-2062.2	Contig132 (47810-48070 p)	95	<p>Identities = 82/86 (95%), Positives = 83/86 (96%)</p> <p>-sp Q9VW03 RS17_STRPN_30S_RIBOSOMAL_PROTEIN_S17- gbl AAD33285.1 AF126059_6 (AF126059) RpS17 [Streptococcus pneumoniae] gbl AAD33274.1 (AF126060) RpS17 [Streptococcus pneumoniae] gbl AAD33283.1 (AF126061) RpS17 [Streptococcus pneumoniae] Length = 86</p>
SeqID 1115	SA-2063.2	Contig132 (47578-47784 p)	88	<p>Identities = 59/68 (85%), Positives = 64/68 (93%)</p> <p>sp Q9VW06 RL29_STRPN_50S_RIBOSOMAL_PROTEIN_L29 gbl AAD33284.1 AF126059_5 (AF126059) Rpl29 [Streptococcus pneumoniae] gbl AAD33273.1 (AF126060) Rpl29 [Streptococcus pneumoniae] gbl AAD33282.1 (AF126061) Rpl29 [Streptococcus pneumoniae] Length = 68</p>
SeqID 1116	SA-2065.1	Contig132 (47165-47588 p)	98	<p>Identities = 135/137 (98%), Positives = 137/137 (99%)</p> <p>sp Q9X5K1 RL16_STRPN_50S_RIBOSOMAL_PROTEIN_L16 gbl AAD33283.1 AF126059_4 (AF126059) Rpl16 [Streptococcus pneumoniae] Length = 137</p>
SeqID 1117	SA-2066.1	Contig132 (46498-47151 p)	91	<p>Identities = 200/208 (96%), Positives = 203/208 (97%)</p> <p>sp Q9VW03 RS3_STRPN_30S_RIBOSOMAL_PROTEIN_S3 gbl AAD33282.1 AF126059_3 (AF126059) RpS3 [Streptococcus pneumoniae] gbl AAD33271.1 (AF126060) RpS3 [Streptococcus pneumoniae] gbl AAD33280.1 (AF126061) RpS3 [Streptococcus pneumoniae] Length = 208</p>
SeqID 1118	SA-2067.1	Contig132 (46141-46485 p)	89	<p>Identities = 99/114 (86%), Positives = 106/114 (92%)</p> <p>sp Q9VW06 RL22_STRPN_50S_RIBOSOMAL_PROTEIN_L22 gbl AAD33281.1 AF126059_2 (AF126059) Rpl22 [Streptococcus pneumoniae] gbl AAD33270.1 (AF126060) Rpl22 [Streptococcus pneumoniae] gbl AAD33279.1 (AF126061) Rpl22 [Streptococcus pneumoniae] Length = 114</p>

SeqID 1119	SA-2069.1	Contig132 (45847-46125 p)	86	<p>Identities = 92/93 (98%), Positives = 93/93 (99%) sp G5W12IRS19_STRPN-30S_RIBOSOMAL_PROTEIN_S19 gb AAD33260.1 AF126059_1 (AF126059) Rps19 [Streptococcus pneumoniae] gb AAD33269.1 AF126060 Rps19 [Streptococcus pneumoniae] gb AAD33278.1 AF126061 Rps19 [Streptococcus pneumoniae] Length = 93</p>
SeqID 1120	SA-207.1	Contig136 (56373-58190 m)	47	<p>Identities = 183/492 (37%), Positives = 292/492 (59%) Gaps = 30/492 (6%) gb AAEF72343.1 AF192329_4 (AF192329) Trk-like protein [Enterococcus faecalis] Length = 584</p>
SeqID 1121	SA-2071.1	Contig132 (44915-45748 p)	84	<p>Identities = 207/277 (74%), Positives = 239/277 (86%) gb AAC45959.1 (U43929) L2 [Bacillus subtilis] Length = 277</p>
SeqID 1122	SA-2072.1	Contig132 (44601-44897 p)	60	<p>Identities = 58/92 (60%), Positives = 67/92 (71%) Gaps = 1/92 (1%) sp Q929L2 RL23_BACHD 50S_RIBOSOMAL_PROTEIN_L23 pir I744385 ribosomal protein L23 [imported] - Bacillus halodurans dbj BA75273.1 (AB017508) rplW homologue (identity of 71 to B. subtilis%) [Bacillus halodurans] dbj BAB03855.1 (AP001507) ribosomal protein L23 [Bacillus halodurans] Length = 96</p>
SeqID 1123	SA-2073.1	Contig132 (43978-44601 p)	73	<p>Identities = 130/207 (62%), Positives = 160/207 (76%) sp P42921 RL4_BACSU 50S_RIBOSOMAL_PROTEIN_L4 pir I469694 ribosomal protein L4 rplD - Bacillus subtilis dbj BAA08832.1 (D50302) Ribosomal Protein L4 [Bacillus subtilis] gb AAC45957.1 (U43929) L4 [Bacillus subtilis] emb CAB11893.1 (Z99104) ribosomal protein L4 [Bacillus subtilis] Length = 207</p>
SeqID 1124	SA-2074.2	Contig132 (43328-43954 p)	82	<p>Identities = 157/208 (75%), Positives = 180/208 (86%) Gaps = 2/208 (0%) sp P42920 RL3_BACSU 50S_RIBOSOMAL_PROTEIN L3 (BL3) pir IG99994 ribosomal protein L3 (BL3) rplC - Bacillus subtilis gb AAC45956.1 (U43929) L3 [Bacillus subtilis] emb CAB11892.1 (Z99104) ribosomal protein L3 (BL3) [Bacillus subtilis] Length = 209</p>

SeqID 1125	SA-2075.2	Contig132 (42915-43223 p)	94	Identities = 98/102 (96%), Positives = 102/102 (99%) sp P4853 RS10_STRMU 30S RIBOSOMAL PROTEIN S10 gb AA846363.1 (L28637) S10 ribosomal protein [Streptococcus mutans] Length = 102
SeqID 1126	SA-2076.2	Contig132 (42879-43280 m)	No Hits found	Identities = 241/259 (93%), Positives = 248/259 (95%) emb CAB90834.1 (A250837) putative transposase [Streptococcus dysgalactiae] Length = 259
SeqID 1127	SA-2077.1	Contig92 (5603-6382 p)	84	Identities = 93/96 (96%), Positives = 94/96 (97%) emb CAB90833.1 (A250837) hypothetical protein [Streptococcus dysgalactiae] Length = 96
SeqID 1128	SA-2078.1	Contig92 (5277-5567 p)	86	
SeqID 1129	SA-2079.1	Contig92 (4012-5049 m)	No Hits found	
SeqID 1130	SA-208.1	Contig136 (56111-56353 m)	No Hits found	
SeqID 1131	SA-2082.1	Contig92 (24-3476 m)	98	Identities = 1141/1150 (99%), Positives = 1142/1150 (99%) gb AAB17762.1 (U56908) SCPB [Streptococcus agalactiae] Length = 1150
SeqID 1132	SA-2083.2	Contig102 (16409-17926 m)	74	Identities = 322/472 (68%), Positives = 378/472 (79%) pir S68568 sucrose-6-phosphate hydrolase ScrB - Streptococcus sobrinus (strain 6715) Length = 479
SeqID 1133	SA-2084.1	Contig102 (15445-16407 m)	84	Identities = 225/320 (70%), Positives = 273/320 (85%) sp Q54430 ISCRR_STRMU SUCROSE OPERON REPRESSOR (SCR OPERON REGULATORY PROTEIN) gb AAC31628.1 (U46902) ScrR [Streptococcus mutans] Length = 320
SeqID 1134	SA-2085.1	Contig102 (14924-15356 p)	56	Identities = 51/129 (39%), Positives = 82/129 (63%) Gaps = 9/129 (6%) sp P54520 NUSB_BACSU N UTILIZATION SUBSTANCE PROTEIN B HOMOLOG (NUSB PROTEIN) pir F69960 transcription termination factor nusB homolog ynfZ [similarly] - Bacillus subtilis dbj BAA12571.1 (D84432) YnfZ [Bacillus subtilis] emb CAB14363.1 (Z99116) similar to transcription termination [Bacillus subtilis] Length = 131

SeqID 1135	SA-2086.1	- Contig102 (14542-14931 p)	53	Identities = 42/107 (39%), Positives = 70/107 (65%), Gaps = 4/107 (3%) dbj BA06505.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 132
SeqID 1136	SA-2087.1	Contig102 (13893-14453 p)	64	Identities = 89/186 (47%), Positives = 120/186 (63%), Gaps = 1/186 (0%) sp P49778 EFP_BACSU ELONGATION FACTOR P (EF-P) p p A69620 translation elongation factor EF-P elfp - Bacillus subtilis dbj BA012558.1 (D64432) YqHU [Bacillus subtilis] emb CAB114376.1 (Z99116) elongation factor P [Bacillus subtilis] Length = 186
SeqID 1137	SA-2090.1	Contig102 (10993-12714 p)	52	Identities = 174/568 (30%), Positives = 300/568 (52%), Gaps = 7/568 (1%) gb AAD10394.1 (U46488) NrpB [Proteus mirabilis] Length = 575
SeqID 1138	SA-2091.1	Contig102 (10920-11162 m)	No Hits found	
SeqID 1139	SA-2092.2	Contig102 (9291-11003 p)	50	Identities = 186/593 (31%), Positives = 305/593 (51%), Gaps = 14/593 (2%) gb AAD10393.1 (U46488) NrpA [Proteus mirabilis] Length = 588
SeqID 1140	SA-2095.2	Contig119 (7199-8548 m)	90	Identities = 377/449 (83%), Positives = 414/449 (91%) p p T51720 glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - Streptococcus mutans gb AAD33517.1 AF132127.2 (AF132127) glucose-6-phosphate isomerase [Streptococcus mutans] Length = 449
SeqID 1141	SA-2096.1	Contig119 (6350-6877 m)	71	Identities = 96/173 (55%), Positives = 129/173 (74%) dbj BA028715.1 (AB001582) hypothetical protein [Streptococcus mutans] Length = 178
SeqID 1142	SA-2097.1	Contig119 (5682-6359 m)	72	Identities = 126/218 (57%), Positives = 166/218 (75%) emb CAB90755.1 (AJ400707) hypothetical protein [Streptococcus uberis] Length = 223

SeqID 1143	SA-2099.1	Contig119 (4507-5550 m)	80	Identities = 148/349 (42%), Positives = 223/349 (63%), Gaps = 16/349 (4%) sp O05252 YUFN_BACSU HYPOTHETICAL LIPOPROTEIN YUFN PRECURSOR pil C70009 ABC transporter (lipoprotein) homolog yufN - Bacillus subtilis emb CAB07936.1 (Z33937) unknown [Bacillus subtilis] emb CAB15143.1 (Z99120) similar to ABC transporter (lipoprotein) [Bacillus subtilis] Length = 350
SeqID 1144	SA-21.1	Contig137 (24502-24849 p)	No Hits found	
SeqID 1145	SA-210.1	Contig136 (55240-56094 m)	39	Identities = 56/262 (21%), Positives = 121/262 (45%), Gaps = 28/262 (10%) gb AAAF72344.1 AF192329_5 (AF192329) unknown [Enterococcus faecalis] Length = 287
SeqID 1146	SA-2100.1	Contig119 (3517-4416 p)	93	Identities = 263/299 (87%), Positives = 287/299 (95%) db JBA28714.1 (AB001562) glucose-1-phosphate uridylyltransferase [Streptococcus mutans] Length = 306
SeqID 1147	SA-2101.1	Contig119 (2464-3480 p)	66	Identities = 177/333 (53%), Positives = 241/333 (72%) sp P46919 GPDA_BACSU GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD(P)+] [NAD(P)H-DEPENDENT DIHYDROXYACETONE-PHOSPHATE REDUCTASE] gb AA486746.1 (U32164) NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis] Length = 345
SeqID 1148	SA-2102.1	Contig119 (1965-2294 m)	54	Identities = 52/109 (47%), Positives = 77/109 (69%), Gaps = 1/109 (0%) pdb 1A6F Rhase P Protein From Bacillus Subtilis Length = 119
SeqID 1149	SA-2103.2	Contig119 (1137-1952 m)	71	Identities = 149/267 (55%), Positives = 197/267 (72%), Gaps = 3/267 (1%) gb AAK04227.1 AC006251_3 (AC006251) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 269
SeqID 1150	SA-2104.2	Contig133 (64785-66146 m)	39	Identities = 100/451 (22%), Positives = 180/451 (39%), Gaps = 81/451 (17%) emb CAB39034.1 (AL034559) hypothetical protein, PFC0940c [Plasmodium falciparum] Length = 806
SeqID 1151	SA-2105.1	Contig133 (65147-67238 m)	No Hits found	

SeqID 1152	- SA-2108.1	Contig133 (67478-68422 m)	50	Identities = 100/317 (31%), Positives = 168/317 (52%), Gaps = 83/17 (2%) djb BAC05608.1 AP001513 unknown conserved protein [Bacillus halodurans] Length = 325
SeqID 1153	SA-2107.1	Contig133 (68486-68815 m)	No Hits found	Identities = 35/91 (38%), Positives = 51/91 (55%) sp P34159 YH51_CLOAB_HYPOTHETICAL_11.0_KD_PROTEIN_IN_HSP18_3_REGION (ORFA1) emb CAA46375.1 (X65276) ORFA1 [Clostridium acetobutylicum] Length = 96
SeqID 1154	SA-2109.1	Contig133 (69774-70190 p)	No Hits found	
SeqID 1155	SA-2111.1	Contig136 (54825-55058 m)	No Hits found	
SeqID 1156	SA-2110.1	Contig133 (70239-70357 p)	No Hits found	
SeqID 1157	SA-2112.1	Contig133 (70808-71098 p)	49	Identities = 260/311 (83%), Positives = 283/311 (90%) sp P6875 PPAC_STRGC_PROBABLE_MANGANESE-DEPENDENT_INORGANIC_PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHOLASE) (PPASE) gb AAB39104.1 (U57759) intragenetic coaggregation-relevant adhesin [Streptococcus gordonii] Length = 311
SeqID 1158	SA-2113.1	Contig133 (71260-71571 p)	No Hits found	
SeqID 1159	SA-2115.1	Contig133 (71861-72589 p)	No Hits found	
SeqID 1160	SA-2116.1	Contig133 (72806-73078 p)	No Hits found	
SeqID 1161	SA-2117.1	Contig133 (73197-73502 m)	No Hits found	Identities = 261/793 (32%), Positives = 436/793 (54%), Gaps = 36/793 (4%) gb AAAF72347.1 AF192329.8 (AF192329) TrsE-like protein [Enterococcus faecalis] Length = 789
SeqID 1162	SA-2118.2	Contig133 (73790-74143 m)	No Hits found	
SeqID 1163	SA-2119.2	Contig118 (5080-6015 p)	88	
SeqID 1164	SA-2121	Contig136 (52523-54868 m)	54	
SeqID 1165	SA-2120.1	Contig118 (4175-4963 p)	80	Identities = 185/260 (71%), Positives = 218/260 (83%) sp O68575 PFLA_STRMU_PYRUVATE_FORMATATE-LYASE ACTIVATING ENZYME (PFL-ACTIVATING ENZYME) gb AAC05773.1 (AF051356) pyruvate-formate lyase activating enzyme [Streptococcus mutans] djb BAA34998.1 (AB018417) PFL-activating enzyme [Streptococcus mutans] Length = 263

SeqID 1166	SA-2122.1	- Contig118 (2773-4107 p)	90	Identities = 348/445 (78%), Positives = 404/445 (90%), Gaps = 1/445 (0%) gblAAC05772.1 (AF061356) putative nemoysin [Streptococcus mutans] Length = 445
SeqID 1167	SA-2123.1	Contig118 (2027-2593 p)	62	Identities = 80/184 (43%), Positives = 119/184 (64%), Gaps = 3/184 (1%) pirl[G81942 hypothetical protein NMA0960 [imported] Neisseria meningitidis (group A strain Z2491) embICAB84230.1 (AL162754) hypothetical protein NMA0960 [Neisseria meningitidis] Length = 188
SeqID 1168	SA-2124.1	Contig118 (1099-2034 p)	69	Identities = 161/302 (53%), Positives = 220/302 (72%), Gaps = 4/302 (1%) pirl[D69999 conserved hypothetical protein ytaA - Bacillus subtilis gblAAC00380.1 (AF008220) YtaA [Bacillus subtilis] embICAB15026.1 (Z99119) similar to hypothetical proteins [Bacillus subtilis] Length = 322
SeqID 1169	SA-2125.1	Contig118 (355-1006 p)	42	Identities = 62/159 (38%), Positives = 93/159 (57%), Gaps = 3/159 (1%) pirl[S32217 hypothetical protein 2 - Bacillus megaterium embICAA79986.1 (Z21972) ORF2 [Bacillus megaterium] Length = 216
SeqID 1170	SA-2126.1	Contig118 (1-384 p)	48	Identities = 33/113 (29%), Positives = 62/113 (54%) sp P50726 YPAA_BACSU HYPOTHETICAL 20.5 KD PROTEIN IN SERA-FER INTERGENIC REGION. pirl[E69832 hypothetical protein ypaA - Bacillus subtilis gblAAC83944.1 (L47546) putative [Bacillus subtilis] embICAB14237.1 (Z99116) ypaA [Bacillus subtilis] Length = 190
SeqID 1171	SA-2126.2	Contig92 (6606-6696 p)	51	Identities = 44/74 (59%), Positives = 53/74 (71%) pirl[T44088 probable transposase [imported] - Staphylococcus aureus Length = 74

SeqID 1172	SA-2129.1	Contig92 (7096-7434 p)	60	<p>Identities = 64/135 (47%), Positives = 86/135 (63%), Gaps = 1/135 (0%) ref NP_052792.1 pXO1-96 [Bacillus anthracis] pir H59102 hypothetical protein pXO1-96 - Bacillus anthracis virulence plasmid pXO1 gb AA74027.1 (U30714) ORFB [Bacillus anthracis] gb AA74029.1 (U30715) ORFB [Bacillus anthracis] gb AAD32400.1 AAD32400 (AF065404) pXO1-96 [Bacillus anthracis] Length = 274</p>
SeqID 1173	SA-2130.1	Contig92 (7421-7738 p)	62	<p>Identities = 45/98 (45%), Positives = 66/98 (66%) ref NP_052792.1 pXO1-96 [Bacillus anthracis] pir H59102 hypothetical protein pXO1-96 - Bacillus anthracis virulence plasmid pXO1 gb AA74027.1 (U30714) ORFB [Bacillus anthracis] gb AA74029.1 (U30715) ORFB [Bacillus anthracis] gb AAD32400.1 AAD32400 (AF065404) pXO1-96 [Bacillus anthracis] Length = 274</p>
SeqID 1174	SA-2131.1	Contig92 (7784-8017 p)	74	<p>Identities = 69/72 (95%), Positives = 69/72 (95%) pir T09011 probable transposase TnpA - Streptococcus pyogenes (fragment) gb AAB92607.1 (AF026542) TnpA [Streptococcus pyogenes] Length = 364</p>
SeqID 1175	SA-2132.1	Contig92 (8216-10684 m)	98	<p>Identities = 809/822 (98%), Positives = 816/822 (98%) pir T46758 hypothetical 92.4K protein - Streptococcus agalactiae gb AAD13797.1 (AF062533) unknown [Streptococcus agalactiae] Length = 822</p>
SeqID 1176	SA-2133.1	Contig92 (10597-11617 m)	99	<p>Identities = 303/306 (99%), Positives = 304/306 (99%) pir T46758 lipoprotein lmb [Validated] - Streptococcus agalactiae gb AAD13796.1 (AF062533) lmb [Streptococcus agalactiae] Length = 306</p>
SeqID 1177	SA-2134.2	Contig139 (98649-99302 p)	79	<p>Identities = 131/218 (60%), Positives = 176/218 (80%), Gaps = 1/218 (0%) gb AAD25108.1 AF140356.1 (AF140356) VncR [Streptococcus pneumoniae] emb CAB54582.1 (AJ006399) response regulator [Streptococcus pneumoniae] Length = 218</p>

SeqID 1178	SA-2136.1	Contig139 (99299-100618 p)	63	Identities = 178/435 (40%), Positives = 281/435 (63%), Gaps = 1/435 (0%) gblA25109.1 (AF140356.2) (AF140356) YncS [Streptococcus pneumoniae] embICAB54583.1 (AJ006399) histidine kinase [Streptococcus pneumoniae] Length = 442
SeqID 1179	SA-2137.1	Contig139 (100670-101284 m)	90	Identities = 197/209 (94%), Positives = 200/209 (95%) prfIT09011 probable transposase TnpA - Streptococcus pyogenes (fragment) gblAAB2607.1 (AF026542) TnpA [Streptococcus pyogenes] Length = 364
SeqID 1180	SA-2138.1	Contig139 (101495-101695 p)	No Hits found	
SeqID 1181	SA-2139.1	Contig139 (101737-101925 p)	No Hits found	
SeqID 1182	SA-214.1	Contig138 (49726-52500 m)	6	Identities = 45/117 (38%), Positives = 60/117 (50%), Gaps = 10/117 (8%) gblAAC61959.1 (AF051917) putative membrane protein TraG [Staphylococcus aureus] prfJ2004267H traG protein [Staphylococcus sp.] Length = 358
SeqID 1183	SA-2140.1	Contig139 (102329-103555 p)	56	Identities = 142/392 (36%), Positives = 237/392 (60%), Gaps = 23/392 (5%) sfpP398041YWCF_BACSU HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION prfJ339697 cell-division protein homolog ywcf - Bacillus subtilis embICAA51598.1 (X73124) ipa-42d [Bacillus subtilis] embICAB15838.1 (Z39123) alternate gene name: ipa-42c-similar to cell-division protein [Bacillus subtilis] Length = 393
SeqID 1184	SA-2141.1	Contig139 (103794-104234 p)	54	Identities = 82/142 (57%), Positives = 105/142 (73%) prfJA57362 gyro protein - Streptococcus pneumoniae (fragment) embICAA58770.1 (X83517) oriGrbB [Streptococcus pneumoniae] embICAA91552.1 (Z67740) unidentified [Streptococcus pneumoniae] Length = 144
SeqID 1185	SA-2143.2	Contig139 (104235-105187 p)	94	Identities = 574/650 (88%), Positives = 618/650 (94%), Gaps = 2/650 (0%) embICAA91553.1 (Z67740) DNA gyrase [Streptococcus pneumoniae] Length = 648

SeqID 1186	SA-2145.1	Contig1114 (17381-18035 m)	64	Identities = 98/223 (43%), Positives = 145/223 (64%), Gaps = 5/223 (2%) dbj BAB04091.1 (AP001508) two-component response regulator [Bacillus halodurans] Length = 222
SeqID 1187	SA-2146.1	Contig1114 (18391-18525 m)	69	Identities = 33/44 (75%), Positives = 39/44 (88%) sp P23376 RL34_BACST 50S RIBOSOMAL PROTEIN L34 p P C48396 ribosomal protein L34 - Bacillus stearothermophilus gb AAE20570.1 BstL34=50S ribosomal subunit protein [Bacillus stearothermophilus, Peptide, 44 aa] gb AAB21085.1 ribosomal protein L34 [Bacillus stearothermophilus, Peptide, 44 aa] p P 1718186C ribosomal protein L34 [Bacillus stearothermophilus] Length = 44
SeqID 1188	SA-2147.1	Contig1114 (18709-20064 m)	66	Identities = 211/459 (45%), Positives = 308/459 (66%), Gaps = 7/459 (1%) dbj BAB07866.1 (AP001520) unknown conserved protein [Bacillus halodurans] Length = 460
SeqID 1189	SA-2148.1	Contig1114 (20311-22038 m)	73	Identities = 343/568 (60%), Positives = 426/568 (74%), Gaps = 2/568 (0%) gb AAAF37879.1 AF234619.2 (AF234619) OpuABC [Lactococcus lactis] Length = 573
SeqID 1190	SA-2149.1	Contig1114 (22057-23280 m)	81	Identities = 274/402 (68%), Positives = 337/402 (83%) gb AAAF37878.1 AF234619.1 (AF234619) OpuAA [Lactococcus lactis] Length = 408
SeqID 1191	SA-2156.2	Contig98 (4979-5518 m)	62	Identities = 90/175 (51%), Positives = 118/175 (67%), Gaps = 2/175 (1%) sp P36264 NUSG_STACA TRANSCRIPTION ANTITERMINATION PROTEIN NUSG p P S38870 transcription antitermination factor nusG - Staphylococcus carnosus emb CAA63738.1 (X76134) nusG [Staphylococcus carnosus] Length = 182
SeqID 1192	SA-2157.1	Contig98 (3727-4932 p)	38	Identities = 98/259 (37%), Positives = 155/259 (59%), Gaps = 10/259 (3%) gb AAAF28353.1 AF224467.2 (AF224467) putative glycosyl transferase [Haemophilus ducreyi] Length = 269

SeqID 1193	SA-2158.1	Contig98 (2466-3662 p)	37	<p>Identities = 88/259 (33%), Positives = 156/259 (59%), Gaps = 11/259 (4%) gb AAAF28363.1 AF224467.2 (AF224467) putative glycosyl transferase [Haemophilus ducreyi] Length = 269</p> <p>Identities = 75/260 (28%), Positives = 123/260 (46%), Gaps = 22/260 (8%) sp P39407 YJUJ_ECOLI_HYPOTHETICAL 39.8 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION (O357) p IIS6601 hypothetical 39.8K protein (osmY-deoC intergenic region) - Escherichia coli gb AAAG7273.1 (U14003) ORF_0357 [Escherichia coli] gb AAC77330.1 (AE000508) orf, hypothetical protein [Escherichia coli K12] Length = 357</p> <p>Identities = 84/265 (31%), Positives = 133/285 (49%), Gaps = 14/265 (5%) gb AA852383.1 (U36837) AbiEII [Lactococcus lactis] Length = 298</p>
SeqID 1194	SA-2159.1	Contig98 (1416-2225 m)	43	<p>Identities = 139/391 (35%), Positives = 221/391 (55%), Gaps = 4/391 (1%) sp P71369 YB04_HAEN_HYPOTHETICAL METABOLITE TRANSPORT PROTEIN H1104 p IIC64167 hypothetical protein H1104 - Haemophilus influenzae (strain Rd KW20) gb AAC22759.1 (U32790) transporter protein [Haemophilus influenzae Rd] Length = 407</p>
SeqID 1195	SA-216.1	Contig136 (48774-49622 p)	45	<p>Identities = 35/101 (34%), Positives = 52/101 (50%), Gaps = 1/101 (0%) pdb 1BUJ C Chain C, Structure Of The Ternary Microplasma-Staphylokinase-Microplasma Complex: A Proteinase-Cofactor-Substrate Complex In Action Length = 128</p>
SeqID 1196	SA-2160.1	Contig98 (126-1373 p)	52	
SeqID 1197	SA-2161.1	Contig81 (8-1291 m)	11	
SeqID 1198	SA-2162.1	Contig81 (1758-2456 p)	No Hits found	

SeqID 1199	SA-2163.1	Contig81 (2627-3571 p)	46	<p>Identities = 102/331 (30%), Positives = 172/331 (51%), Gaps = 26/331 (7%) sp P33019 YEIH_ECOLI HYPOTHETICAL 36 9 KD PROTEIN IN LYS-P-NFO INTERGENIC REGION prf E64984 hypothetical 36.9 kD protein in lysP-nfo intergenic region - Escherichia coli (strain K-12) gb AA60511.1 (U00007) yeiH [Escherichia coli] gb AAC75219.1 (AE000305)orf. hypothetical protein [Escherichia coli K12] prf 2014253BD yeiH gene [Escherichia coli] Length = 349</p>
SeqID 1200	SA-2165.1	Contig81 (3645-5021 p)	63	<p>Identities = 229/455 (50%), Positives = 305/455 (66%), Gaps = 5/455 (1%) gb AAD19405.1 (AF102543) succinic semialdehyde dehydrogenase [Zymomonas mobilis] Length = 458</p>
SeqID 1201	SA-2166.1	Contig81 (5164-5708 p)	68	<p>Identities = 93/178 (52%), Positives = 127/178 (71%) sp P64417 OPUD_BACSU GLYCINE BETAINE TRANSPORTER OPUD prf G69670 glycine betaine transporter opuB - Bacillus subtilis gb AAC44388.1 (U50082) glycine betaine transporter Opud [Bacillus subtilis] gb AAC00408.1 (AF008220) putative transporter [Bacillus subtilis] emb CAB14985.1 (Z99119) glycine betaine transporter [Bacillus subtilis] Length = 512</p>
SeqID 1202	SA-2167.1	Contig81 (5710-6711 p)	70	<p>Identities = 183/324 (56%), Positives = 236/324 (72%), Gaps = 1/324 (0%) prf T48645 glycine betaine transport protein betL [validated] - Listeria monocytogenes gb AAD30266.1 AF102174.1 (AF102174) glycine betaine transporter BetL [Listeria monocytogenes] Length = 507</p>

SeqID 1203	SA-2168.1	Contig81 (6734-7219 m)	58	<p>Identities = 68/152 (44%), Positives = 94/152 (61%), Gaps = 3/152 (1%) p[ri]A70081 conserved hypothetical protein yxkH - <i>Bacillus subtilis</i> dbj[BAA11724.1] (D83026) homologous to SwissProt:YADE_ECOLI; hypothetical [Bacillus subtilis] emb[CAB15906.1] (Z99123) similar to hypothetical proteins [Bacillus subtilis] Length = 279</p>
SeqID 1204	SA-2169.1	Contig81 (7060-7620 m)	29	<p>Identities = 38/122 (31%), Positives = 56/122 (45%), Gaps = 17/122 (13%) p[ri]A70081 conserved hypothetical protein yxkH - <i>Bacillus subtilis</i> dbj[BAA11724.1] (D83026) homologous to SwissProt:YADE_ECOLI; hypothetical [Bacillus subtilis] emb[CAB15906.1] (Z99123) similar to hypothetical proteins [Bacillus subtilis] Length = 279</p>
SeqID 1205	SA-217.1	Contig136 (48187-48777 p)	44	<p>Identities = 53/219 (24%), Positives = 93/219 (42%), Gaps = 30/219 (13%) gb AAB52382.1 (U36837) AbiE1 [Lactococcus lactis] Length = 287</p>
SeqID 1206	SA-2170.1	Contig81 (7797-8006 p)	58	<p>Identities = 35/69 (50%), Positives = 50/69 (71%) sp P52985 DHOM_LACLA HOMOSERINE DEHYDROGENASE (HDH) p[ri]JC6049 homoserine dehydrogenase [EC 1.1.1.3] - Lactococcus lactis emb CA465713.1 (X96988) hom [Lactococcus lactis] Length = 428</p>
SeqID 1207	SA-2172.1	Contig80 (5804-7288 p)	61	<p>Identities = 220/470 (46%), Positives = 311/470 (65%), Gaps = 16/470 (3%) p[ri]A82294 probable carbon starvation protein A VC0687 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAFG3852.1 (AE004154) carbon starvation protein A, putative [Vibrio cholerae] Length = 494</p>
SeqID 1208	SA-2173.1	Contig80 (4914-5648 p)	59	<p>Identities = 93/245 (37%), Positives = 150/245 (60%), Gaps = 3/245 (1%) gb AAB48183.1 (L42945) lytR [Staphylococcus aureus] Length = 246</p>
SeqID 1209	SA-2174.1	Contig80 (3163-4902 p)	67	<p>Identities = 265/582 (45%), Positives = 394/582 (67%), Gaps = 2/582 (0%) gb AAB48182.1 (L42945) lytS [Staphylococcus aureus] Length = 584</p>
SeqID 1210	SA-2175.1	Contig80 (2618-2782 p)	No Hits found	

SeqID 1211	SA-2177.2	Contig80 (2239-2418 p)	No Hits found	Identities = 283/489 (57%), Positives = 361/489 (72%), Gaps = 14/489 (2%) gblAAD20136.1 (AF091502) autoaggregation-mediated protein [Lactobacillus reuteri] Length = 497
SeqID 1212	SA-2178.1	Contig80 (1241-1618 p)	No Hits found	
SeqID 1213	SA-2180.2	Contig80 (529-852 p)	No Hits found	
SeqID 1214	SA-2182.2	Contig80 (2-181 p)	No Hits found	
SeqID 1215	SA-2184.1	Contig129 (22347-23933 m)	66	Identities = 89/237 (37%), Positives = 132/237 (55%), Gaps = 3/237 (1%) pirJC81348 probable periplasmic protein Cj0771c [Imported] - Campylobacter jejuni (strain NCTC 11168) embjCAB73036.1 (AL139076) putative periplasmic protein [Campylobacter jejuni] Length = 256
SeqID 1216	SA-2185.1	Contig129 (24168-24998 m)	46	
SeqID 1217	SA-2186.1	Contig129 (25014-25676 m)	56	Identities = 80/206 (38%), Positives = 127/206 (60%), Gaps = 4/206 (1%) pirJ082957 probable permease of ABC transporter PA5504 [Imported] - Pseudomonas aeruginosa (strain PAO1) gblAAG08889.1AE004963.2 (AE004963) probable permease of ABC transporter [Pseudomonas aeruginosa] Length = 225
SeqID 1218	SA-2187.1	Contig129 (25669-26403 m)	56	
SeqID 1219	SA-2188.1	Contig129 (26524-26904 m)	69	Identities = 84/221 (38%), Positives = 138/221 (62%), Gaps = 5/221 (2%) spP44785ABC_HAEIN ATP-BINDING PROTEIN ABC pirJC64082 ATP-binding protein homolog H10821 - Haemophilus influenzae (strain Rd KW20) gblAAC22280.1 (U32744) ABC transporter, ATP-binding protein [Haemophilus influenzae Rd] Length = 345
SeqID 1219	SA-2188.1	Contig129 (26524-26904 m)	69	Identities = 74/125 (59%), Positives = 92/125 (73%) pirJA69854 hypothetical protein yj0A - Bacillus subtilis embjCAB13104.1 (Z59110) yj0A [Bacillus subtilis] gblAA887515.1 (AF034138) unknown [Bacillus subtilis] Length = 125

SeqID 1220	SA-2190.1	Contig129 (26990-28534 m)	75	Identities = 311/518 (60%), Positives = 393/518 (75%), Gaps = 9/518 (1%) sp 066490 RF3_STAAU PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3) emb CAA74739.1 (Y14370) peptide chain release factor 3 [Staphylococcus aureus] Length = 521
SeqID 1221	SA-2192.2	Contig129 (28711-30249 m)	26	Identities = 92/358 (25%), Positives = 142/358 (39%), Gaps = 55/358 (15%) gp AAAG54632.1 AE005207 putative adhesin [Escherichia coli O157:H7] Length = 1417
SeqID 1222	SA-2195.2	Contig109 (153-1748 m)	56	Identities = 243/373 (65%), Positives = 302/373 (80%), Gaps = 1/373 (0%) sp P34001 YWAP_STRMU HYPOTHETICAL PROTEIN IN WAPA 3 REGION pir S06993 hypothetical protein (wapa 3 region) - Streptococcus mutans (fragment) gp AAA88609.1 (M37842) unknown protein [Streptococcus mutans] Length = 373
SeqID 1223	SA-2196.1	Contig109 (1867-3537 m)	87	Identities = 432/556 (77%), Positives = 492/556 (87%) sp Q59925 FTHS_STRMU FORMATE--TETRAHYDROFOLATE LIGASE (FORMYL-TETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) gp AAB49329.1 (U39612) formyl-tetrahydrofolate synthetase [Streptococcus mutans] Length = 556
SeqID 1224	SA-2197.1	Contig109 (3526-4645 m)	60	Identities = 131/331 (39%), Positives = 207/331 (61%), Gaps = 5/331 (1%) pir G69830 lipote-protein ligase homolog ynfJ - Bacillus subtilis emb CAA74631.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CAB12865.1 (Z99109) similar to lipote-protein ligase [Bacillus subtilis] Length = 331
SeqID 1225	SA-2198.2	Contig109 (4672-5550 m)	No Hits found	Identities = 228/571 (39%), Positives = 347/571 (59%), Gaps = 24/571 (4%) pir EB1869 probable ATP-dependent proteinase ATP-binding protein NMA1045 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB84311.1 (AL162755) putative ATP-dependent protease ATP-binding protein [Neisseria meningitidis] Length = 759
SeqID 1226	SA-22.1	Contig137 (22578-24410 p)	52	

SeqID 1227	SA-220.1	Contig136 (43070-47860 m)	36	<p>Identities = 420/1385 (30%), Positives = 606/1385 (43%), Gaps = 308/1385 (22%) gb AAC44100.1 (U40026) SspB precursor [Streptococcus gordonii] Length = 1500</p> <p>Identities = 385/427 (90%), Positives = 404/427 (94%) sp O573Q1TG_STRPY_TRIGGER_FACTOR (TF) gb AAC82391.1 (AF073822) RopA [Streptococcus pyogenes] Length = 427</p> <p>Identities = 105/261 (40%), Positives = 150/261 (57%), Gaps = 2/261 (0%) db BAB06385.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 276</p>
SeqID 1228	SA-2200.2	Contig78 (4809-5092 p)	92	<p>Identities = 91/176 (51%), Positives = 115/176 (64%) sp P39157 YWLJG_BACSU_HYPOTHETICAL_19.4_KD_PROTEIN IN SPOIR-GLYC INTERGENIC REGION pf J40482 hypothetical protein ywlg - Bacillus subtilis emb CA86108.1 (Z38002) Unknown [Bacillus subtilis] emb CAB15708.1 (Z99122) alternate gene name: ipc-33d [Bacillus subtilis] pf J2108403H ipc-33d gene [Bacillus subtilis] Length = 180</p>
SeqID 1229	SA-2201.1	Contig78 (3810-4652 m)	52	<p>Identities = 46/148 (31%), Positives = 78/148 (52%), Gaps = 9/148 (6%) pf G75153 hypothetical protein PAB2090 - Pyrococcus abyssi (strain Orsay) emb CAB49310.1 (AJ248284) hypothetical protein [Pyrococcus abyssi] Length = 199</p>
SeqID 1230	SA-2202.1	Contig78 (3204-3773 p)	58	<p>Identities = 95/253 (37%), Positives = 150/253 (58%), Gaps = 13/253 (5%) sp P39610 THID_BACSU PHOSPHOMETHYLPIRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE) pf J339707 phosphomethylpyrimidine kinase thid - Bacillus subtilis emb CAA51608.1 (X73124) ipa-52r [Bacillus subtilis] emb CAB15828.1 (Z99123) phosphomethylpyrimidine kinase [Bacillus subtilis] Length = 271</p>
SeqID 1231	SA-2203.1	Contig78 (2743-3207 p)	49	
SeqID 1232	SA-2204.1	Contig78 (1975-2733 p)	58	

SeqID 1233	SA-2205.1	Contig78 (1236-2012 p)	56	Identities = 105/240 (43%), Positives = 147/240 (60%), Gaps = 2/240 (0%) sp G9Z9.0 TRUA_BACHD tRNA PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE) p J14415 pseudouridylyl synthase I trua [imported] - Bacillus halodurans dbj BA75303.1 (AB017508) trua homologue (identity of 62 to B. subtilis%) [Bacillus halodurans] dbj BAB03866.1 (AP001507) tRNA pseudouridine synthase A (pseudouridylyl synthase I) [Bacillus halodurans] Length = 263
SeqID 1234	SA-2206.1	Contig78 (2-1165 p)	62	Identities = 173/347 (49%), Positives = 241/347 (68%), Gaps = 3/347 (0%) db AAD24445.1 AF118389_2 (AF118389) unknown [Streptococcus suis] Length = 419
SeqID 1235	SA-2207.2	Contig139 (46557-47384 p)	73	Identities = 162/270 (60%), Positives = 202/270 (74%), Gaps = 3/270 (1%) dbj BAB06497.1 (AP001516) hemolysin-like protein [Bacillus halodurans] Length = 272
SeqID 1236	SA-2208.2	Contig139 (47371-47844 p)	50	Identities = 49/153 (32%), Positives = 84/153 (54%), Gaps = 4/153 (2%) emb CAA09428.1 (AJ010954) arginine repressor [Bacillus stearothermophilus] Length = 149
SeqID 1237	SA-2210.1	Contig139 (47856-48514 p)	63	Identities = 245/567 (43%), Positives = 366/567 (64%), Gaps = 18/567 (3%) sp P17894 RECN_BACSU DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N) p J1835128 DNA repair and genetic recombination protein recN - Bacillus subtilis gb AA22691.1 (M30297) recombination protein (tg start codon) [Bacillus subtilis] dbj BAA12579.1 (D84432) RecN [Bacillus subtilis] emb CAB14355.1 (Z99116) recN [Bacillus subtilis] Length = 576
SeqID 1238	SA-2212.1	Contig139 (49627-50463 p)	54	Identities = 93/277 (33%), Positives = 152/277 (54%), Gaps = 4/277 (1%) dbj BAB07346.1 (AP001519) unknown conserved protein [Bacillus halodurans] Length = 283

SeqID 1239	SA-2213.1	Contig139 (50531-51295 p)	69	Identities = 149/274 (54%), Positives = 208/274 (75%), Gaps = 9/274 (3%) [emb(CAA72096.1) (Y11213) hypothetical protein [Streptococcus thermophilus] Length = 280
SeqID 1240	SA-2214.2	Contig139 (51270-51872 p)	57	Identities = 75/185 (40%), Positives = 116/185 (62%), Gaps = 3/185 (1%) [emb(CAA72097.1) (Y11213) hypothetical protein [Streptococcus thermophilus] Length = 189
SeqID 1241	SA-2215.1	Contig77 (5615-5663 m)	55	Identities = 31/84 (36%), Positives = 51/84 (59%) [pir B69770 conserved hypothetical protein ydaS - Bacillus subtilis db BAA19274.1 (AB001488) FUNCTION UNKNOWN. [Bacillus subtilis] emb(CAB12244.1) (Z99106) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] Length = 85
SeqID 1242	SA-2216.1	Contig77 (5019-5570 m)	No Hits found	Identities = 27/61 (44%), Positives = 45/61 (73%) gb AAA86382.1 (U23376) putative 6-kDa protein [Lactococcus lactis] Length = 62
SeqID 1243	SA-2217.1	Contig77 (4815-5009 m)	66	Identities = 95/157 (60%), Positives = 121/157 (76%) gb AAA86383.1 (U23376) putative 20-kDa protein [Lactococcus lactis] Length = 183
SeqID 1244	SA-2218.1	Contig77 (4217-4759 m)	64	Identities = 20/43 (46%), Positives = 29/43 (66%), Gaps = 1/43 (2%) gb AAG19662.1 (AE005054) calcium-binding protein homology. Cbp [Halobacterium sp. NRC-1] Length = 385
SeqID 1245	SA-222.1	Contig136 (42878-43069 m)	45	Identities = 24/61 (39%), Positives = 37/61 (60%), Gaps = 1/61 (1%) gb AAB66851.1 (AF034574) putative cruciform DNA binding protein [Glomus versiforme] Length = 99
SeqID 1246	SA-2220.1	Contig77 (3961-4158 m)	53	Identities = 83/153 (54%), Positives = 110/153 (71%) gb AAA86383.1 (U23376) putative 20-kDa protein [Lactococcus lactis] Length = 183
SeqID 1247	SA-2221.1	Contig77 (3368-3939 m)	58	

SeqID 1248	SA-2222.1	Contig777 (2583-3224 m)	15	<p>Identities = 22/48 (45%), Positives = 35/48 (72%)</p> <p>ref NP_070072.1 A. fulgidus predicted coding region AF1244 [Archaeoglobus fulgidus] pif C68405 hypothetical protein AF1244 - Archaeoglobus fulgidus gb AAB90005.1 (AE001018) A. fulgidus predicted coding region AF1244 - -- [Archaeoglobus fulgidus] Length = 161</p>
SeqID 1249	SA-2223.1	Contig777 (1814-2578 m)	46	<p>Identities = 67/262 (25%), Positives = 121/262 (45%), Gaps = 21/262 (8%) pif B72352 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb AAD35735.1 AE001738_15 (AE001738) conserved hypothetical protein [Thermotoga maritima] Length = 268</p>
SeqID 1250	SA-2224.1	Contig777 (1155-1814 m)	52	<p>Identities = 67/218 (30%), Positives = 120/218 (54%), Gaps = 5/218 (2%) emb CAB40581.1 (AJ010128) DNA alkylation repair enzyme [Bacillus cereus] Length = 237</p>
SeqID 1251	SA-2225.1	Contig777 (588-1082 m)	85	<p>Identities = 119/163 (73%), Positives = 145/163 (88%) sp P31308 TPX_STRSA PROBABLE THIOLE PEROXIDASE pif B43583 thioredoxin peroxidase (EC 1.1.1.1) - Streptococcus sanguis gb AAC88427.1 (M63481) 20-kDa protein [Streptococcus sanguinis] Length = 163</p>
SeqID 1252	SA-2226.1	Contig777 (3-512 p)	No Hits found	
SeqID 1253	SA-2227.2	Contig133 (18629-19093 m)	46	<p>Identities = 39/135 (28%), Positives = 76/135 (55%), Gaps = 9/135 (6%) gb AAC09977.1 AF248038_6 (AF248038) GalA [Streptococcus agalactiae] Length = 149</p>
SeqID 1254	SA-2228.1	Contig133 (18322-18627 m)	No Hits found	
SeqID 1255	SA-2231.1	Contig133 (16834-18282 m)	40	<p>Identities = 112/408 (27%), Positives = 197/408 (47%), Gaps = 21/408 (5%) sp P39365 SGCC_ECOLI_PUTATIVE PHOSPHOTRANSFERASE ENZYME II, C COMPONENT SGCC pif S56529 probable phosphotransferase enzyme II - Escherichia coli gb AA497200.1 (U14003) ORF_437 [Escherichia coli] gb AAC77260.1 (AE000501) putative PTS system enzyme IIC component [Escherichia coli K12] Length = 437</p>

SeqID 1256	SA-2232.2	Contig133 (14146-16596 m)	45	Identities = 294/504 (58%), Positives = 380/504 (75%), Gaps = 10/504 (1%) sp Q59595 NANA_STRPN_SIALIDASE_A PRECURSOR (NEURAMINIDASE A) p T30287 exo-alpha-sialidase (EC 3.2.1.18) - Streptococcus pneumoniae emb CAA51473.1 (X72967) neuraminidase [Streptococcus pneumoniae] Length = 1035
SeqID 1257	SA-2233.2	Contig101 (6129-7064 p)	25	Identities = 57/146 (39%), Positives = 81/146 (55%), Gaps = 8/146 (5%) gb AAFP18951.1 AF155805_5 (AF155805) CpsH [Streptococcus suis] Length = 143
SeqID 1258	SA-2235.1	Contig101 (5072-6127 p)	47	Identities = 108/327 (33%), Positives = 170/327 (51%), Gaps = 22/327 (6%) emb CAC14890.1 AJ295156) d-TDP-glucose dehydratase [Phragmites australis] Length = 350
SeqID 1259	SA-2236.1	Contig101 (4347-5089 p)	52	Identities = 77/231 (33%), Positives = 131/231 (56%), Gaps = 6/231 (2%) p TJSS6119 conserved hypothetical protein yacM - Bacillus subtilis db BAA05324.1 (D26185) unknown [Bacillus subtilis] emb CAB11866.1 (Z89104) similar to hypothetical proteins [Bacillus subtilis] Length = 232
SeqID 1260	SA-2237.1	Contig101 (3523-4347 p)	50	Identities = 85/274 (31%), Positives = 141/274 (51%), Gaps = 16/274 (5%) gb AAD37093.1 AF106539_2 (AF106539) LicD1 [Streptococcus pneumoniae] Length = 267
SeqID 1261	SA-2238.1	Contig101 (1765-3498 p)	No Hits found	Identities = 27/109 (24%), Positives = 55/109 (49%) db BAA19645.1 (AB002668) unnamed protein product [Actinobacillus actinomycetemcomitans] Length = 126
SeqID 1262	SA-2239.1	Contig101 (1419-1772 p)	46	
SeqID 1263	SA-224.1	Contig136 (42343-42894 m)	No Hits found	
SeqID 1264	SA-2240.1	Contig101 (691-1422 p)	59	Identities = 118/240 (49%), Positives = 152/240 (63%), Gaps = 1/240 (0%) gb AAC35924.1 (AF071085) putative glycosyl transferase [Enterococcus faecalis] Length = 241

SeqID 1265	SA-2241.2	Contig101 (3-689 p)	75	Identities = 123/231 (53%), Positives = 174/231 (75%), Gaps = 7/231 (3%) pif1 T00087 rhamnosyltransferase - Streptococcus mutans dbj BA32090.1 (AB010970) rhamnosyltransferase [Streptococcus mutans] Length = 311
SeqID 1266	SA-2242.2	Contig115 (41-406 p)	75	Identities = 77/118 (65%), Positives = 102/118 (86%) gb AAK04288.1 AE006256_11 (AE006256) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 122
SeqID 1267	SA-2244.2	Contig115 (406-2070 p)	78	Identities = 354/539 (65%), Positives = 438/539 (80%), Gaps = 8/39 (1%) gb AAK04288.1 AE006256_10 (AE006256) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 535
SeqID 1268	SA-2245.1	Contig115 (2254-3102 p)	56	Identities = 127/275 (46%), Positives = 174/275 (63%), Gaps = 1/275 (0%) gb AAAF68390.1 AF236374_1 (AF236374) hypersensitive-induced response protein [Zea mays] Length = 284
SeqID 1269	SA-2246.1	Contig115 (4134-4664 p)	31	Identities = 39/110 (35%), Positives = 55/110 (49%), Gaps = 3/110 (2%) pif1 G72536 hypothetical protein APE1580 - Aeropyrum pernix (strain K1) dbj BA80580.1 (AP000062) 114aa long hypothetical protein [Aeropyrum pernix] Length = 114
SeqID 1270	SA-2247.1	Contig115 (4184-4924 m)	71	Identities = 132/241 (54%), Positives = 178/241 (73%), Gaps = 1/241 (0%) pif1 F81363 probable glutamine transport ATP-binding protein Cj0902 [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73160.1 (AL138076) putative glutamine transport ATP-binding protein [Campylobacter jejuni] Length = 242
SeqID 1271	SA-2248.2	Contig115 (4934-6484 m)	49	Identities = 147/534 (27%), Positives = 255/534 (47%), Gaps = 75/534 (14%) pif1 S77250 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj BA17584.1 (D90907) glutamine-binding periplasmic protein [Synechocystis sp.] Length = 530
SeqID 1272	SA-225.1	Contig136 (41699-42292 m)	No Hits found	

SeqID 1273	SA-2253.1	Contig104 (9163-9489 p)	47	<p>Identities = 35/95 (36%), Positives = 56/95 (58%), Gaps = 3/95</p> <p>- (3%) spjP46339YQGH_BACSU PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGH pirjB69956 phosphate ABC transporter (permease) homolog yqgH - Bacillus subtilis dbjBAA09582.1 (D58414) ORF72 [Bacillus subtilis] dbjBAA12511.1 (D84432) YqgH [Bacillus subtilis] embICAB14428.1 (Z99116) alternate gene name: yzmC-similar to phosphate ABC transporter (permease) [Bacillus subtilis] Length = 309</p>
SeqID 1274	SA-2252.1	Contig104 (9422-9700 p)	45	<p>Identities = 35/54 (64%), Positives = 44/54 (80%)</p> <p>spjP46339YQGH_BACSU PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGH pirjB69956 phosphate ABC transporter (permease) homolog yqgH - Bacillus subtilis dbjBAA09582.1 (D58414) ORF72 [Bacillus subtilis] dbjBAA12511.1 (D84432) YqgH [Bacillus subtilis] embICAB14428.1 (Z99116) alternate gene name: yzmC-similar to phosphate ABC transporter (permease) [Bacillus subtilis] Length = 309</p>
SeqID 1275	SA-2253.1	Contig104 (9663-10082 p)	62	<p>Identities = 78/161 (48%), Positives = 113/161 (69%), Gaps = 1/161 (0%) spjP46339YQGH_BACSU PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGH pirjB69956 phosphate ABC transporter (permease) homolog yqgH - Bacillus subtilis dbjBAA09582.1 (D58414) ORF72 [Bacillus subtilis] dbjBAA12511.1 (D84432) YqgH [Bacillus subtilis] embICAB14428.1 (Z99116) alternate gene name: yzmC-similar to phosphate ABC transporter (permease) [Bacillus subtilis] Length = 309</p>

SeqID 1276	SA-2254.1	Contig104 (10072-10959 p)	74	<p>Identities = 157/294 (53%), Positives = 225/294 (76%)</p> <p>spiP46340YQGJ, BACSU PROBABLE ABC TRANSPORTER PERMEASE PROTEIN YQGJ, priIJC68956 phosphate ABC transporter (permease) homolog yqgi - Bacillus subtilis dbj BAA09583.1 (D58414) ORF73 [Bacillus subtilis] dbj BAA12512.1 (D84432) Yqgi [Bacillus subtilis] emb CAB14427.1 (Z99116) alternate gene name: yzmD-similar to phosphate ABC transporter (permease) [Bacillus subtilis] Length = 294</p>
SeqID 1277	SA-2255.1	Contig104 (10971-11774 p)	74	<p>Identities = 154/247 (62%), Positives = 204/247 (82%)</p> <p>spiQ58418PSTB, METUA PROBABLE PHOSPHATE TRANSPORT ATP-BINDING PROTEIN PSTB, priIJC64426 phosphate transport system ATP-binding protein - Methanococcus jannaschii gb AA899016.1 (U67544) phosphate specific transport complex component (pstB) [Methanococcus jannaschii] Length = 252</p>
SeqID 1278	SA-2256.1	Contig104 (11786-12544 p)	74	<p>Identities = 148/248 (59%), Positives = 189/248 (75%)</p> <p>spiP46341YQGJ, BACSU HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YQGJ, priIJD69566 phosphate ABC transporter (ATP-binding protein) homolog yqgi - Bacillus subtilis dbj BAA09584.1 (D58414) ORF74 [Bacillus subtilis] dbj BAA12513.1 (D84432) Yqgi [Bacillus subtilis] emb CAB14426.1 (Z99116) alternate gene name: yzmE-similar to phosphate ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 269</p>
SeqID 1279	SA-2258.2	Contig104 (12578-13231 p)	72	<p>Identities = 116/217 (53%), Positives = 167/217 (76%)</p> <p>gb AAK05813.1 AE006402.1 (AE006402) phosphate transport system regulator [Lactococcus lactis subsp. lactis] Length = 217</p>

SeqID 1280	SA-2259.1	Contig76 (2249-4879 p)	25	<p>Identities = 107/531 (20%), Positives = 224/531 (42%), Gaps = 62/531 (11%) ref NP_070647.1 A. fulgidus predicted coding region AF1820 [Archaeoglobus fulgidus] prj C69477 hypothetical protein AF1820 - Archaeoglobus fulgidus gb AA89436.1 (AE000977) A. fulgidus predicted coding region AF1820 [Archaeoglobus fulgidus] Length = 791</p>
SeqID 1281	SA-2260.1	Contig76 (1536-2237 p)	70	<p>Identities = 112/230 (48%), Positives = 167/230 (71%) ref NP_070646.1 ABC transporter, ATP-binding protein [Archaeoglobus fulgidus] prj B69477 ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus gb AA89431.1 (AE000977) ABC transporter, ATP-binding protein [Archaeoglobus fulgidus] Length = 231</p>
SeqID 1282	SA-2261.1	Contig76 (158-1399 p)	76	<p>Identities = 278/469 (59%), Positives = 355/469 (75%), Gaps = 10/469 (2%) sp Q3K423 TOP1_BACHD DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE) db JBA806186.1 (AP001515) DNA topoisomerase I [Bacillus halodurans] Length = 690</p>
SeqID 1283	SA-2263.1	Contig127 (39359-39559 p)	No Hits found	<p>Identities = 126/284 (44%), Positives = 185/284 (64%) sp P37550 SPE_BACSU_4.DIPHOSPHOCYTIDYL-2-C-METHYL-D-ERYTHRITOL KINASE (CNK) (4-CYTIDINE-5 - DIPHOSPHO)-2-C-METHYL-D-ERYTHRITOL KINASE prj S66075 conserved hypothetical protein yabH - Bacillus subtilis db BAA05281.1 (D26185) unknown [Bacillus subtilis] emb CAB11822.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 289</p>
SeqID 1284	SA-2264.2	Contig127 (39121-39972 m)	64	
SeqID 1285	SA-2265.2	Contig127 (38592-39035 m)	73	<p>Identities = 77/146 (52%), Positives = 117/146 (79%) prj I46753 repressor protein adR [imported] - Streptococcus pneumoniae emb CA96184.1 (Z71552) AdcR protein [Streptococcus pneumoniae] Length = 146</p>

SeqID 1286	SA-2266.2	Contig127 (37879-38589 m)	84	<p>Identities = 182/231 (78%), Positives = 206/231 (88%) pii T46754 AdcC protein [imported] - Streptococcus pneumoniae emb CAA96186.1 Z71552 AdcC protein [Streptococcus pneumoniae] Length = 234</p>
SeqID 1287	SA-2267.1	Contig127 (37077-37889 m)	77	<p>Identities = 197/263 (74%), Positives = 236/263 (88%) pii T46754 membrane protein adCB [imported] - Streptococcus pneumoniae emb CAA96187.1 Z71552 AdcB protein [Streptococcus pneumoniae] Length = 268</p>
SeqID 1288	SA-2268.2	Contig127 (35834-36865 p)	41	<p>Identities = 116/216 (53%), Positives = 150/216 (68%) Gaps = 9/216 (4%) gbl AAK04254.1 AE008253_5 AE008253 HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 263</p>
SeqID 1289	SA-2269.1	Contig134 (81376-82521 m)	61	<p>Identities = 169/374 (45%), Positives = 235/374 (62%) Gaps = 18/374 (4%) sp O05005 AAPA_BACSU AMINO ACID PERMEASE AAPA pii I869580 amino acid permease apaA - Bacillus subtilis emb CAA63459.1 X92868 amino acid permease [Bacillus subtilis] emb CAB14651.1 Z99117 amino acid permease [Bacillus subtilis] Length = 459</p>
SeqID 1290	SA-2271.1	Contig134 (80825-81282 p)	86	<p>Identities = 121/155 (78%), Positives = 139/155 (89%) gbl AAC23745.1 AF062209 VacB homolog [Streptococcus pneumoniae] Length = 441</p>
SeqID 1291	SA-2272.2	Contig134 (78417-80822 p)	61	<p>Identities = 350/815 (42%), Positives = 501/815 (60%) Gaps = 49/815 (6%) sp O32231 RN_R_BACSU RIBONUCLEASE R (RNASE R) (VACB PROTEIN HOMOLOG) pii G70027 conserved hypothetical protein ywaJ - Bacillus subtilis emb CAB15366.1 Z99121 similar to hypothetical proteins [Bacillus subtilis] Length = 779</p>
SeqID 1292	SA-2274.1	Contig123 (1-786 m)	76	<p>Identities = 169/260 (65%), Positives = 210/260 (80%) Gaps = 1/260 (0%) gbl AFAF86640.1 AF162694_1 AF162694 ABC transporter [Enterococcus gallinarum] Length = 269</p>

SeqID 1293	SA-2276.1	Contig123 (791-1687 m)	57	Identities = 114/285 (40%), Positives = 175/285 (61%), Gaps = 3/285 (1%) pilJF63165 probable permease of ABC transporter PA3837 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07224.1 AE004801_2 (AE004801) probable permease of ABC transporter [Pseudomonas aeruginosa] Length = 296
SeqID 1294	SA-2278.1	Contig123 (1703-2647 m)	50	Identities = 103/283 (36%), Positives = 165/283 (57%), Gaps = 1/283 (0%) pilJE83185 hypothetical protein PA3836 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07223.1 AE004801_1 (AE004801) hypothetical protein [Pseudomonas aeruginosa] Length = 325
SeqID 1295	SA-2279.1	Contig123 (3130-3939 m)	54	Identities = 89/261 (34%), Positives = 151/261 (57%), Gaps = 4/261 (1%) sp P44447 Y003_HAEN PROTEIN HI0003 pilJ64139 hypothetical protein HI0003 - Haemophilus influenzae (strain Rd KW20) gb AAC21682.1 U32686 conserved hypothetical protein [Haemophilus influenzae Rd] Length = 262
SeqID 1296	SA-2280.1	Contig123 (4113-4973 p)	43	Identities = 86/275 (31%), Positives = 143/275 (51%), Gaps = 6/275 (2%) db JBA07024.1 AP001518 unknown conserved protein [Bacillus halodurans] Length = 286
SeqID 1297	SA-2281.2	Contig123 (5016-5747 p)	58	Identities = 97/240 (40%), Positives = 151/240 (62%), Gaps = 1/240 (0%) gb AAD24446.1 AF118389_3 (AF118389) unknown [Streptococcus suis] Length = 244
SeqID 1298	SA-2282.1	Contig104 (20416-20709 p)	No Hits found	
SeqID 1299	SA-2283.1	Contig104 (20191-20379 p)	No Hits found	
SeqID 1300	SA-2285.1	Contig104 (18504-20069 p)	92	Identities = 437/522 (83%), Positives = 484/522 (92%), Gaps = 7/522 (1%) sp Q64431 SR64_STRIMU SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) gb AAB48050.1 AAB48050 (U88582) Ffh [Streptococcus mutans] Length = 516
SeqID 1301	SA-2287.1	Contig104 (18154-18486 p)	84	Identities = 95/110 (86%), Positives = 103/110 (93%) gb AAB48049.1 AAB48049 (U88582) Ynm [Streptococcus mutans] Length = 110

SeqID 1302	SA-2288.2	Contig104 (16752-18065 p)	89	Identities = 219/420 (52%), Positives = 306/420 (72%), Gaps = 4/420 (0%) pIQ54955(CIAH_STRPN SENSOR PROTEIN CIAH- pIIFJ54954 hisidine kinase - Streptococcus pneumoniae emb CAA54486.1 (X77249) histidine kinase (Streptococcus pneumoniae) emb CAB54565.1 (AJ005928) histidine kinase [Streptococcus pneumoniae] Length = 444
SeqID 1303	SA-2288.2	Contig129 (21139-21903 p)	73	Identities = 152/245 (62%), Positives = 193/245 (78%), Gaps = 1/245 (0%) gb AAK05239.1 AE006442.6 (AE006442) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 250
SeqID 1304	SA-2291.1	Contig129 (20284-21004 m)	44	Identities = 66/200 (33%), Positives = 111/200 (55%), Gaps = 10/200 (5%) pIIE68826 probable 1-acylglycerol-3-phosphate O- acyltransferase (EC 2.3.1.51) yndO - Bacillus subtilis emb CAA74489.1 (Y14082) hypothetical protein [Bacillus subtilis] emb CAB12793.1 (Z99109) similar to 1-acylglycerol-3-phosphate O-acyltransferase [Bacillus subtilis] Length = 199
SeqID 1305	SA-2292.1	Contig129 (19511-20164 m)	60	Identities = 96/217 (44%), Positives = 138/217 (63%), Gaps = 4/217 (1%) gb AAC23741.1 (AF052208) competence protein [Streptococcus pneumoniae] Length = 216
SeqID 1306	SA-2293.1	Contig129 (18655-19527 m)	60	Identities = 120/286 (41%), Positives = 180/286 (61%), Gaps = 1/286 (0%) gb AAC23742.1 (AF052208) competence protein [Streptococcus pneumoniae] Length = 753
SeqID 1307	SA-2284.1	Contig129 (17289-18554 m)	64	Identities = 205/419 (48%), Positives = 298/419 (70%), Gaps = 2/419 (0%) gb AAC23742.1 (AF052208) competence protein [Streptococcus pneumoniae] Length = 753
SeqID 1308	SA-2295.2	Contig129 (16354-17163 m)	61	Identities = 120/287 (44%), Positives = 177/287 (65%), Gaps = 6/287 (2%) gb AAK04342.1 AE006562.1 (AE006562) conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 270

SeqID 1309	SA-2298.2	Contig101 (10807-11655 p)	57	Identities = 112/278 (40%), Positives = 163/278 (59%), Gaps = 2/278 (0%) emb(CAB59237.1) [Z88171] EpsQ protein [Streptococcus thermophilus] Length = 279
SeqID 1310	SA-2297.1	Contig101 (11645-12784 p)	51	Identities = 108/395 (27%), Positives = 196/395 (49%), Gaps = 29/395 (7%) pirID54433 hypothetical protein MJ1069 - Methanococcus jannaschii gpAAB907.1.1 (U67549) galactosyltransferase isolog [Methanococcus jannaschii] Length = 392
SeqID 1311	SA-2298.1	Contig101 (12836-14385 m)	54	Identities = 172/492 (34%), Positives = 289/492 (57%), Gaps = 2/492 (0%) gpAAC97147.1 (U49397) Nra [Streptococcus pyogenes] Length = 511
SeqID 1312	SA-23.1	Contig137 (20828-22576 p)	53	Identities = 218/608 (35%), Positives = 323/608 (52%), Gaps = 52/608 (8%) gpAAC38606.1 (AF007787) type I topoisomerase [Enterococcus faecalis] Length = 714
SeqID 1313	SA-230.1	Contig136 (35495-41695 m)	29	Identities = 373/1243 (30%), Positives = 614/1243 (49%), Gaps = 97/1243 (7%) refNP_066874.1 similar to jhp0928 gene in Helicobacter pylori [Agrobacterium rhizogenes] dbjBAB16212.1 (AP002086) similar to jhp0928 gene in Helicobacter pylori [Agrobacterium rhizogenes] Length = 1693
SeqID 1314	SA-2300.3	Contig101 (14589-17354 p)	9	Identities = 58/176 (32%), Positives = 83/176 (46%), Gaps = 19/176 (10%) gpAAD33086.1 (AF071083.1) (AF071083) fibronectin-binding protein I [Streptococcus pyogenes] Length = 1161
SeqID 1315	SA-2302.2	Contig79 (4055-5029 p)	67	Identities = 138/315 (43%), Positives = 222/315 (69%), Gaps = 6/315 (1%) pirIC69763 ferrichrome ABC transporter (permease) homolog ydO - Bacillus subtilis dbjBAA09013.1 (D50453) homologue of ferric anguibactin transport system permease protein FstC of V. anguillarum [Bacillus subtilis] emb(CAB12189.1) (Z99106) similar to ferrichrome ABC transporter (permease) [Bacillus subtilis] Length = 315

SeqID 1316	SA-2303.1	Contig79 (3086-4056 p)	67	<p>Identities = 149/304 (49%), Positives = 234/304 (76%) prf[B9763 ferrichrome ABC transporter (permease) homolog yclN - Bacillus subtilis dbj[BAA09012.1] (D50453) homolog of ferric anguibacillin transport system permease protein Fcd of V. anguillarum [Bacillus subtilis] emb[CAB12188.1] (Z99106) similar to ferrichrome ABC transporter (permease) [Bacillus subtilis] Length = 316</p>
SeqID 1317	SA-2304.1	Contig79 (2309-2857 p)	63	<p>Identities = 93/182 (51%), Positives = 125/182 (68%), Gaps = 2/182 (1%) dbj[BAB06720.1] (AP001517) maltose transacetylase (maltose O-acetyltransferase) [Bacillus halodurans] Length = 186</p>
SeqID 1318	SA-2305.1	Contig79 (1524-2288 p)	64	<p>Identities = 128/249 (51%), Positives = 168/249 (67%) splO3174[RNRH2_BACSU RIBONUCLEASE HII (RNAse HII)] prf[C99893 ribonuclease H rnh - Bacillus subtilis emb[CAB13479.1] (Z99112) ribonuclease H [Bacillus subtilis] Length = 255</p>
SeqID 1319	SA-2306.1	Contig79 (689-1540 p)	66	<p>Identities = 141/281 (50%), Positives = 198/281 (69%), Gaps = 5/281 (1%) dbj[BAA75381.1] (AB013365) YqF [Bacillus halodurans] dbj[BAB06195.1] (AP001515) unknown conserved protein [Bacillus halodurans] Length = 284</p>
SeqID 1320	SA-2307.1	Contig79 (72-413 p)	62	<p>Identities = 61/135 (45%), Positives = 86/135 (63%), Gaps = 4/135 (2%) prf[A69760 conserved hypothetical protein yclB - Bacillus subtilis dbj[BAA09899.1] (D50453) yclB [Bacillus subtilis] emb[CAB12129.1] (Z99105) similar to hypothetical proteins [Bacillus subtilis] Length = 194</p>
SeqID 1321	SA-2308.1	Contig79 (5434-6534 m)	40	<p>Identities = 85/336 (25%), Positives = 158/336 (46%), Gaps = 28/336 (8%) prf[E71665 bicyclomycin resistance protein (bcr1) RP603 - Rickettsia prowazekii emb[CAA15047.1] (AJ255272) BICYCLOMYCIN RESISTANCE PROTEIN (bcr1) [Rickettsia prowazekii] Length = 407</p>

SeqID 1322	SA-2309.1	Contig74 (4435-5382 m)	53	Identities = 127/269 (47%), Positives = 177/269 (65%), Gaps = 82/269 (2%) gblAAC23746.1 (AF052209) competence protein [Streptococcus pneumoniae] Length = 266
SeqID 1323	SA-231.1	Contig136 (35124-35423 m)	No Hits found	Identities = 593/601 (98%), Positives = 597/601 (98%) spIQ53778PEPB_STRAG_GROUP_B_OLIGOPEPTIDASE_PEPB pflT51748 thimet oligopeptidase (EC 3.4.24.15) PepB [validated] Streptococcus agalactiae gblAAC42415.1 (U49821) group B oligopeptidase PepB [Streptococcus agalactiae] Length = 601
SeqID 1324	SA-2311.1	Contig74 (2614-4419 m)	98	Identities = 391/117 (33%), Positives = 67/117 (56%), Gaps = 9/117 (7%) pflJAE7362 gyrB protein - Streptococcus pneumoniae (fragment) embICAA58770.1 (X83917) onfgyrB [Streptococcus pneumoniae] embICAA91552.1 (Z87740) unidentified [Streptococcus pneumoniae] Length = 144
SeqID 1325	SA-2312.1	Contig74 (1793-2419 m)	28	Identities = 131/227 (57%), Positives = 169/227 (73%) embICAA68045.1 (X99710) methyltransferase [Lactococcus lactis] Length = 227
SeqID 1326	SA-2313.1	Contig74 (1012-1719 m)	69	Identities = 101/307 (32%), Positives = 151/307 (48%), Gaps = 17/307 (5%) spIP15294IPRTM_LACLA_PROTEASE MATURATION PROTEIN PRECURSOR pflJIS08083 probable protein export protein prfM precursor - Lactococcus lactis subsp. cremoris (strain NCDO 763) plasmid pLP763 embICAA32349.1 (X14130) ORF (AA 1 to 299) [Lactococcus lactis subsp. cremoris] Length = 299
SeqID 1327	SA-2314.1	Contig74 (22-951 m)	48	Identities = 539/725 (74%), Positives = 616/725 (84%), Gaps = 7/725 (0%) gblJAA00215.1 (U73336) anaerobic ribonucleotide reductase [Lactobacillus lactis subsp. cremoris] Length = 747
SeqID 1328	SA-2315.2	Contig123 (8457-10655 m)	82	
SeqID 1329	SA-2316.1	Contig123 (8239-8382 m)	No Hits found	

SeqID 1330	SA-2317.1	Contig123 (7294-8226 m)	46	Identities = 91/299 (30%), Positives = 147/299 (48%), Gaps = 7/299 (2%) emb(CAB5794.1)[AL359949] putative oxidoreductase [Streptomyces coelicolor A3(2)] Length = 301
SeqID 1331	SA-2318.1	Contig123 (6794-7285 m)	40	Identities = 52/129 (40%), Positives = 70/129 (53%), Gaps = 5/129 (3%) dbj(BAB04222.1)[AP001508] unknown conserved protein in others [Bacillus halodurans] Length = 174
SeqID 1332	SA-2319.2	Contig123 (6104-6721 m)	79	Identities = 152/198 (76%), Positives = 176/198 (88%) gb(AAD00216.1)[U73336] anaerobic ribonucleotide reductase activator protein [Lactococcus lactis subsp. cremoris] Length = 199
SeqID 1333	SA-232.1	Contig136 (34814-35113 m)	No Hits found	
SeqID 1334	SA-2322.2	Contig118 (25662-27211 p)	76	Identities = 275/450 (61%), Positives = 347/450 (77%), Gaps = 1/450 (0%) dbj(BAA76640.1)[AB019579] glutathione reductase (GR) [Streptococcus mutans] Length = 450
SeqID 1335	SA-2324.1	Contig118 (27254-27706 m)	50	Identities = 45/156 (28%), Positives = 79/156 (49%), Gaps = 3/156 (1%) gb(AAF67093.1)[AF167576.1](AF167576) secreted antigen SagB [Enterococcus hirae] Length = 576
SeqID 1336	SA-2326.1	Contig118 (27953-29098 p)	60	Identities = 175/353 (49%), Positives = 234/353 (65%), Gaps = 1/353 (0%) sp P31672 NIFS_LACDE NIFS PROTEIN HOMOLOG pri S16047 nitrogenase cofactor synthesis protein nifs - Lactobacillus delbrueckii emb CAA43493.1] (X61190) nifs-like gene [Lactobacillus delbrueckii] Length = 355
SeqID 1337	SA-2327.2	Contig118 (29100-30314 p)	74	Identities = 264/385 (68%), Positives = 312/385 (80%) gb AAK04477.1 AE006275.1 (AE006275) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 406
SeqID 1338	SA-2329.3	Contig118 (30416-31594 p)	28	Identities = 68/224 (30%), Positives = 117/224 (51%), Gaps = 10/224 (4%) ref NP_053211.1 pXO2-56 [Bacillus anthracis] gb AAAF13661.1 AF188935_59 (AF188935) pXO2-56 [Bacillus anthracis] Length = 411

SeqID	SA-2333.1	Contig136 (34011-34712 m)	No Hits found	
SeqID 1340	SA-2330.1	Contig73 (1490-2371 m)	93	Identities = 260/293 (88%), Positives = 276/293 (93%) dbj BAB16889.1 AB050113 class-II aldolase [Streptococcus bovis] Length = 293
SeqID 1341	SA-2331.1	Contig73 (488-1405 p)	60	Identities = 175/306 (57%), Positives = 220/306 (71%), Gaps = 3/306 (0%) sp P14295DHL2_LACCO L-2- HYDROXYISOCAPROATE DEHYDROGENASE (L-HICDH) pirl J00114 L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)- Lactobacillus confusus gb AA488213.1 (M31425) L-2- hydroxyisocaproate dehydrogenase [Weissella confusa] Length = 310
SeqID 1342	SA-2332.1	Contig73 (61-249 m)	72	Identities = 45/62 (72%), Positives = 53/62 (84%) sp P37807 RL28_BACSU 50S RIBOSOMAL PROTEIN L28 pirl S3982 ribosomal protein L28 (rplB) - Bacillus subtilis gb AAC36810.1 (L12244) ribosomal protein L28 [Bacillus subtilis] emb CAA74255.1 (Y13937) putative RplB protein [Bacillus subtilis] emb CAB13455.1 (Z99112) ribosomal protein L28 [Bacillus subtilis] Length = 62
SeqID 1343	SA-2334.1	Contig101 (17522-19501 p)	13	Identities = 65/236 (27%), Positives = 92/236 (38%), Gaps = 47/236 (19%) pirl S2348 hypothetical protein 2 - Lactobacillus leichmannii emb CAA57459.1 (X81859) orf2 [Lactobacillus leichmannii] Length = 507
SeqID 1344	SA-2335.2	Contig101 (19712-20491 p)	50	Identities = 91/298 (30%), Positives = 155/298 (51%), Gaps = 13/298 (4%) gb AAK04857.1 AE006309.6 (AE006309) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 432
SeqID 1345	SA-2336.1	Contig101 (20491-21375 p)	46	Identities = 95/271 (35%), Positives = 139/271 (51%), Gaps = 16/271 (6%) gb AAC13546.1 (AF019629) putative fibrin- associated protein [Actinomyces naeslundii] Length = 365
SeqID 1346	SA-2337.1	Contig101 (21423-22298 p)	30	Identities = 62/245 (25%), Positives = 96/245 (38%), Gaps = 45/245 (19%) dbj BAB04080.1 (AP001508) unknown [Bacillus halodurans] Length = 1661

SeqID 1347	SA-2339.2	Contig135 (2828-3526 p)	95	Identities = 228/232 (98%), Positives = 229/232 (98%), Gaps = 3/232 (1%) dbjBAA82278.1 (AB028896) CpsIad [Streptococcus agalactiae] Length = 229
SeqID 1348	SA-234.1	Contig136 (32865-3970 m)	38	Identities = 103/342 (30%), Positives = 155/342 (45%), Gaps = 50/342 (14%) efINP_053232.1, pXO2-78 [Bacillus anthracis] gb AAAF13682.1 AF188935_80 (AF188935) pXO2-78 [Bacillus anthracis] Length = 344
SeqID 1349	SA-2340.2	Contig135 (3539-4827 p)	95	Identities = 448/449 (99%), Positives = 448/449 (99%) pir T44643 galactosyl transferase cpsD [imported] - Streptococcus agalactiae gb AAD53066.1 AF163833_6 (AF163833) CpsE [Streptococcus agalactiae] Length = 449
SeqID 1350	SA-2341.1	Contig135 (4951-5400 p)	93	Identities = 149/149 (100%), Positives = 149/149 (100%) pir T44644 glycosyl transferase activity enhancer cpsG [imported] - Streptococcus agalactiae gb AAD53067.1 AF163833_7 (AF163833) CpsF [Streptococcus agalactiae] Length = 149
SeqID 1351	SA-2342.1	Contig135 (5400-5873 p)	94	Identities = 155/157 (98%), Positives = 155/157 (98%) pir T44645 glycosyl transferase cpsH [imported] - Streptococcus agalactiae gb AAD53068.1 AF163833_8 (AF163833) CpsG [Streptococcus agalactiae] Length = 157
SeqID 1352	SA-2343.1	Contig135 (6870-7016 p)	99	Identities = 380/381 (99%), Positives = 380/381 (99%) pir T44646 capsular polysaccharide repeating unit polymerase cpsI [imported] - Streptococcus agalactiae gb AAD53069.1 AF163833_9 (AF163833) CpsI [Streptococcus agalactiae] Length = 381
SeqID 1353	SA-2344.1	Contig135 (7012-7980 p)	98	Identities = 318/322 (98%), Positives = 320/322 (98%) pir T44647 glycosyl transferase cpsJ [imported] - Streptococcus agalactiae gb AAD53070.1 AF163833_10 (AF163833) CpsJ [Streptococcus agalactiae] Length = 322

SeqID 1354	SA-2346.1	Contig135 (8014-8961 p)	96	Identities = 314/315 (99%), Positives = 315/315 (99%) dbjBAA33750.1 [AB017355] galactosyltransferase [Streptococcus agalactiae] dbjBAA62284.1 [AB028896] CpsIA [Streptococcus agalactiae] Length = 315
SeqID 1355	SA-2346.2	Contig135 (9045-10001 p)	98	Identities = 318/318 (100%), Positives = 318/318 (100%) dbjBAA33751.1 [AB017355] cpsJ [Streptococcus agalactiae] dbjBAA62285.1 [AB028896] CpsIAK [Streptococcus agalactiae] Length = 318
SeqID 1356	SA-2347.1	Contig75 (158-718 p)	51	Identities = 64/234 (27%), Positives = 122/234 (51%), Gaps = 3/234 (1%) spIO320951UEF_BACSU HYPOTHETICAL 40.9 KDA PROTEIN IN DEQO-ALD INTERGENIC REGION pirIG70007 conserved hypothetical protein yueF - Bacillus subtilis embICAB15168.1 [Z99120] similar to hypothetical proteins [Bacillus subtilis] Length = 369
SeqID 1357	SA-2348.1	Contig75 (814-1494 p)	57	Identities = 90/210 (42%), Positives = 136/210 (63%) spIO02170RADCBACSU DNA REPAIR PROTEIN RADCB HOMOLOG (ORF) pirJB45239 DNA repair protein homolog ysxA - Bacillus subtilis gbIAAA22396.1 [M96343] homologous to E. coli radC gene product and to unidentified protein from Staphylococcus aureus [Bacillus subtilis] gbIAAA22583.1 [L08793] putative [Bacillus subtilis] embICAB14764.1 [Z99118] similar to DNA repair protein [Bacillus subtilis] Length = 231
SeqID 1358	SA-2349.1	Contig75 (1507-2145 m)	64	Identities = 96/202 (47%), Positives = 140/202 (68%), Gaps = 4/202 (1%) pirJA69787 hypothetical protein ydH - Bacillus subtilis dbjBAA19721.1 [D88802] ydH [Bacillus subtilis] Length embICAB12416.1 [Z99107] ydH [Bacillus subtilis] = 215
SeqID 1359	SA-2350.1	Contig136 (32600-32830 m)	No Hits found	
SeqID 1360	SA-2350.1	Contig75 (2300-2847 m)	No Hits found	

SeqID 1361	SA-2351.1	Contig75 (2648-3767 m)	63	Identities = 173/373 (46%), Positives = 236/373 (62%), Gaps = 6/373 (1%) dbj BA04979.1 (AF001511) Fe-S cluster formation protein [Bacillus halodurans] Length = 386
SeqID 1362	SA-2352.1	Contig75 (3768-4043 m)	68	Identities = 42/89 (47%), Positives = 63/69 (70%), Gaps = 2/89 (2%) gb AAAF15359.1 (AF201954.1) (AF201954) phosphoribosylpyrophosphate synthetase [Plasmodium falciparum] Length = 323
SeqID 1363	SA-2353.1	Contig72 (5600-5809 p)	82	Identities = 48/70 (68%), Positives = 58/70 (82%) pir T00087 rhamnosyltransferase - Streptococcus mutans dbj BAA32090.1 (AB010870) rhamnosyltransferase [Streptococcus mutans] Length = 311
SeqID 1364	SA-2354.1	Contig72 (4453-5610 p)	66	Identities = 234/362 (64%), Positives = 284/362 (77%) pir T00086 igpAc protein - Streptococcus mutans dbj BAA32089.1 (AB010870) igpAc [Streptococcus mutans] Length = 362
SeqID 1365	SA-2355.1	Contig72 (3485-4339 p)	92	Identities = 257/283 (90%), Positives = 273/283 (95%) gb AAC38675.1 (AF030359) dTDP-L-rhamnose synthase [Streptococcus pneumoniae] gb AAC38686.1 (AF030361) dTDP-L-rhamnose synthase [Streptococcus pneumoniae] gb AAC38701.1 (AF030364) dTDP-L-rhamnose synthase [Streptococcus pneumoniae] gb AAD10184.1 (AF026471) Cps20 [Streptococcus pneumoniae] Length = 283
SeqID 1366	SA-2356.1	Contig72 (3054-3395 p)	82	Identities = 92/108 (85%), Positives = 100/108 (92%) dbj BAA21508.1 (AB000631) unnamed protein product [Streptococcus mutans] Length = 111
SeqID 1367	SA-2357.1	Contig72 (1803-2945 p)	93	Identities = 345/367 (94%), Positives = 358/367 (97%) dbj BAA21507.1 (AB000631) sigma 42 protein [Streptococcus mutans] Length = 371
SeqID 1368	SA-2358.1	Contig72 (20-1828 p)	64	Identities = 271/637 (42%), Positives = 389/637 (60%), Gaps = 56/637 (8%) sp Q04505 PRIM_LACLA DNA PRIMASE pir J02485 DNA primase (EC 2.7.7.-) dnaG - Lactococcus lactis pir T106154A DNA primase [Lactococcus lactis] Length = 642

SeqID 1369	SA-2359.2	Contig71 (2968-3543 m)	63	Identities = 98/195 (49%), Positives = 138/195 (70%), Gaps = 15/195 (7%) gblAAK04732.1(AE006296_6 (AE006296) DNA-directed RNA polymerase delta chain (EC 2.7.7.6) [Lactococcus lactis subsp. lactis] Length = 187
SeqID 1370	SA-236.1	Contig136 (32214-32603 m)	No Hits found	Identities = 421/535 (78%), Positives = 481/535 (89%) embICA09021.2 (AJO10153) CTP synthetase [Lactococcus lactis subsp. cremoris] Length = 535
SeqID 1371	SA-2360.1	Contig71 (1091-2695 m)	89	Identities = 157/312 (50%), Positives = 212/312 (67%), Gaps = 9/312 (2%) gblAAK04219.1(AE006250_6 (AE006250) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 311
SeqID 1372	SA-2361.2	Contig71 (56-982 m)	67	Identities = 62/235 (26%), Positives = 108/235 (46%), Gaps = 12/235 (5%) pflJ34651 probable transmembrane protein - Streptomyces coelicolor embICAA22372.1 (AL034446) putative transmembrane protein [Streptomyces coelicolor A3(2)] Length = 307
SeqID 1373	SA-2363.1	Contig104 (71-529 m)	No Hits found	Identities = 106/440 (24%), Positives = 206/440 (46%), Gaps = 65/440 (14%) pflJC82901 conserved hypothetical UU367 [imported] - Ureaplasma urealyticum
SeqID 1374	SA-2364.1	Contig104 (3-842 p)	38	gblAAEF30776.1(AE002133_9 (AE002133) conserved hypothetical [Ureaplasma urealyticum] Length = 507
SeqID 1375	SA-2365.1	Contig104 (949-1539 p)	No Hits found	Identities = 39/145 (26%), Positives = 68/145 (46%), Gaps = 7/145 (4%) pflJD69831 conserved hypothetical protein yH10 - Bacillus subtilis embCAA74538.1 (Y14084) hypothetical protein [Bacillus subtilis] embICAB12871.1 (Z99109) similar to hypothetical proteins [Bacillus subtilis] Length = 149
SeqID 1376	SA-2366.1	Contig104 (1573-2844 p)	47	
SeqID 1377	SA-2367.1	Contig104 (2857-3288 p)	45	

SeqID 1378	SA-2368.1	Contig104 (3380-4264 p)	64	Identities = 145/283 (51%), Positives = 191/283 (67%), Gaps = 12/283 (4%) dbj BA806129.1 (AP001515) RNA pseudouridine 5S synthase [Bacillus halodurans] Length = 304
SeqID 1379	SA-2369.2	Contig104 (4277-5209 p)	98	Identities = 310/311 (99%), Positives = 311/311 (99%) gb AA864408.1 (U92073) macrolide-efflux protein [Streptococcus agalactiae] Length = 311
SeqID 1380	SA-237.1	Contig136 (31877-32062 m)	No Hits found	
SeqID 1381	SA-2370.3	Contig124 (2287-4089 m)	59	Identities = 252/598 (42%), Positives = 358/598 (59%), Gaps = 54/598 (9%) gb AAK04733.1 (AE006296.7 (AE006296) conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 550
SeqID 1382	SA-2371.1	Contig124 (1732-2214 m)	68	Identities = 86/154 (55%), Positives = 114/154 (73%), Gaps = 1/154 (0%) sp P80240 GREA_BACSU TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA) (GENERAL STRESS PROTEIN 20M) (GSP20M) pir A69637 transcription elongation factor grea - Bacillus subtilis emb CAB14674.1 (Z99117) transcription elongation factor [Bacillus subtilis] Length = 157
SeqID 1383	SA-2372.1	Contig124 (168-1628 m)	54	Identities = 182/488 (37%), Positives = 267/488 (54%), Gaps = 17/488 (3%) pir C75543 6-aminohexanoate-cyclic-dimer hydrolase - Deinococcus radiodurans (strain R1) gb AA09821.1 (AE001885.5 (AE001885) 6-aminohexanoate-cyclic-dimer hydrolase [Deinococcus radiodurans] Length = 561
SeqID 1384	SA-2373.1	Contig93 (16319-16855 p)	54	Identities = 65/206 (31%), Positives = 110/206 (52%), Gaps = 16/206 (7%) gb AA027630.1 (M88350) hydrophobic protein [unidentified bacterium] Length = 251

SeqID 1385	SA-2374.1	Contig83 (15061-16188 m)	22	<p>Identities = 54/192 (28%), Positives = 89/192 (46%), Gaps = 14/192 (7%) sp P50736 YPDA_BACSU HYPOTHETICAL 36.3 KD PROTEIN IN RECQ-CMK INTERGENIC REGION</p> <p>pir JA69334 thioredoxin reductase homolog ypdA - Bacillus subtilis gb AAC33954.1 (L47548) putative [Bacillus subtilis] emb CAB14211.1 (Z99115) similar to thioredoxin reductase [Bacillus subtilis] emb CAB14227.1 (Z99116) similar to thioredoxin reductase [Bacillus subtilis] Length = 324</p>
SeqID 1386	SA-2376.1	Contig83 (14038-16024 p)	78	<p>Identities = 213/322 (66%), Positives = 260/322 (80%), Gaps = 5/322 (1%) gb AB81912.1 (U92974) unknown [Lactobacoccus lactis] Length = 319</p>
SeqID 1387	SA-2377.1	Contig83 (13570-13875 m)	No Hits found	
SeqID 1388	SA-2378.2	Contig93 (12039-13412 p)	52	<p>Identities = 174/321 (54%), Positives = 241/321 (74%), Gaps = 4/321 (1%) pir JC5050 sugar phosphate transport protein - Shigella flexneri gb AAC44575.1 (U28354) IS629 ORF8 fused with sequences similar to E. coli GpT and UnpT proteins, Swiss-Prot Accession Number P08194 and P09836; Method: conceptual translation supplied by author [Shigella flexneri] Length = 333</p>
SeqID 1389	SA-238.1	Contig136 (31331-31807 m)	19	<p>Identities = 23/57 (40%), Positives = 36/57 (62%) ref NP_049417.1 putative cro-like regulatory protein [Streptococcus thermophilus bacteriophage DT1] gb AAD21905.1 (AF065222) putative cro-like regulatory protein [Streptococcus thermophilus bacteriophage DT1] Length = 67</p>
SeqID 1390	SA-2380.2	Contig130 (2285-3055 p)	55	<p>Identities = 112/253 (44%), Positives = 151/253 (63%), Gaps = 1/253 (0%) sp Q9RGS6 THIM_STACA HYDROXYETHYLTHIAZOLE KINASE (4-METHYL-5-BETA-HYDROXYETHYLTHIAZOLE KINASE) (TH KINASE) (TH KINASE) gb AF25543.1 (AF109218) Thim [Staphylococcus carnosus] Length = 264</p>

SeqID 1391	SA-2381.1	Contig130 (1486-2283 p)	- - 67	Identities = 139/258 (53%), Positives = 186/258 (71%), Gaps = 4/258 (1%) gb AAAF25542.1 AF109218_2 (AF109218) TnD [Staphylococcus carnosus] Length = 273
SeqID 1392	SA-2382.1	Contig130 (805-1461 p)	52	Identities = 74/213 (34%), Positives = 122/213 (56%), Gaps = 13/213 (5%) gb AAAF25541.1 AF109218_1 (AF109218) TnA [Staphylococcus carnosus] Length = 228
SeqID 1393	SA-2383.1	Contig130 (181-305 p)	No Hits found	
SeqID 1394	SA-2384.1	Contig130 (20-721 p)	41	Identities = 49/216 (22%), Positives = 98/216 (45%), Gaps = 3/216 (1%) emb CAA91230.1 Z55283 orf2 [Lactobacillus helveticus] Length = 217
SeqID 1395	SA-2386.1	Contig101 (9385-10610 p)	64	Identities = 189/462 (40%), Positives = 313/462 (66%) emb CAB52225.1 Z98171 EpsU protein [Streptococcus thermophilus] Length = 471
SeqID 1396	SA-2387.1	Contig101 (8022-9386 p)	No Hits found	
SeqID 1397	SA-2388.2	Contig101 (7073-8020 p)	23	Identities = 53/116 (45%), Positives = 75/116 (63%), Gaps = 4/116 (3%) gb AAAF18951.1 AF155805_5 (AF155805) Cps9H [Streptococcus suis] Length = 143
SeqID 1398	SA-239.1	Contig136 (30561-31331 m)	58	Identities = 99/260 (38%), Positives = 157/260 (60%), Gaps = 3/260 (1%) pri S45085 hypotrichal protein zeta - Streptococcus pyogenes plasmid pDB101 and pBT233 pri S6806 hypotrichal protein zeta - Streptococcus pyogenes plasmid pBT233 emb CAA45934.1 XG4695 ORF zeta [Streptococcus pyogenes] emb CAA47091.1 XG6468 orf zeta [Streptococcus pyogenes] emb CAA47092.1 XG6468 orf zeta [Streptococcus pyogenes] Length = 287

SeqID 1399	SA-2390.2	Contig136 (91497-93569 p)	38	Identities = 178/535 (33%), Positives = 269/535 (50%), Gaps = 55/535 (10%) sp P54602 YHCR_BACSU HYPOTHETICAL 132.7 KDA PROTEIN IN CSPB-GLTP INTERGENIC REGION pir F69823 probable phosphatase (EC 3.1.-) yHCR - Bacillus subtilis emb CA65702.1 (X96983) hypothetical protein [Bacillus subtilis] emb CAB12747.1 (Z99106) similar to 5 - nucleotidase [Bacillus subtilis] Length = 1217
SeqID 1400	SA-2391.1	Contig136 (93606-94016 m)	70	Identities = 72/136 (52%), Positives = 96/136 (69%) sp O06450 DEF_CLOBE POLYPEPTIDE DEFORMYLASE (PDF) (FORMYL METHIONINE DEFORMYLASE) emb CAB09662.1 (Z96934) peptide deformylase [Clostridium beijerinckii] Length = 136
SeqID 1401	SA-2392.1	Contig136 (94086-95393 m)	81	Identities = 292/436 (66%), Positives = 356/436 (80%), Gaps = 2/436 (0%) dbj BAB05620.1 (AP001514) NADP-specific glutamate dehydrogenase [Bacillus halodurans] Length = 458
SeqID 1402	SA-2394.2	Contig89 (9769-11001 m)	29	Identities = 63/243 (25%), Positives = 120/243 (48%) dbj BAB03800.1 (AP001507) BH0081-unknown conserved protein in others [Bacillus halodurans] Length = 251
SeqID 1403	SA-2395.1	Contig69 (11041-12582 m)	81	Identities = 352/509 (69%), Positives = 421/509 (82%), Gaps = 1/509 (0%) pir F69813 ABC transporter (ATP-binding protein) homolog yfmM - Bacillus subtilis dbj BA22327.1 (D86417) YfmM [Bacillus subtilis] emb CAB12571.1 (Z99108) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 518
SeqID 1404	SA-2396.2	Contig88 (2596-3666 p)	60	Identities = 138/358 (38%), Positives = 220/358 (60%), Gaps = 18/358 (5%) pir F71373 probable regulatory protein (pfsSR) - syphilis spirochete gb AAC65034.1 (AE001189) regulatory protein (pfsSR) [Treponema pallidum] Length = 350

SeqID 1405	SA-2397.1	Contig88 (1467-2459 p)	67	Identities = 163/325 (50%), Positives = 222/325 (68%), Gaps = 3/325 (0%) djBjAB07127.1 (AP001518) thioredoxin reductase [Bacillus halodurans] Length = 330
SeqID 1406	SA-2398.1	Contig88 (731-1486 p)	73	Identities = 144/246 (58%), Positives = 186/246 (75%), Gaps = 6/246 (2%) djBjAB06198.1 (AP001515) rRNA methyltransferase [Bacillus halodurans] Length = 246
SeqID 1407	SA-2399.1	Contig88 (1-744 p)	51	Identities = 88/174 (50%), Positives = 128/174 (72%), Gaps = 1/174 (0%) spJO317401RIMM_BACSU PROBABLE 16S RRNA PROCESSING PROTEIN RIMM prfJ69880 conserved hypothetical protein yjQE - Bacillus subtilis embiCAB13475.1 (Z39112) similar to hypothetical proteins [Bacillus subtilis] Length = 174
SeqID 1408	SA-240.2	Contig 136 (28308-30459 m)	15	Identities = 65/236 (27%), Positives = 117/236 (49%), Gaps = 27/236 (11%) prfJH83403 hypothetical protein PA1939 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb AA05327.1 AE004620.6 (AE004620) hypothetical protein [Pseudomonas aeruginosa] Length = 665
SeqID 1409	SA-2404.1	Contig122 (33097-35049 m)	77	Identities = 412/632 (65%), Positives = 506/632 (79%), Gaps = 6/632 (0%) prfJ585599 phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific - Streptococcus sobrius (strain 6715) Length = 632
SeqID 1410	SA-2405.1	Contig70 (5129-5893 m)	98	Identities = 252/254 (99%), Positives = 253/254 (99%) gb AA05975.1 AF248038.4 (AF248038) methyltransferase [Streptococcus agalactiae] Length = 254
SeqID 1411	SA-2406.1	Contig70 (4770-5108 m)	95	Identities = 112/112 (100%), Positives = 112/112 (100%) gb AA05974.1 AF248038.3 (AF248038) unknown [Streptococcus agalactiae] Length = 112
SeqID 1412	SA-2407.1	Contig70 (4463-4768 m)	94	Identities = 101/101 (100%), Positives = 101/101 (100%) gb AA05973.1 AF248038.2 (AF248038) acetate kinase [Streptococcus agalactiae] Length = 101

SeqID 1413	SA-2409.2	Contig70 (3708-4245 p)	52	Identities = 105/107 (98%), Positives = 106/107 (98%) gb AAC09972.1 AF248038.1 (AF248038) integrase [Streptococcus agalactiae] Length = 108
SeqID 1414	SA-2411.2	Contig138 (3783-38351 m)	55	Identities = 74/175 (42%), Positives = 98/175 (55%), Gaps = 6/175 (3%) sp P50838 YPSA_BACSU HYPOTHETICAL 21.1 KD PROTEIN IN COTD-KOUD INTERGENIC REGION pir D69941 conserved hypothetical protein ypsA - Bacillus subtilis gb JAB38471.1 (L47838) putative [Bacillus subtilis] emb CAB14136.1 (Z99115) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] Length = 180
SeqID 1415	SA-2410.1	Contig70 (3110-3544 p)	42	Identities = 40/123 (32%), Positives = 63/123 (50%), Gaps = 9/123 (7%) gb AAD00258.1 (U77495) putative integrase [Leuconostoc oenos bacteriophage 10MC] Length = 348
SeqID 1416	SA-2411.1	Contig70 (2734-3060 p)	33	Identities = 24/72 (33%), Positives = 38/72 (52%), Gaps = 2/72 (2%) db JBA07266.1 (AP001519) unknown conserved protein in others [Bacillus halodurans] Length = 79
SeqID 1417	SA-2412.1	Contig70 (2007-2561 p)	No Hits found	Identities = 70/211 (33%), Positives = 101/211 (47%), Gaps = 5/211 (2%) pir JHC204 hypothetical 30.5K protein precursor - Enterococcus faecalis plasmid pAM-beta-1 gb AAC38600.1 (AF007787) orfC [Enterococcus faecalis] Length = 288
SeqID 1418	SA-2414.1	Contig70 (1022-1783 p)	38	
SeqID 1419	SA-2415.1	Contig70 (440-997 p)	No Hits found	
SeqID 1420	SA-2416.1	Contig70 (12-440 p)	No Hits found	
SeqID 1421	SA-2418.2	Contig104 (16088-16768 p)	88	Identities = 202/246 (82%), Positives = 223/246 (90%), Gaps = 7/246 (2%) emb CAB54564.1 (AJ005926) response regulator [Streptococcus pneumoniae] Length = 246
SeqID 1422	SA-2419.2	Contig104 (13377-15926 p)	76	Identities = 555/847 (65%), Positives = 673/847 (78%), Gaps = 4/847 (0%) emb CAB50785.1 (AJ007700) aminopeptidase N [Streptococcus thermophilus] Length = 847

SeqID 1423	SA-242.2	Contig1138 (38426-39025 p)	78	Identities = 143/166 (72%), Positives = 165/196 (83%), Gaps = 1/196 (0%) sp Q00579 RECU_STOR RECOMBINATION PROTEIN U HOMOLOG gb AA26957.1 (M90328) ORF [Streptococcus oralis] Length = 198
SeqID 1424	SA-2420.2	Contig1118 (31784-32098 p)	70	Identities = 82/104 (78%), Positives = 92/104 (87%) gb AAK05177.1 AE006340.10 (AE006340) 50S ribosomal protein L21 [Lactococcus lactis subsp. lactis] Length = 104
SeqID 1425	SA-2421.2	Contig1118 (31661-32134 m)	No Hits found	
SeqID 1426	SA-2422.2	Contig1118 (32105-32443 p)	53	Identities = 38/107 (35%), Positives = 61/107 (56%), Gaps = 5/107 (4%) gb AAK05178.1 AE006340.11 (AE006340) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 111
SeqID 1427	SA-2423.1	Contig1118 (32465-32758 p)	76	Identities = 70/90 (77%), Positives = 80/90 (88%) sp P05657 RL27_BACSU 50S RIBOSOMAL PROTEIN L27 (BL30) (BL24) p rl C21895 ribosomal protein L27 - Bacillus subtilis emb CAA26482.1 (X02658) homologous to E.coli ribosomal protein L27 [Bacillus subtilis] emb CAB14754.1 (Z99118) ribosomal protein L27 (BL24) [Bacillus subtilis] Length = 94
SeqID 1428	SA-2424.1	Contig1118 (32974-33878 p)	53	Identities = 105/287 (35%), Positives = 164/297 (64%), Gaps = 4/297 (1%) p rl T44638 capsular polysaccharide biosynthesis protein cpsY [Imported] - Streptococcus agalactiae emb CAB36980.1 (Y17218) CpsY protein [Streptococcus agalactiae] emb CAB39982.2 (Y17241) CpsY protein [Streptococcus agalactiae] gb AAD53064.1 AF163833.1 (AF163833) CpsY [Streptococcus agalactiae] Length = 307
SeqID 1429	SA-2425.1	Contig1118 (33888-34352 p)	58	Identities = 61/144 (42%), Positives = 94/144 (64%), Gaps = 1/144 (0%) sp Q48729 LSPA_LACLC LIPOPROTEIN SIGNAL PEPTIDASE (PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II) Length = 150

SeqID 1430	SA-2426.2	Contig118 (34336-34836 p)	80	Identities = 115/188 (68%), Positives = 140/168 (82%) gb AAK05096.1 AE006334.2 (AE006334.2) pseudouridine synthase [Lactococcus lactis subsp. lactis] Length = 301
SeqID 1431	SA-2428.1	Contig67 (20-2098 p)	87	Identities = 536/692 (77%), Positives = 613/692 (88%) emb CAC08927.1 (A248559) translation elongation factor G, EF G [Bacillus stearothermophilus] Length = 692
SeqID 1432	SA-2429.2	Contig135 (26612-27559 m)	23	Identities = 42/173 (24%), Positives = 80/173 (45%), Gaps = 2/173 (1%) ref NP_052734.1 pXO1-38 [Bacillus anthracis] pilJF5905 hypothetical protein pXO1-38 - Bacillus anthracis virulence plasmid pXO1 gb AAD32342.1 AAD32342 (AF065404) pXO1-38 [Bacillus anthracis] Length = 276
SeqID 1433	SA-2430.1	Contig135 (25417-26483 m)	64	Identities = 153/350 (43%), Positives = 234/350 (66%), Gaps = 4/350 (1%) ref NP_049990.1 orf359 gp [Streptococcus thermophilus bacteriophage Sf21] emb CAAG4931.1 (X95646) integrase [Streptococcus thermophilus bacteriophage Sf21] gb AAC03454.1 (AF020796) integrase homolog [Streptococcus thermophilus bacteriophage TP-J34] gb AAD44086.1 AF115103.25 (AF115103) orf359 gp [Streptococcus thermophilus bacteriophage Sf21] Length = 359
SeqID 1434	SA-2431.3	Contig135 (23774-25237 p)	63	Identities = 251/401 (62%), Positives = 312/401 (77%), Gaps = 4/401 (0%) gb AAK04938.1 AE006317.5 (AE006317) 30S ribosomal protein S1 [Lactococcus lactis subsp. lactis] Length = 408

SeqID 1435	SA-2432.3	Contig135 (24255-25128 m)	38	<p>Identities = 73/265 (27%), Positives = 111/265 (41%), Gaps = 40/265 (15%) ref NP_014442.1 anchorage subunit of a- agglutinin, Aga1p [Saccharomyces cerevisiae]</p> <p>sp P32323 JAGA1_YEAST A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR pr JAA1258 a-agglutinin core protein AGA1 - yeast [Saccharomyces cerevisiae] gb AA34382.1 (M60560) a-agglutinin core subunit [Saccharomyces cerevisiae] emb CAA96325.1 (Z71659) ORF YNR044w [Saccharomyces cerevisiae] Length = 725</p>
SeqID 1436	SA-2433.2	Contig96 (1705-2137 m)	42	<p>Identities = 47/137 (34%), Positives = 71/137 (51%), Gaps = 5/137 (3%) dbj BA04953.1 (AP001511) small multidrug export related protein [Bacillus halodurans] Length = 134</p>
SeqID 1437	SA-2434.3	Contig96 (507-1547 p)	81	<p>Identities = 242/338 (71%), Positives = 290/338 (85%) gb AAK06250.1 (AE008444.1) (AE008444) elongation factor Ts [Lactococcus lactis subsp. lactis] Length = 342</p>
SeqID 1438	SA-2435.3	Contig96 (3-413 p)	83	<p>Identities = 102/131 (77%), Positives = 115/131 (88%), Gaps = 2/131 (1%) gb AAK06251.1 (AE008444.2) (AE008444) 30S ribosomal protein S2 [Lactococcus lactis subsp. lactis] Length = 255</p>
SeqID 1439	SA-2436.3	Contig96 (2-316 m)	30	<p>Identities = 28/59 (47%), Positives = 32/59 (53%) emb CA867155.1 (AJ271079) hypothetical protein [Onchocerca elata subsp. hooker] Length = 94</p>
SeqID 1440	SA-2437.2	Contig135 (2125-2817 p)	93	<p>Identities = 229/230 (99%), Positives = 229/230 (99%) sp Q04662 CP8B_STRAG CP8B PROTEIN pr IS34975 polysaccharide chain length regulator cpsB [Imported] - Streptococcus agalactiae gb AA00382.1 (AF163833) CpsC [Streptococcus agalactiae] Length = 230</p>
SeqID 1441	SA-2438.1	Contig135 (1385-2116 p)	96	<p>Identities = 242/243 (99%), Positives = 243/243 (99%) dbj BA042276.1 (AB028696) CpsIAB [Streptococcus agalactiae] Length = 243</p>
SeqID 1442	SA-2439.1	Contig135 (80-427 m)	No Hits found	

SeqID 1443	SA-244.2	Contig138 (39012-41258 p)	71	Identities = 412/725 (56%), Positives = 537/725 (73%), Gaps = 25/725 (3%) gb AAAF17262.1 AF210752.1 (AF210752) penicillin-binding protein 1A [Streptococcus pneumoniae] Length = 719
SeqID 1444	SA-2440.1	Contig135 (12-1379 p)	99	Identities = 450/453 (99%), Positives = 452/453 (99%) emb CAB36981.1 Y17218) CpsX protein [Streptococcus agalactiae] dbj BAAB2275.1 (AB028866) CpslaA [Streptococcus agalactiae] Length = 485
SeqID 1445	SA-2441.1	Contig123 (43050-43538 m)	No Hits found	
SeqID 1446	SA-2442.1	Contig123 (42359-42814 p)	No Hits found	
SeqID 1447	SA-2443.1	Contig123 (41388-42402 p)	No Hits found	
SeqID 1448	SA-2445.2	Contig123 (39711-40976 p)	48	Identities = 138/398 (34%), Positives = 208/398 (51%), Gaps = 17/398 (4%) ref NP_076752.1 integrate [bacteriophage bIL310] gb AAK04145.1 AE006243.9 (AE006243) prophage p81 protein 23, integrate [Lactococcus lactis subsp. lactis] gb AAK08405.1 AF323671.1 (AF323671) integrate [bacteriophage bIL310] Length = 394
SeqID 1449	SA-2446.2	Contig136 (2790-3302 m)	48	Identities = 78/191 (40%), Positives = 112/191 (57%), Gaps = 9/191 (4%) dbj BAA21095.1 (D88438) repB [Lactobacillus acidophilus] Length = 193
SeqID 1450	SA-2447.1	Contig136 (2553-2756 m)	No Hits found	
SeqID 1451	SA-2448.1	Contig136 (1354-2535 m)	41	Identities = 101/370 (27%), Positives = 167/370 (44%), Gaps = 39/370 (10%) pir J13289 probable integrase - Streptococcus phage phi-O1205 gb AAC79517.1 (U88974) ORF1 [Streptococcus thermophilus temperate bacteriophage O1205] Length = 359
SeqID 1452	SA-2450.2	Contig135 (78598-79290 m)	No Hits found	
SeqID 1453	SA-2452.1	Contig66 (2566-2703 m)	No Hits found	

SeqID 1454	SA-2453.1	Contig66 (1714-2415 m)	67	<p>Identities = 112/244 (45%), Positives = 164/244 (66%), Gaps = 10/244 (4%) sp O31458 YBET_BACSU HYPOTHETICAL 27.3 KD PROTEIN IN GLTP-CW/LJ INTERGENIC REGION pir E89750 glucosamine-6-phosphate isomerase homolog ynfT - Bacillus subtilis emb CAB12030.1 (Z99105) similar to glucosamine-6-phosphate isomerase [Bacillus subtilis] dbj BAA33133.1 (AB006424) ynfT [Bacillus subtilis] Length = 249</p>
SeqID 1455	SA-2454.1	Contig66 (686-1642 p)	70	<p>Identities = 197/318 (61%), Positives = 243/318 (75%) pir S76960 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj BAA18872.1 (D80917) hypothetical protein [Synechocystis sp.] Length = 319</p>
SeqID 1456	SA-2455.1	Contig66 (3-590 m)	60	<p>Identities = 91/196 (46%), Positives = 120/196 (60%), Gaps = 1/196 (0%) dbj BAB08992.1 (AP001518) 16S pseudouridy/late synthase [Bacillus halodurans] Length = 238</p>
SeqID 1457	SA-2457.3	Contig132 (33811-35607 p)	45	<p>Identities = 151/620 (24%), Positives = 273/620 (43%), Gaps = 57/620 (9%) gb AAK08205.1 (AE008439_2) (AE008439) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 605</p>
SeqID 1458	SA-2458.3	Contig132 (33590-33632 p)	39	<p>Identities = 33/63 (39%), Positives = 51/63 (60%) pir E83144 hypothetical protein PA4016 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07403.1 (AE004818_9) (AE004818) hypothetical protein [Pseudomonas aeruginosa] Length = 579</p>
SeqID 1459	SA-2459.3	Contig91 (5194-5715 p)	61	<p>Identities = 72/165 (43%), Positives = 112/165 (67%), Gaps = 2/165 (1%) sp P39667 YRXA_BACSU HYPOTHETICAL 19.7 KDA PROTEIN IN PHEA-NIFS INTERGENIC REGION (ORF1) pir J47071 hypothetical protein ynfA - Bacillus subtilis emb CAB14749.1 (Z99118) ynfA [Bacillus subtilis] Length = 178</p>

SeqID 1460	SA-246.1	Contig138 (41304-42638 m)	90	<p>Identities = 363/445 (81%), Positives = 408/445 (91%) sp G56115 EPC_STRT AMINOPEPTIDASE C pil[S46143 cysteine aminopeptidase C - Streptococcus thermophilus emb CAA62960.1 (Z30315) aminopeptidase C [Streptococcus thermophilus] Length = 445</p>
SeqID 1461	SA-2460.1	Contig91 (4551-5126 p)	56	<p>Identities = 97/188 (51%), Positives = 133/188 (70%) gb AAC18360.1 (AF064763) putative membrane spanning protein [Lactococcus lactis subsp. cremoris] Length = 186</p>
SeqID 1462	SA-2461.1	Contig91 (3911-4414 p)	No Hits found	
SeqID 1463	SA-2462.1	Contig91 (3130-3873 p)	59	<p>Identities = 106/246 (43%), Positives = 150/246 (60%), Gaps = 7/246 (2%) pi G56984 RNA methylase homolog ysgA - Bacillus subtilis emb CA99902.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14825.1 (Z99118) similar to RNA methylase [Bacillus subtilis] Length = 248</p>
SeqID 1464	SA-2463.1	Contig91 (2820-3377 m)	29	<p>Identities = 35/91 (38%), Positives = 54/91 (59%), Gaps = 3/91 (3%) pir G72240 hypothetical protein TM1564 - Thermotoga maritima (strain MSB8) gb AAD36630.1 AE001801_17 (AE001801) acylphosphatase, putative [Thermotoga maritima] Length = 90</p>
SeqID 1465	SA-2464.2	Contig91 (1803-2693 m)	63	<p>Identities = 140/307 (45%), Positives = 201/307 (64%), Gaps = 19/307 (6%) gb AAK04667.1 AE006291_1 (AE006291) conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 307</p>

SeqID 1466	SA-2465.1	Contig139 (189466-189870 m)	45	<p>Identities = 42/105 (40%), Positives = 62/105 (59%) spIP45678PEB1_CAMJIE MAJOR CELL-BINDING FACTOR PRECURSOR (CBF1) (PEB1) pirIA48518 probable ABC-type amino-acid transporter periplasmic solute-binding protein Cj0921c precursor [Imported] - Campylobacter jejunii (strain NCTC 11168) gbAAA02919.1 (L13662) major cell- binding factor [Campylobacter jejuni] embICAB73178.1 (AL139076) probable ABC-type amino-acid transporter periplasmic solute-binding protein [Campylobacter jejuni] Length = 259</p>
SeqID 1467	SA-2466.1	Contig139 (188758-189453 m)	68	<p>Identities = 112/226 (49%), Positives = 161/226 (70%), Gaps = 3/226 (1%) pirJG381365 probable ABC-type amino-acid transporter permease protein Cj0920c: [Imported] - Campylobacter jejuni (strain NCTC 11168) embICAB73177.1 (AL139076) putative ABC-type amino-acid transporter permease protein [Campylobacter jejuni] Length = 250</p>
SeqID 1468	SA-2467.1	Contig139 (188096-188746 m)	58	<p>Identities = 85/216 (39%), Positives = 132/216 (60%), Gaps = 6/216 (2%) pirJF69533 glutamine ABC transporter (membrane protein) glnP - Bacillus subtilis embICAB14687.1 (Z99117) glutamine ABC transporter (integral membrane protein) [Bacillus subtilis] embICAB14704.1 (Z99118) glutamine ABC transporter (integral membrane protein) [Bacillus subtilis] Length = 218</p>
SeqID 1469	SA-2468.2	Contig139 (187481-188047 p)	42	<p>Identities = 43/167 (27%), Positives = 83/167 (52%), Gaps = 9/167 (5%) dbjBAB04094.1 (AP001508) BH0375-unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 194</p>
SeqID 1470	SA-2469.2	Contig139 (186295-187314 p)	No Hits found	

SeqID 1471	SA-2471.1	Contig138 (42751-43572 m)	75		Identities = 173/275 (62%), Positives = 215/275 (77%), Gaps = 1/275 (0%) spIP18643INADE_ECOLI_NH(3)-DEPENDENT NAD(+) SYNTHETASE (NITROGEN-REGULATORY PROTEIN) pIIJID4933 NAD+ synthase (EC 6.3.1.5) nadE [validated] - Escherichia coli (strain K-12) dbjBAA15529.1 (D90817) NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1) (Nitrogen-regulatory protein), [Escherichia coli] dbjBAA15535.1 (D90818) NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1) (Nitrogen-regulatory protein), [Escherichia coli] gb AAC74810.1 (AE000269) NAD synthetase, prefers NH3 over glutamine [Escherichia coli K12] Length = 275
SeqID 1472	SA-2470.1	Contig65 (2150-2422 m)	No Hits found		
SeqID 1473	SA-2471.1	Contig65 (1678-2109 p)	67		Identities = 69/152 (45%), Positives = 101/152 (66%), Gaps = 12/152 (7%) pIIJIT11571 hypothetical protein 2 - Streptococcus mutans gb AAD15622.1 (U75480) unknown [Streptococcus mutans] Length = 151
SeqID 1474	SA-2472.1	Contig65 (1283-1681 p)	77		Identities = 88/129 (68%), Positives = 112/129 (86%) pIIJIT11570 hypothetical protein 1 - Streptococcus mutans gb AAD15621.1 (U75480) unknown [Streptococcus mutans] Length = 131
SeqID 1475	SA-2473.1	Contig65 (495-1288 p)	85		Identities = 184/258 (71%), Positives = 227/258 (87%) spP72462LGT_STRMU PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE pIIJIT11569 prolipoprotein diacylglycerol transferase (EC 2.4.99.-) Streptococcus mutans gb AAC80171.3 (U75480) putative prolipoprotein diacylglycerol transferase [Streptococcus mutans] Length = 259
SeqID 1476	SA-2474.1	Contig65 (377-502 p)	89		Identities = 68/77 (88%), Positives = 75/77 (97%) sp C92498 HPRK_STRSL HPR(SER) KINASE/PHOSPHATASE gb AAD12781.1 (AF069743) HP(serine) kinase [Streptococcus salivarius] Length = 309

SeqID 1477	SA-2475.1	Contig55 (1-254 p)	95	<p>Identities = 82/84 (97%), Positives = 84/84 (99%) dbj BAA77782.1 (AB027460) Hpr kinase [Streptococcus bovis] Length = 310</p>
SeqID 1478	SA-2476.1	Contig64 (2858-3013 m)	75	<p>Identities = 33/48 (71%), Positives = 39/46 (84%) pir H70958 probable uncl phosphoribosyltransferase (EC 2.4.2.9) - Mycobacterium tuberculosis (strain H37RV) emb CA802640.1 (Z81011) pyrR [Mycobacterium tuberculosis] Length = 193</p>
SeqID 1479	SA-2477.1	Contig64 (1739-2809 m)	72	<p>Identities = 188/352 (53%), Positives = 265/352 (74%) emb CA888872.1 (AJ132624) carbamoyl phosphate synthetase small subunit [Lactococcus lactis] Length = 357</p>
SeqID 1480	SA-2479.1	Contig64 (85-1683 m)	37	<p>Identities = 116/414 (28%), Positives = 204/414 (49%), Gaps = 31/414 (7%) sp P77886 CARB_LACPL CARBAMOYL- PHOSPHATE SYNTHASE PYRIMIDINE-SPECIFIC LARGE CHAIN (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN) emb CAA91005.1 (Z34240) carbamoyl- phosphate synthase [Lactobacillus plantarum] Length = 1058</p>
SeqID 1481	SA-248.1	Contig138 (43569-45029 m)	77	<p>Identities = 309/476 (64%), Positives = 384/476 (79%), Gaps = 2/476 (0%) pir J070008 nicotinate phosphoribosyltransferase homolog yueK - Bacillus subtilis emb CA815163.1 (Z99120) similar to nicotinate phosphoribosyltransferase [Bacillus subtilis] Length = 490</p>
SeqID 1482	SA-2480.2	Contig79 (5026-5787 p)	60	<p>Identities = 125/247 (50%), Positives = 187/247 (75%) pir D69763 ferrichrome ABC transporter (ATP-binding p) homolog ydp - Bacillus subtilis dbj BAA09014.1 (D50453) homologue of iron dicitrate transport ATP-binding protein FecE of E. coli [Bacillus subtilis] emb CAB12190.1 (Z99106) similar to ferrichrome ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 252</p>

SeqID 1483	SA-2482.2	Contig79 (5849-6877 p)	55	Identities = 122/348 (35%), Positives = 201/348 (57%), Gaps = 16/348 (4%) emb CAA06500.1 (AJO05352) lipoprotein [Staphylococcus aureus] Length = 342
SeqID 1484	SA-2483.1	Contig79 (7015-7677 p)	44	Identities = 72/172 (41%), Positives = 108/172 (61%), Gaps = 2/172 (1%) pf C72399 DNA processing chain A - Thermotoga maritima (strain MSB8) gb AAD35341.1 AE001708_9 (AE001708) DNA processing chain A [Thermotoga maritima] Length = 337
SeqID 1485	SA-2486.2	Contig68 (423-1265 m)	64	Identities = 157/281 (55%), Positives = 196/281 (68%), Gaps = 6/281 (2%) gb AAK04366.1 AE006294_5 (AE006294) oxidoreductase [Lactococcus lactis subsp. lactis] Length = 281
SeqID 1486	SA-2488.2	Contig69 (4025-5050 m)	43	Identities = 96/352 (27%), Positives = 164/352 (46%), Gaps = 21/352 (5%) pf C69858 conserved hypothetical protein yknX - Bacillus subtilis emb CAB13308.1 (Z99111) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] gb AAC24909.1 (AF012285) YknX [Bacillus subtilis] Length = 377
SeqID 1487	SA-249.1	Contig138 (45187-46101 m)	74	Identities = 173/302 (57%), Positives = 234/302 (77%) db BAB07290.1 (AP001519) thioredoxin reductase (NADPH) [Bacillus halodurans] Length = 315
SeqID 1488	SA-2480.2	Contig69 (9312-4022 m)	69	Identities = 131/218 (60%), Positives = 169/218 (77%) db BAB06841.1 (AP001517) ABC transporter (ATP-binding protein) [Bacillus halodurans] Length = 227
SeqID 1489	SA-2491.2	Contig69 (2050-3297 m)	57	Identities = 161/419 (38%), Positives = 243/419 (57%), Gaps = 25/419 (5%) sp Q31712 YKNZ_BACSU HYPOTHETICAL 42.1 KDA PROTEIN IN MOAD-FRUR INTERGENIC REGION pf C69858 conserved hypothetical protein yknZ - Bacillus subtilis emb CAB13310.1 (Z99111) similar to hypothetical proteins [Bacillus subtilis] gb AAC24912.1 (AF012285) YknZ [Bacillus subtilis] Length = 397

SeqID 1490	SA-2492.2	Contig105 (19268-21082 p)	72	<p>Identities = 356/604 (58%), Positives = 445/604 (72%), Gaps = 4/604 (0%) spIP39754(GLMS, BACSU GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) pIrljB69633</p> <p>glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) gmsS - <i>Bacillus subtilis</i> gbIAA46422.1 (U21932) L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis] embjCAB11954.1 (Z99104) L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis] embjCAB11971.1 (Z99105) L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis] dbjBAA33071.1 (AB006424) L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDO TRANSFERASE [Bacillus subtilis] Length = 600</p>
SeqID 1491	SA-2493.1	Contig62 (1978-3021 p)	83	<p>Identities = 255/348 (73%), Positives = 298/348 (85%), Gaps = 1/348 (0%) spIP10539IDHAS_STRIMU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE) (ASADH) pIrljA29137 aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - <i>Streptococcus mutans</i> gbIAA26850.1 (J02667) aspartate beta-semialdehyde dehydrogenase (EC 1.2.1.11) [Streptococcus mutans] Length = 357</p>
SeqID 1492	SA-2494.1	Contig62 (640-1494 m)	34	<p>Identities = 71/271 (26%), Positives = 97/271 (35%), Gaps = 5/271 (1%) pIrljS54157 extensin-like protein - cowpea (fragment) Length = 279</p>
SeqID 1493	SA-2495.1	Contig62 (537-1759 p)	42	<p>Identities = 86/373 (23%), Positives = 176/373 (47%), Gaps = 26/373 (6%) gpIAAF-48863.1 (AE003509) CG15040 gene product [Drosophila melanogaster] Length = 1895</p>
SeqID 1494	SA-2497.2	Contig104 (5252-5665 p)	68	<p>Identities = 74/126 (58%), Positives = 101/126 (79%) gbIAAF21893.1 (AF-103794_1 (AF-103794) unknown [Listeria monocytogenes] Length = 131</p>

SeqID 1495	SA-2498.2	Contig104 (5658-5939 p)	47	Identities = 33/78 (42%), Positives = 50/78 (63%) pri[C69864 hypothetical protein ykA - Bacillus subtilis embjCAB1337.1] (Z99111) ykA [Bacillus subtilis] gb AAC2438.1 (AF012285) unknown [Bacillus subtilis] Length = 88
SeqID 1496	SA-2499.3	Contig104 (5929-6693 p)	56	Identities = 121/252 (48%), Positives = 171/252 (67%), Gaps = 4/252 (1%) gb AAK04646.1 AE006288.9 (AE006288) conserved hypothetical protein [Lactococcus lactis subsp. lactis] Length = 255
SeqID 1497	SA-25.1	Contig137 (15915-20645 p)	11	Identities = 117/377 (31%), Positives = 182/377 (48%), Gaps = 73/377 (19%) ref NP_053235.1 pX02-81 [Bacillus anthracis] gb AAF13685.1 AF18935_83 (AF18935) pX02-81 [Bacillus anthracis] Length = 589
SeqID 1498	SA-250.1	Contig138 (46170-46418 m)	No Hits found	
SeqID 1499	SA-2500.3	Contig104 (6761-8071 p)	48	Identities = 139/466 (29%), Positives = 213/466 (44%), Gaps = 36/466 (7%) pri A82193 Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94657.1 (AE004228) Sun/nucleolar protein family protein [Vibrio cholerae] Length = 503
SeqID 1500	SA-2501.2	Contig63 (2458-3795 m)	47	Identities = 111/428 (25%), Positives = 210/428 (48%), Gaps = 39/428 (9%) pri B69855 amino acid permease homolog ykA - Bacillus subtilis embjCAA05566.1 (AJ002871) ykA [Bacillus subtilis] embjCAB13143.1 (Z99110) similar to amino acid permease [Bacillus subtilis] Length = 438
SeqID 1501	SA-2502.2	Contig63 (1737-2285 m)	71	Identities = 111/168 (66%), Positives = 136/168 (80%), Gaps = 3/168 (1%) gb AAK05247.1 AE006347_5 (AE006347) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 169

SeqID 1502	SA-2503.1	Contig63 (432-1601 m)	56	<p>Identities = 130/381 (34%), Positives = 221/381 (57%), Gaps = 4/381 (1%) sp Q08432 PATB_BACSU PUTA.TIVE AMINOTRANSFERASE B. prii S32934.aminotransferase patB - Bacillus subtilis emb CAB07910.1 (Z39363) aminotransferase [Bacillus subtilis] emb CAB07924.1 (U63302) PatB [Bacillus subtilis] gb AAB61979.1 (U63302) PatB [Bacillus subtilis] emb CAB15133.1 (Z99120) aminotransferase [Bacillus subtilis] Length = 387</p>
SeqID 1503	SA-2504.1	Contig63 (179-322 m)	84	<p>Identities = 44/47 (93%), Positives = 45/47 (95%) gb AAAY1926.1 (L08445) uracil phosphoribosyltransferase [Streptococcus salivarius] Length = 128</p>
SeqID 1504	SA-2505.1	Contig63 (3-182 m)	90	<p>Identities = 49/60 (81%), Positives = 54/60 (89%) gb AAAY1926.1 (L08445) uracil phosphoribosyltransferase [Streptococcus salivarius] Length = 128</p>
SeqID 1505	SA-2507.2	Contig132 (1877-2116 p)	57	<p>Identities = 27/75 (36%), Positives = 52/75 (69%) ref NP_050766.1 acyl carrier protein [Guillardia theta] sp P29189 ACP_GUITH.ACYL CARRIER PROTEIN. gb AAC35700.1 (AF041468) acyl carrier protein [Guillardia theta] Length = 81</p>
SeqID 1506	SA-2508.1	Contig132 (874-1866 p)	70	<p>Identities = 174/330 (52%), Positives = 239/330 (71%), Gaps = 2/330 (0%) sp P71018 PLSX_BACSU FATTY ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX prii H69679 involved in fatty acid phospholipid synthesis plxX - Bacillus subtilis emb CAA74248.1 (Y13937) putative PlxX protein [Bacillus subtilis] emb CAB13462.1 (Z99112) alternate gene name: ylpD [Bacillus subtilis] Length = 333</p>
SeqID 1507	SA-2509.1	Contig132 (2-796 p)	26	<p>Identities = 47/154 (30%), Positives = 69/154 (44%), Gaps = 12/154 (7%) prii T34651 probable transmembrane protein - Streptomyces coelicolor emb CAA22372.1 (A1034446) putative transmembrane protein [Streptomyces coelicolor A3(2)] Length = 307</p>

SeqID 1508	SA-251.1	Contig138 (46516-47259 m)	69	<p>Identities = 121/247 (48%), Positives = 176/247 (70%) sp Q34900 YTMN_BACSU PROBABLE AMINO-ACID ABC TRANSPORTER ATP-BINDING PROTEIN YTMN_prl F69641 histidine transport protein hisP - Bacillus subtilis_gblAAC00329.1 (AF008220) putative amino acid transporter [Bacillus subtilis] emb CAB14894.1 (Z99118) histidine transport protein (ATP- binding protein) [Bacillus subtilis] emb CAB14912.1 (Z99119) histidine transport protein (ATP-binding protein) [Bacillus subtilis] Length = 259</p>
SeqID 1509	SA-2510.2	Contig135 (76527-78527 p)	79	<p>Identities = 430/659 (65%), Positives = 537/659 (81%), Gaps = 4/659 (0%) gb AAK04722.1 AE006295.3 (AE006295) potassium uptake protein [Lactococcus lactis subsp. lactis] Length = 671</p>
SeqID 1510	SA-2511.1	Contig135 (75631-76392 p)	67	<p>Identities = 142/248 (57%), Positives = 179/248 (71%), Gaps = 1/248 (0%) sp P45200 YDFG_HAEIN HYPOTHETICAL OXIDOREDUCTASE H11430_prl H64122_ydG protein - Haemophilus influenzae (strain Rd KW20)_gblAAC23077.1 (U32822) short chain dehydrogenase/reductase [Haemophilus influenzae Rd] Length = 252</p>
SeqID 1511	SA-2512.2	Contig135 (74577-75569 p)	70	<p>Identities = 208/323 (64%), Positives = 249/323 (76%), Gaps = 1/323 (0%) gb AAK05757.1 AE006396.8 (AE006396) phosphate acetyltransferase (EC 2.3.1.8) [Lactococcus lactis] Length = 326</p>
SeqID 1512	SA-2513.2	Contig138 (26798-27427 m)	72	<p>Identities = 122/204 (59%), Positives = 156/204 (75%) pir J669878 guanylate kinase homolog yloD - Bacillus subtilis emb CAA74271.1 (Y13937) putative Gmk protein [Bacillus subtilis] emb CAB13441.1 (Z99112) similar to guanylate kinase [Bacillus subtilis] Length = 244</p>

SeqID 1513	SA-2514.1	Contig138 (27594-28298 m)	33	<p>Identities = 48/183 (25%), Positives = 81/183 (44%), Gaps = 11/183 (6%) pirJF69065 hypothetical protein MTH1490 - Methanobacterium thermoautotrophicum (strain Delta H) gb AAB85665.1 (AE000909) unknown [Methanobacterium thermoautotrophicum] Length = 188</p>
SeqID 1514	SA-2515.2	Contig138 (28348-28938 m)	78	<p>Identities = 121/199 (60%), Positives = 157/199 (78%), Gaps = 3/199 (1%) emb CAB54585.1 (AJ006400) response regulator [Streptococcus pneumoniae] Length = 199</p>
SeqID 1515	SA-2516.2	Contig68 (1532-2206 p)	58	<p>Identities = 109/221 (49%), Positives = 150/221 (67%), Gaps = 9/221 (4%) gb AAK02817.1 (AE006110) unknown [Pasteurella multocida] Length = 220</p>
SeqID 1516	SA-2517.1	Contig68 (2294-2886 p)	62	<p>Identities = 59/131 (45%), Positives = 98/131 (65%), Gaps = 2/131 (1%) sp P44638 GLUL_HAEN LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOXETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) pir I6417 lactoylglutathione lyase (EC 4.4.1.5) - Haemophilus influenzae gb AAC21986.1 (U32717) lactoylglutathione lyase (gloA) [Haemophilus influenzae] Rd Length = 135</p>
SeqID 1517	SA-2518.1	Contig68 (2815-3741 p)	64	<p>Identities = 139/308 (45%), Positives = 202/308 (65%), Gaps = 3/308 (0%) sp Q45539 CSBB_BACSU CSBB PROTEIN pir JC5173 stress response protein csbB - Bacillus subtilis gb AAB38423.1 (L77099) 44 identity over 302 residues with hypothetical protein from Synechocystis sp. accession D84006 CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtilis] emb CAB12688.1 (Z59108) stress response protein [Bacillus subtilis] db JBA24480.1 (D86082) yfHn [Bacillus subtilis] Length = 329</p>

SeqID 1518	SA-2519.1	Contig68 (3870-4025 p)	58	<p>identities = 30/46 (65%), Positives = 37/46 (80%)</p> <p>- spIP45495YEV_LACDL HYPOTHETICAL TRANSPORT PROTEIN IN PEV3 REGION (ORF2) pif[S57903 probable amino acid permease - Lactobacillus delbrueckii (fragment)]</p> <p>- embICAA83253.1 (Z31377) potential amino acid permease [Lactobacillus delbrueckii] Length = 175</p>
SeqID 1519	SA-252.1	Contig138 (47259-48047 m)	50	<p>identities = 90/224 (40%), Positives = 137/224 (60%) Gaps = 10/224 (4%) spIP54953YXEN_BACSU PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN YXEN pif[H70075 amino acid ABC transporter (permease) homolog yxN - Bacillus subtilis dbj[BAA08330.1] (D45912) homologous to Gln transport system permease proteins [Bacillus subtilis] embICAB15985.1 (Z99124) similar to amino acid ABC transporter (permease) [Bacillus subtilis] Length = 224</p>
SeqID 1520	SA-2520.2	Contig115 (8665-8494 p)	13	<p>identities = 43/206 (20%), Positives = 91/206 (43%), Gaps = 12/206 (5%) pif[H64496 hypothetical protein MJ1577 - Methanococcus jannaschii gb AAB89606.1 (U67598) M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii] Length = 598</p>
SeqID 1521	SA-2522.2	Contig69 (1649-1921 m)	78	<p>identities = 81/90 (90%), Positives = 85/90 (94%) gb AAK05687.1 AE006387.10 (AE006387) 30S ribosomal protein S16 [Lactococcus lactis subsp. lactis] Length = 90</p>
SeqID 1522	SA-2523.2	Contig69 (1397-1639 m)	75	<p>identities = 39/75 (52%), Positives = 63/75 (84%) gb AAK05686.1 AE006387.9 (AE006387) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 79</p>
SeqID 1523	SA-2524.1	Contig69 (3-1265 m)	46	<p>identities = 115/437 (26%), Positives = 201/437 (45%), Gaps = 26/437 (5%) gb AAC97147.1 (U49397) Nra [Streptococcus pyogenes] Length = 511</p>

SeqID 1524	SA-2525.1	Contig60 (87-1895 m)	89	<p>Identities = 483/603 (78%), Positives = 540/603 (88%) sp P37949 LEPA_BACSU GTP-BINDING PROTEIN LEPA pir JG6949 GTP-binding protein lepA - Bacillus subtilis emb CAA62842.1 (X91655) lepA [Bacillus subtilis] db JBA112460.1 (D84432) YpeC [Bacillus subtilis] emb CAB14493.1 (Z99117) GTP-binding protein [Bacillus subtilis] Length = 612</p>
SeqID 1525	SA-2526.1	Contig61 (969-2801 m)	29	<p>Identities = 95/382 (24%), Positives = 180/382 (46%), Gaps = 26/382 (6%) db BAB06137.1 (AP001515) DNA polymerase III (alpha subunit) [Bacillus halodurans] Length = 1433</p>
SeqID 1526	SA-2528.1	Contig61 (82-843 p)	80	<p>Identities = 217/232 (93%), Positives = 226/232 (96%) emb CAB90834.1 (AJ250337) putative transposase [Streptococcus dysgalactiae] Length = 259</p>
SeqID 1527	SA-253.1	Contig138 (48157-48969 m)	49	<p>Identities = 80/273 (29%), Positives = 136/273 (49%), Gaps = 27/273 (9%) emb CAA68052.1 (X99716) collagen binding protein [Lactobacillus reuteri] Length = 263</p>
SeqID 1528	SA-2531.2	Contig136 (1-1152 p)	26	<p>Identities = 51/228 (22%), Positives = 100/228 (43%), Gaps = 36/228 (15%) emb CAB39029.1 (AL034559) hypothetical protein, PFC0905c [Plasmodium falciparum] Length = 3085</p>
SeqID 1529	SA-2532.1	Contig137 (4715-4921 p)	No Hits found	<p>Identities = 18/34 (52%), Positives = 26/34 (75%) gb AAC98435.1 (L29324) unknown [Streptococcus pneumoniae] Length = 121</p>
SeqID 1530	SA-2533.1	Contig139 (122098-122286 p)	41	<p>Identities = 32/53 (60%), Positives = 39/53 (73%) gb AAC98435.1 (L29324) unknown [Streptococcus pneumoniae] Length = 121</p>
SeqID 1531	SA-2534.1	Contig139 (122022-122204 p)	63	<p>Identities = 85/91 (93%), Positives = 88/91 (96%) gb AAD40808.1 (L36946_1) (L36946) histone-like DNA-binding protein [Streptococcus pyogenes] Length = 91</p>
SeqID 1532	SA-2535.1	Contig139 (51975-52250 p)	88	<p>Identities = 85/91 (93%), Positives = 88/91 (96%) gb AAD40808.1 (L36946_1) (L36946) histone-like DNA-binding protein [Streptococcus pyogenes] Length = 91</p>

SeqID 1533	SA-2536.1	Contig139 (46592-46564 p)	58	<p>Identities = 126/258 (48%), Positives = 175/258 (66%), Gaps = 2/258 (0%) sp O66126 SPA_MICLJ GERANYLTRANSFERASE (FARNESYL-DIPHOSPHATE SYNTHASE) (FPP SYNTHASE) dbj BAA23265.1 (AB003187) farnesyl diphosphate synthase [Micrococcus luteus] Length = 291</p> <p>Identities = 22/77 (28%), Positives = 41/77 (52%), Gaps = 4/77 (5%) pir G99668 hypothetical protein ykuJ - Bacillus subtilis emb CAA10873.1 (AJ222887) YkuJ protein [Bacillus subtilis] emb CAB13283.1 (Z99111) ykuJ [Bacillus subtilis] Length = 79</p>
SeqID 1534	SA-2537.1	Contig139 (38436-38686 p)	39	
SeqID 1535	SA-2539.1	Contig131 (7218-7448 p)	No Hits found	
SeqID 1536	SA-2540.2	Contig138 (95981-96244 p)	No Hits found	
SeqID 1537	SA-2542.1	Contig133 (27162-27320 m)	No Hits found	
SeqID 1538	SA-2543.1	Contig132 (25696-25839 m)	No Hits found	
SeqID 1539	SA-2545.1	Contig127 (19934-20134 p)	No Hits found	
SeqID 1540	SA-2547.1	Contig135 (30113-30319 p)	No Hits found	
SeqID 1541	SA-2548.1	Contig135 (29845-30003 p)	No Hits found	
SeqID 1542	SA-2549.1	Contig135 (27910-28200 m)	No Hits found	
SeqID 1543	SA-2551.1	Contig138 (49107-50450 m)	67	<p>Identities = 215/439 (48%), Positives = 311/439 (69%), Gaps = 5/439 (1%) sp P54475 YQFR_BACSU PROBABLE RNA HELICASE IN COCA-SODA INTERGENIC REGION pir D69954 ATP-dependent RNA helicase homolog yqfR - Bacillus subtilis dbj BAA12495.1 (D84432) YqfR [Bacillus subtilis] emb CAB14444.1 (Z99116) similar to ATP-dependent RNA helicase [Bacillus subtilis] Length = 438</p>
SeqID 1544	SA-2551.2	Contig123 (36802-36984 m)	No Hits found	
SeqID 1545	SA-2554.1	Contig116 (30459-30827 m)	No Hits found	
SeqID 1546	SA-2555.1	Contig116 (60-398 m)	No Hits found	
SeqID 1547	SA-2556.1	Contig134 (78113-78304 p)	45	<p>Identities = 24/75 (32%), Positives = 46/75 (61%) sp O32233 BECG_BACSU PROBABLE PROTEIN-EXPORT MEMBRANE PROTEIN SECQ pir A70028 hypothetical protein yvaI - Bacillus subtilis emb CAB15368.1 (Z99121) yvaI [Bacillus subtilis] Length = 76</p>

SeqID 1548	SA-2557.1	Contig134 (69629-69823 m)	No Hits found	
SeqID 1549	SA-2558.1	Contig 134 (69418-69646 p)	No Hits found	
SeqID 1550	SA-2559.1	Contig 139 (132392-132580 m)	61	Identities = 36/46 (78%), Positives = 39/46 (84%) gb AAC38687.1 (AF030361) transposase [Streptococcus pneumoniae] gb AAC38702.1 (AF030364) transposase [Streptococcus pneumoniae] Length = 418
SeqID 1551	SA-2561.1	Contig 138 (50548-51558 m)	79	Identities = 221/336 (65%), Positives = 271/336 (79%), Gaps = 11/336 (3%) sp Q3ZHA5 MRAY_STRPN PHOSPHO-N-ACETYL MURAMYL-PENTAPEPTIDE-TRANSFERASE (UDP-MURNAAC-PENTAPEPTIDE PHOSPHOTRANSFERASE) gb AAC39457.1 (AF068903) undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase [Streptococcus pneumoniae] Length = 326
SeqID 1552	SA-2560.1	Contig 139 (133610-133768 p)	37	Identities = 23/35 (65%), Positives = 28/35 (79%) gb AAG38044.1 (AF295925_9) (AF295925) Orf28 [Streptococcus pneumoniae] Length = 371
SeqID 1553	SA-2561.1	Contig 139 (154195-154389 p)	No Hits found	
SeqID 1554	SA-2562.1	Contig 125 (24635-24835 p)	No Hits found	
SeqID 1555	SA-2564.1	Contig 112 (19746-19868 p)	47	Identities = 22/40 (55%), Positives = 27/40 (67%), Gaps = 1/40 (2%) db JBA04083.1 (AP01508) transcriptional regulator [Bacillus halodurans] Length = 66
SeqID 1556	SA-2565.1	Contig 112 (19523-19741 p)	No Hits found	
SeqID 1557	SA-2566.1	Contig 111 (15881-16075 p)	No Hits found	
SeqID 1558	SA-2567.1	Contig 111 (13119-13307 p)	No Hits found	
SeqID 1559	SA-257.1	Contig 138 (51560-53821 m)	73	Identities = 405/741 (54%), Positives = 556/741 (74%), Gaps = 107/741 (1%) gb AAAF17266.1 (AF210736_1) (AF210736) penicillin-binding protein 2A [Streptococcus pneumoniae] Length = 750
SeqID 1560	SA-2571.1	Contig 106 (21708-21950 p)	41	Identities = 32/83 (38%), Positives = 46/83 (54%) sp P55661 Y4TG_RHISN PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN Y4TG gb AAB91860.1 (AE000098) Y4G [Rhizobium sp. NGR234] Length = 231

SeqID 1561	SA-2572.1	Contig106 (21244-21573 p)	79	<p>Identities = 79/110 (71%), Positives = 91/110 (81%), Gaps = 1/110 (0%) sp P16680 PHNA_ECOLI PHNA PROTEIN pir J335718 alkylphosphonate uptake protein phnA [imported] - Escherichia coli gb AAA24337.1 (J05260) phnA protein [Escherichia coli] gb AAAG7007.1 (U14003) phnA gene product [Escherichia coli] gb AAC77069.1 (AE000483) orf, hypothetical protein [Escherichia coli K12] Length = 111</p>
SeqID 1562	SA-2574.1	Contig135 (83485-83640 p)	No Hits found	
SeqID 1563	SA-2575.1	Contig125 (16287-16571 m)	No Hits found	
SeqID 1564	SA-2576.2	Contig134 (50208-50895 p)	85	<p>Identities = 190/228 (83%), Positives = 204/228 (89%) gb AAK06098.1 AE006430.3 (AE006430) 50S ribosomal protein L1 [Lactococcus lactis subsp. lactis] Length = 229</p>
SeqID 1565	SA-2577.1	Contig135 (69410-69703 m)	42	<p>Identities = 35/72 (48%), Positives = 42/72 (57%) pir J59084 hypothetical protein 28.1 - red alga (Chondrus crispus) mitochondrion emb CAA87600.1 (Z47547) unique orf (Chondrus crispus) Length = 79</p>
SeqID 1566	SA-258.1	Contig138 (53822-54148 m)	50	<p>Identities = 44/89 (44%), Positives = 71/89 (71%) emb CA801928.1 (Z79691) FlsL (Streptococcus pneumoniae) gb AAC85455.1 (AF068903) Y1D (Streptococcus pneumoniae) Length = 105</p>
SeqID 1567	SA-2582.1	Contig89 (20-172 m)	53	<p>Identities = 27/42 (64%), Positives = 35/42 (83%) gb AAD09220.1 (U74080) unknown [Streptococcus gordonii] Length = 50</p>
SeqID 1568	SA-2583.1	Contig133 (74342-74776 m)	62	<p>Identities = 51/145 (35%), Positives = 91/145 (62%), Gaps = 3/145 (2%) pir JH70091 hypothetical protein yjdJ - Bacillus subtilis dbj BAA11272.1 (D78193) yjdJ [Bacillus subtilis] emb CAB16051.1 (Z99124) yjdJ [Bacillus subtilis] Length = 240</p>
SeqID 1569	SA-2584.1	Contig133 (74719-75069 m)	60	<p>Identities = 47/106 (44%), Positives = 71/106 (66%) pir JH70091 hypothetical protein yjdJ - Bacillus subtilis dbj BAA11272.1 (D78193) yjdJ [Bacillus subtilis] emb CAB16051.1 (Z99124) yjdJ [Bacillus subtilis] Length = 240</p>

SeqID 1570	SA-2586.1	Contig80 (961-1092 m)	No Hits found	
SeqID 1571	SA-2588.2	Contig95 (1977-2162 p)	No Hits found	
SeqID 1572	SA-259.1	Contig138 (54163-55110 m)	84	Identities = 265/316 (83%), Positives = 268/316 (90%) gb/AAC55454.1 (AF068903) Y1C (Streptococcus pneumoniae) Length = 316
SeqID 1573	SA-2593.1	Contig65 (2145-2339 p)	No Hits found	
SeqID 1574	SA-2594.1	Contig62 (165-344 p)	No Hits found	
SeqID 1575	SA-2596.1	Contig91 (939-1604 p)	75	Identities = 117/217 (53%), Positives = 168/217 (78%) sp P42399 YCKA_BACSU PROBABLE AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN YCKA pir C89780 amino acid ABC transporter (permease) homolog yckA - Bacillus subtilis dbj BA006425.1 (D30762) homolog of glutamine permease of H. influenzae [Bacillus subtilis] dbj BA008971.1 (D50453) homolog of glutamine permease of H. influenzae [Bacillus subtilis] emb CAB12131.1 (Z99105) similar to amino acid ABC transporter (permease) [Bacillus subtilis] Length = 226
SeqID 1576	SA-2597.1	Contig91 (58-915 p)	62	Identities = 127/276 (46%), Positives = 183/276 (66%), Gaps = 12/276 (4%) sp P42400 YCKB_BACSU PROBABLE ABC TRANSPORTER EXTRACELLULAR BINDING PROTEIN YCKB PRECURSOR (ORF2) pir D89760 amino acid ABC transporter (binding protein) homolog yckB - Bacillus subtilis emb CAB12132.1 (Z99105) similar to amino acid ABC transporter (binding protein) [Bacillus subtilis] Length = 287

SeqID 1577	SA-2598.1	Contig104 (8256-8870 p)	67	<p>Identities = 109/218 (50%), Positives = 146/218 (66%), Gaps = 15/218 (6%) spIP46338YQGG_BACSU PROBABLE ABC TRANSPORTER BINDING PROTEIN YQGG PRECURSOR</p> <p>prfJ469956 phosphate ABC transporter (binding protein) homolog yqgG - Bacillus subtilis dbjBAA09581.1 (D58414) ORF108 [Bacillus subtilis] dbjBAA12510.1 (D84432) YqgG [Bacillus subtilis] embICAB14423.1 (Z99116) alternate gene name: yzmB-similar to phosphate ABC transporter (binding protein) [Bacillus subtilis] Length = 300</p>
SeqID 1578	SA-2599.1	Contig135 (79561-80901 p)	54	<p>Identities = 153/445 (34%), Positives = 250/445 (55%), Gaps = 11/445 (2%) embICAB61253.1 (AJ250422) ORFC [Onococcus cent]</p>
SeqID 1579	SA-26.1	Contig137 (15639-15896 p)	No Hits found	Identities = 303/417 (72%), Positives = 356/417 (84%), Gaps = 1/417 (0%) spIP96489PROA_STRTX GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE) embICAA63148.1 (X92418) gamma-glutamyl phosphate reductase [Streptococcus thermophilus] Length = 416
SeqID 1581	SA-2600.1	Contig110 (3263-3451 m)	No Hits found	Identities = 63/115 (54%), Positives = 83/115 (71%), Gaps = 1/115 (0%) spIO35048YQCD_BACSU HYPOTHETICAL 36.4 KDA PROTEIN IN CSAA-DES INTERGENIC REGION
SeqID 1582	SA-2602.1	Contig110 (3909-4259 p)	70	<p>prfJA69901 immunity to bacteriotoxins homolog yocD - Bacillus subtilis gbIAAB4435.1 (AF027868) YocD [Bacillus subtilis] embICAB13809.1 (Z99114) similar to immunity to bacteriotoxins [Bacillus subtilis] Length = 325</p>
SeqID 1583	SA-2603.1	Contig111 (11745-11921 p)	No Hits found	

SeqID 1584	SA-2604.1	Contig116 (30551-30826 m)	34	Identities = 30/51 (58%), Positives = 32/51 (61%) pir F71245 hypothetical protein PHS004 - Pyrococcus horikoshii dbj BA229293.1 (AP000001) 58aa long hypothetical protein [Pyrococcus horikoshii] Length = 58
SeqID 1585	SA-2605.1	Contig116 (7428-7886 p)	80	Identities = 122/123 (99%), Positives = 123/123 (99%) gb AAG09868.1 (AF248037_3) (AF248037) caton efflux system protein [Streptococcus agalactiae] Length = 287
SeqID 1586	SA-2606.1	Contig138 (96371-96607 p)	No Hits found	
SeqID 1587	SA-2608.1	Contig139 (135435-135725 m)	No Hits found	
SeqID 1588	SA-2609.1	Contig139 (132781-132939 m)	No Hits found	
SeqID 1589	SA-2611.1	Contig138 (56456-57259 m)	86	Identities = 200/285 (75%), Positives = 235/265 (88%) sp P96489 PROB_STRTTR GLUTAMATE 5-KINASE (GAMMA- GLUTAMYL KINASE) (GK) emb CAA63147.1 (X92418) gamma- glutamyl kinase [Streptococcus thermophilus] Length = 267
SeqID 1590	SA-2610.1	Contig139 (132368-132517 p)	60	Identities = 19/36 (52%), Positives = 30/36 (82%) pir T50042 hypothetical protein lasA [imported] - Streptococcus pneumoniae emb CAA59773.1 (X85787) lasA [Streptococcus pneumoniae] Length = 359
SeqID 1591	SA-2612.1	Contig139 (93559-93832 p)	No Hits found	
SeqID 1592	SA-2615.1	Contig139 (52350-52646 m)	No Hits found	
SeqID 1593	SA-2618.1	Contig139 (18458-18772 m)	35	Identities = 30/71 (42%), Positives = 37/71 (51%), Gaps = 1/71 (1%) pir G72514 hypothetical protein APE2092 - Aeropyrum pernix (strain K1) dbj BA81103.1 (AP000063) 101aa long hypothetical protein [Aeropyrum pernix] Length = 101
SeqID 1594	SA-2620.1	Contig138 (81930-82160 m)	No Hits found	

SeqID 1595	SA-263.1	Contig138 (57400-58785 p)	57	<p>Identities = 174/447 (38%), Positives = 267/447 (59%), Gaps = 10/447 (2%) p[1]T747097 hypothetical protein N17C [Imported] - <i>Bacillus subtilis</i> dbj BA006652.1 (D31856) hypothetical protein [Bacillus subtilis] dbj BA006256.1 (D29885) hypothetical 64.7-kDa protein [Bacillus subtilis] emb CAB15963.1 (Z99124) phosphotransferase system (PTS) beta-glucoside-specific enzyme IIAABC component [Bacillus subtilis] Length = 609</p>
SeqID 1596	SA-2632.1	Contig137 (26599-29556 p)	No Hits found	
SeqID 1597	SA-2635.1	Contig136 (45825-45980 p)	No Hits found	
SeqID 1598	SA-264.1	Contig135 (58993-60997 m)	No Hits found	
SeqID 1599	SA-2642.1	Contig135 (29120-29389 m)	No Hits found	
SeqID 1600	SA-2646.1	Contig134 (73407-73562 m)	No Hits found	
SeqID 1601	SA-2649.1	Contig133 (70298-70522 p)	No Hits found	
SeqID 1602	SA-265.1	Contig138 (60601-61335 m)	65	<p>Identities = 95/243 (39%), Positives = 164/243 (67%), Gaps = 2/243 (0%) p[1]H75077 abc transporter, ATP-binding protein PAB1696 - <i>Pyrococcus abyssi</i> (strain Orsay) emb CAB49925.1 (AJ248286) ABC transporter, ATP-binding protein [Pyrococcus abyssi] Length = 253</p>
SeqID 1603	SA-2650.1	Contig133 (68864-69245 p)	No Hits found	
SeqID 1604	SA-2651.1	Contig133 (60101-60367 p)	No Hits found	
SeqID 1605	SA-2654.1	Contig132 (48100-48423 m)	34	<p>Identities = 34/73 (46%), Positives = 37/73 (50%), Gaps = 3/73 (4%) p[1]E71186 hypothetical protein PH1769 - <i>Pyrococcus horikoshii</i> dbj BA330884.1 (AP000007) 100aa long hypothetical protein [Pyrococcus horikoshii] Length = 100</p>
SeqID 1606	SA-2655.1	Contig132 (48095-48463 p)	93	<p>Identities = 116/122 (95%), Positives = 120/122 (98%) sp Q9WVZ2 RL14_STRPN 50S RIBOSOMAL PROTEIN L14 gb AAD33266.1 AF126059.7 (AF126059) Rpl14 [Streptococcus pneumoniae] gb AAD33275.1 (AF126060) Rpl14 [Streptococcus pneumoniae] gb AAD33284.1 (AF126061) Rpl14 [Streptococcus pneumoniae] Length = 122</p>

SeqID 1607	SA-2657.1	Contig132 (25921-26223 p)	No Hits found	77	Identities = 403661 (60%), Positives = 520661 (77%), Gaps = 8661 (1%) dbj BA06071.1 (AP001515) transketolase [Bacillus halodurans] Length = 666
SeqID 1608	SA-266.1	Contig138 (61355-61660 m)	No Hits found		
SeqID 1609	SA-2664.1	Contig131 (2878-3129 m)	No Hits found		
SeqID 1610	SA-2666.1	Contig130 (70425-70709 p)	No Hits found		
SeqID 1611	SA-2668.1	Contig130 (38146-38331 m)	No Hits found		
SeqID 1612	SA-2669.1	Contig130 (27964-28215 p)	No Hits found	53	Identities = 4083 (48%), Positives = 6483 (76%) pir A69742 conserved hypothetical protein yzaA - Bacillus subtilis emb CAB11811.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 99
SeqID 1613	SA-267.1	Contig138 (61873-63858 m)	No Hits found		
SeqID 1614	SA-2670.1	Contig129 (57906-58148 m)	No Hits found		
SeqID 1615	SA-2672.1	Contig129 (47951-48133 p)	No Hits found		
SeqID 1616	SA-2673.1	Contig129 (21896-22162 p)	No Hits found		
SeqID 1617	SA-268.1	Contig138 (63983-65413 m)	18	18	Identities = 48191 (25%), Positives = 88191 (45%), Gaps = 9191 (4%) emb CAB65412.1 (AJ243530) putative Mga-like regulatory protein [Streptococcus dysgalactiae subsp. dysgalactiae] Length = 487
SeqID 1618	SA-2681.1	Contig126 (41736-42008 p)	No Hits found		
SeqID 1619	SA-2683.1	Contig126 (33663-34071 p)	No Hits found		
SeqID 1620	SA-2687.1	Contig125 (36866-37171 m)	No Hits found		
SeqID 1621	SA-2689.1	Contig124 (23609-23926 p)	33		
SeqID 1622	SA-269.1	Contig138 (65404-66741 m)	44	44	Identities = 105423 (24%), Positives = 198423 (45%), Gaps = 15423 (3%) sp P37061 NAOX_ENTFA NADH OXIDASE (NOXASE) pir S26965 NADH oxidase - Enterococcus faecalis emb CAA48728.1 (X68847) NADH oxidase [Enterococcus faecalis] Length = 446
SeqID 1623	SA-2690.1	Contig123 (39402-39596 p)	No Hits found		

SeqID 1624	SA-2691.1	Contig123 (39313-39621 p)	36	<p>Identities = 21/61 (34%), Positives = 38/61 (61%), Gaps = 1/61 (1%) ref NP_075759.1 Orf18 [bacteriophage bIL310] gb AAK04132.1 AE006242_11 (AE006242) prophage ps1 protein 10 [Lactococcus lactis subsp. lactis] gb AAK08422.1 AF323671_18 (AF323671) Orf18 [bacteriophage bIL310] Length = 93</p>
SeqID 1625	SA-2696.1	Contig122 (25328-25630 m)	34	<p>Identities = 22/56 (39%), Positives = 35/56 (62%), Gaps = 4/56 (7%) sp P36471 GBF_DICDI G-BOX BINDING FACTOR (GBF) pir JAS3185 G-box-binding factor - slime mold (Dictyostelium discoideum) gb AAA21021.1 (L29075) G-box binding factor [Dictyostelium discoideum] Length = 708</p>
SeqID 1626	SA-2701.1	Contig138 (66829-67542 m)	81	<p>Identities = 150/230 (65%), Positives = 194/230 (84%), Gaps = 1/230 (0%) sp P52281 GLPF_STRPN GLYCEROL UPTAKE FACILITATOR PROTEIN pir S67937 glycerol uptake facilitator GlpF - Streptococcus pneumoniae (strain P13) gb AAA91618.1 (U12567) glycerol uptake facilitator [Streptococcus pneumoniae] Length = 233</p>
SeqID 1627	SA-2703.1	Contig119 (308-1129 m)	50	<p>Identities = 94/304 (30%), Positives = 152/304 (49%), Gaps = 32/304 (10%) gb AAK04228.1 AE006251_4 (AE006251) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 304</p>
SeqID 1628	SA-2705.1	Contig118 (27339-27527 p)	No Hits found	<p>Identities = 52/66 (78%), Positives = 60/66 (90%) gb AAK05941.1 AE006414_7 (AE006414) 50S ribosomal protein L35 [Lactococcus lactis subsp. lactis] Length = 66</p>
SeqID 1629	SA-2707.1	Contig118 (17969-18169 p)	80	<p>Identities = 112/169 (66%), Positives = 134/169 (79%) sp O53084 f3_LUSMO TRANSLATION INITIATION FACTOR IF- 3 emb CACAG6820.1 (Y07640) translation initiation factor, IF3 [<i>Listeria monocytogenes</i>] Length = 171</p>
SeqID 1630	SA-2709.1	Contig118 (17399-17929 p)	74	<p>Identities = 464/608 (76%), Positives = 539/608 (88%) gb AAC34740.1 (U94770) alpha-glycerophosphate oxidase [Streptococcus pneumoniae] Length = 608</p>
SeqID 1631	SA-271.1	Contig138 (67539-69368 m)	87	

SeqID 1632	SA-2710.1	Contig118 (16555-17238 p)	73	Identities = 139/223 (62%), Positives = 171/223 (76%), Gaps = 3/223 (1%) gb AAK05801.1 AE006401.2 cytidine monophosphate kinase (EC 2.7.4.14) [Lactococcus subsp. lactis] Length = 220
SeqID 1633	SA-2711.1	Contig118 (16244-16408 m)	No Hits found	Identities = 46/167 (27%), Positives = 82/167 (48%), Gaps = 15/167 (8%) gb AAK05013.1 AE006326.2 telohic acid ABC transporter ATP binding protein [Lactococcus lactis subsp. lactis] Length = 466
SeqID 1634	SA-2712.1	Contig118 (16020-16544 p)	42	
SeqID 1635	SA-2715.1	Contig117 (11081-11336 p)	No Hits found	
SeqID 1636	SA-2718.1	Contig116 (21405-21707 p)	No Hits found	
SeqID 1637	SA-2719.1	Contig116 (19624-19911 p)	No Hits found	
SeqID 1638	SA-272.1	Contig138 (69381-70889 m)	85	Identities = 383/501 (76%), Positives = 442/501 (87%), Gaps = 1/501 (0%) sp Q34154 GLPK_ENTFA_GLYCEROL KINASE (ATP-GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) gb AA66986.1 (U94356) glycerol kinase [Enterococcus faecalis] Length = 501
SeqID 1639	SA-2722.1	Contig115 (26094-26351 m)	45	Identities = 36/58 (62%), Positives = 39/58 (67%) gb AAG12204.1 AF287482.5 (AF287482) Orf122 [Chlorobium tepidum] Length = 121
SeqID 1640	SA-2726.1	Contig113 (25585-25693 p)	No Hits found	
SeqID 1641	SA-273.1	Contig138 (71003-71266 m)	43	Identities = 36/79 (45%), Positives = 46/79 (60%), Gaps = 1/79 (1%) pir J083401 hypothetical protein PA1960 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05348.1 AE004622.10 (AE004622) hypothetical protein [Pseudomonas aeruginosa] Length = 240
SeqID 1642	SA-2733.1	Contig108 (18783-18911 p)	No Hits found	
SeqID 1643	SA-274.1	Contig138 (71355-71612 m)	58	Identities = 41/72 (56%), Positives = 58/72 (76%), Gaps = 1/72 (1%) pir J089894 hypothetical protein yncC - Bacillus subtilis emb CAB13672.1 (Z99113) yncC [Bacillus subtilis] Length = 77
SeqID 1644	SA-2741.1	Contig102 (13042-13308 p)	No Hits found	
SeqID 1645	SA-2747.1	Contig98 (8006-8278 p)	No Hits found	

SeqID 1646	SA-275.1	Contig138 (71624-73663 m)	65	<p>Identities = 315/687 (45%), Positives = 445/687 (63%), Gaps = 21/687 (3%) sp P54381 SYGB_BACSU GLYCYL-TRNA SYNTHETASE BETA CHAIN (GLYCINE--TRNA LIGASE BETA CHAIN) (GLYS) pr J89696 glycine--RNA ligase (EC 6.1.1.14) beta chain gys - Bacillus subtilis dbj BA112485.1 (D84432) YrK [Bacillus subtilis] emb CAB14455.1 (Z99116) glycol-RNA synthetase (beta subunit) [Bacillus subtilis] emb CAB14468.1 (Z99117) glycol-RNA synthetase (beta subunit) [Bacillus subtilis] Length = 679</p>
SeqID 1647	SA-2752.1	Contig94 (10312-10587 p)	No Hits found	Identities = 32/79 (40%), Positives = 48/79 (60%) gb AAK05381.1 AE006360.10 (AE006360) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 79
SeqID 1648	SA-2756.1	Contig91 (6477-6716 p)	60	
SeqID 1649	SA-2757.1	Contig91 (6359-6622 m)	No Hits found	
SeqID 1650	SA-2758.1	Contig91 (5806-6126 m)	No Hits found	
SeqID 1651	SA-2759.1	Contig91 (5708-6319 p)	46	Identities = 66/153 (43%), Positives = 94/153 (61%), Gaps = 2/153 (1%) gb AAK05259.1 AE006348.4 (AE006348) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 199
SeqID 1652	SA-276.1	Contig138 (73667-74164 m)	45	Identities = 64/176 (36%), Positives = 99/176 (55%), Gaps = 6/176 (3%) gb AAD24436.1 AF112858.1 (AF112858) NAD(P)H dehydrogenase [Bacillus stearothermophilus] Length = 211
SeqID 1653	SA-2760.1	Contig91 (613-960 m)	45	Identities = 33/106 (31%), Positives = 53/106 (49%), Gaps = 8/106 (7%) emb CAA33190.1 (X15081) MURF2 protein (AA 1-348) [Cnithidia fasciculata] Length = 347
SeqID 1654	SA-2761.1	Contig80 (10903-11157 m)	No Hits found	
SeqID 1655	SA-2763.1	Contig90 (3-899 p)	99	Identities = 298/298 (100%), Positives = 298/298 (100%) gb AAK14387.1 AF338416.1 (AF338416) glyceraldehyde 3-phosphate dehydrogenase [Streptococcus agalactiae] Length = 336
SeqID 1656	SA-2766.1	Contig85 (11550-11849 m)	No Hits found	

SeqID 1657	SA-2767.1	Contig84 (10458-10913 m)	67	Identities = 79/142 (55%), Positives = 102/142 (71%), Gaps = 5/142 (3%) gb AAK05046.1 AE006329.5 (AE006329) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis] Length = 159
SeqID 1658	SA-2768.1	Contig84 (10038-10448 m)	50	Identities = 38/131 (29%), Positives = 70/131 (53%), Gaps = 5/131 (3%) pir B83475 hypothetical protein PA1353 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04742.1 AE004585.1 (AE004585) hypothetical protein [Pseudomonas aeruginosa] Length = 137
SeqID 1659	SA-2769.1	Contig83 (5598-5870 p)	No Hits found	Identities = 221/287 (77%), Positives = 250/287 (87%) sp Q9KDX9 SYGA_BACHD GLYCYL-TRNA SYNTHETASE ALPHA CHAIN (GLYCINE-TRNA LIGASE ALPHA CHAIN) (GLYRS) db BAB03089.1 (AP001511) glycol-HRNA synthetase (alpha subunit) [Bacillus halodurans] Length = 297
SeqID 1660	SA-2771.1	Contig138 (74308-75225 m)	72	Identities = 17/58 (29%), Positives = 27/58 (46%), Gaps = 1/58 (1%) ref NP_042981.1 U88 [Human herpesvirus 6] emb CAA58337.1 (X83413) U88 [Human herpesvirus 6] Length = 413
SeqID 1661	SA-2770.1	Contig83 (3561-3887 p)	24	Identities = 26/51 (50%), Positives = 37/51 (71%), Gaps = 2/51 (3%) gb AAK04732.1 AE006296.5 (AE006296) DNA-directed RNA polymerase delta chain (EC 2.7.7.6) [Lactococcus lactis subsp. lactis] Length = 187
SeqID 1662	SA-2771.1	Contig80 (1912-2166 m)	No Hits found	
SeqID 1663	SA-2772.1	Contig80 (902-1168 p)	No Hits found	
SeqID 1664	SA-2773.1	Contig78 (6209-6433 p)	49	Identities = 26/51 (50%), Positives = 37/51 (71%), Gaps = 2/51 (3%) gb AAK04732.1 AE006296.5 (AE006296) DNA-directed RNA polymerase delta chain (EC 2.7.7.6) [Lactococcus lactis subsp. lactis] Length = 187
SeqID 1665	SA-2776.1	Contig69 (2000-2224 p)	No Hits found	
SeqID 1666	SA-278.2	Contig138 (75535-76077 m)	57	Identities = 71/168 (42%), Positives = 105/168 (62%) pir F81147 probable integral membrane protein NMA1102 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) gb AAFA41294.1 (AE002440) conserved hypothetical protein [Neisseria meningitidis MC58] emb CAB84365.1 (AL162755) putative integral membrane protein [Neisseria meningitidis Z2491] Length = 169

SeqID 1667	SA-279.1	Contig126 (42614-42796 p)	No Hits found	Identities = 96/354 (27%), Positives = 161/354 (45%), Gaps = 61/354 (17%) ref NP_053236.1 pX02-84 [Bacillus anthracis] gb AAAF13688.1 AF188935_88 [AF188935] pX02-84 [Bacillus anthracis] Length = 490
SeqID 1668	SA-28.1	Contig137 (13147-15513 p)	20	
SeqID 1669	SA-280.1	Contig126 (42553-46098 m)	69	Identities = 629/1241 (50%), Positives = 825/1241 (65%), Gaps = 75/1241 (6%) gb AAG33958.1 AF217414_1 (AF217414) pullulanase [Streptococcus pneumoniae] Length = 1287
SeqID 1670	SA-282.1	Contig126 (41501-42421 m)	61	Identities = 134/299 (44%), Positives = 197/299 (65%) db JBAB08178.1 (AB036768) exfoliative toxin A [Staphylococcus hyicus] Length = 306
SeqID 1671	SA-283.1	Contig126 (41283-41459 p)	No Hits found	
SeqID 1672	SA-285.1	Contig126 (40282-41184 m)	62	Identities = 139/311 (44%), Positives = 200/311 (63%), Gaps = 21/311 (6%) sp Q9KAC3 MIAA_BACHD TRNA DELTA(2)-ISOPENTENYL-PYROPHOSPHATE TRANSFERASE (IPP TRANSFERASE) (ISOPENTENYL-DIPHOSPHATE:TRNA ISOPENTENYL TRANSFERASE) (IPTASE) (IPPT) db JBAB06085.1 (AP001515) RNA isopentenylpyrophosphate transferase [Bacillus halodurans] Length = 314
SeqID 1673	SA-286.1	Contig126 (38953-40191 m)	61	Identities = 183/406 (45%), Positives = 255/406 (62%), Gaps = 12/406 (2%) db JBAB06081.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 418
SeqID 1674	SA-287.1	Contig126 (38313-38960 m)	No Hits found	
SeqID 1675	SA-288.1	Contig126 (37342-38271 m)	64	Identities = 156/309 (50%), Positives = 209/309 (67%), Gaps = 5/309 (1%) sp P54548 YQJ_K_BACSU HYPOTHETICAL 34.0 KDA PROTEIN IN GLN-ANSR INTERGENIC REGION pi I C69964 conserved hypothetical protein yqjK - Bacillus subtilis db JBAA12617.1 (D84432) YqjK [Bacillus subtilis] emb CAB14316.1 (Z99116) similar to hypothetical proteins [Bacillus subtilis] Length = 307
SeqID 1676	SA-29.1	Contig137 (12635-13093 p)	No Hits found	

SeqID 1677	SA-290.1	Contig126 (36579-37340 m)	59	<p>Identities = 100/253 (39%), Positives = 152/253 (59%), Gaps = 2/253 (0%) sp P54554 YQJQ_BACSU HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION pir A09986 ketoacyl reductase homolog yqJ - Bacillus subtilis db BAA12823.1 (D84432) YqJ [Bacillus subtilis] emb CAB14310.1 (Z99116) similar to ketoacyl reductase [Bacillus subtilis] Length = 259</p>
SeqID 1678	SA-291.1	Contig126 (34384-36582 m)	60	<p>Identities = 276/772 (35%), Positives = 447/772 (57%), Gaps = 45/772 (5%) pi H6980 single-strand DNA-specific exonuclease homolog yvE - Bacillus subtilis emb CAB14721.1 (Z99118) similar to single-strand DNA-specific exonuclease [Bacillus subtilis] Length = 786</p>
SeqID 1679	SA-292.1	Contig126 (31688-34187 m)	12	<p>Identities = 65/220 (29%), Positives = 104/220 (46%), Gaps = 33/220 (15%) sp P11701 SACB_STRIMU LEVANSUCRASE PRECURSOR (BETA-D-FRUCTOFURANOSYL TRANSFERASE) pi B26551 levansucrase (EC 2.4.1.10) precursor - Streptococcus mutans (strain GS-5) gb AAA88584.1 (M18954) fructosyltransferase [Streptococcus mutans] Length = 797</p>
SeqID 1680	SA-293.1	Contig126 (31027-31545 m)	74	<p>Identities = 110/170 (64%), Positives = 135/170 (78%) sp O34443 APT_BACSU ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT) pi B69587 adenine phosphoribosyltransferase (EC 2.4.2.7) - Bacillus subtilis gb AAC46040.1 (U86377) adenine phosphoribosyltransferase; Apt [Bacillus subtilis] emb CAB14720.1 (Z99118) adenine phosphoribosyltransferase [Bacillus subtilis] Length = 170</p>
SeqID 1681	SA-294.1	Contig126 (30228-30909 m)	78	<p>Identities = 140/227 (61%), Positives = 179/227 (78%) db BAA11244.1 (D78182) ORF2 [Streptococcus mutans] Length = 231</p>
SeqID 1682	SA-295.1	Contig126 (29442-30125 m)	71	<p>Identities = 132/226 (58%), Positives = 168/226 (73%) db BAA11245.1 (D78182) ORF3 [Streptococcus mutans] Length = 232</p>

SeqID 1683	SA-296.1	Contig126 (28664-29455 m)	83	Identities = 186/262 (70%), Positives = 224/262 (84%) dbj BAA11246.1 (D78182) ORF4 [Streptococcus mutans] Length = 262
SeqID 1684	SA-297.1	Contig126 (27552-28655 m)	55	Identities = 147/368 (39%), Positives = 210/368 (56%), Gaps = 13/368 (3%) sp Q359 YURR_BACSU HYPOTHETICAL 39.4 KD OXIDOREDUCTASE IN HOM-MRGA INTERGENIC REGION pri A70019 opine catabolism homolog yurR - Bacillus subtilis emb CAB15253.1 (Z59120) similar to opine catabolism [Bacillus subtilis] Length = 372
SeqID 1685	SA-298.3	Contig126 (26639-27493 m)	89	Identities = 247/275 (89%), Positives = 260/275 (93%) gb AAD19913.1 (AF105113) glucose-1-phosphate thymidyl transferase [Streptococcus pneumoniae] Length = 289
SeqID 1686	SA-298.3	Contig126 (26032-26625 m)	86	Identities = 162/198 (81%), Positives = 183/198 (91%) gb AAC78675.1 (AF094575) dTDP-4-keto-6-deoxyglucose-3,5-epimerase Cps19aM [Streptococcus pneumoniae] Length = 198
SeqID 1687	SA-3.1	Contig137 (40498-42447 p)	50	Identities = 188/659 (28%), Positives = 327/659 (49%), Gaps = 23/659 (4%) ref NP_053164.1 pXO2.09 [Bacillus anthracis] gb AAF13614.1 (AF188935_12 (AF188935) pXO2.09 [Bacillus anthracis] Length = 643
SeqID 1688	SA-30.1	Contig137 (11818-12618 p)	22	Identities = 48/115 (41%), Positives = 64/115 (54%), Gaps = 3/115 (2%) emb CAA59264.1 (X84793) streptodornase [Streptococcus pyogenes] Length = 385
SeqID 1689	SA-301.1	Contig126 (24779-25825 m)	91	Identities = 325/347 (93%), Positives = 340/347 (97%) sp P95780 RWLB_STRMU DTD-GLUCOSE 4-6-DEHYDRATASE dbj BAA11249.1 (D78182) dTDP-glucose-4,6-dehydratase [Streptococcus mutans] Length = 348
SeqID 1690	SA-303.1	Contig126 (22366-22569 m)	No Hits found	
SeqID 1691	SA-305.1	Contig126 (21509-24727 p)	99	Identities = 107/1072 (99%), Positives = 1071/1072 (99%) emb CAA59665.1 (Y15903) hyaluronate lyase [Streptococcus agalactiae] Length = 1072

SeqID 1692	SA-308.1	Contig126 (20810-21292 m)	88	Identities = 132/160 (82%), Positives = 146/160 (90%), Gaps = 1/160 (0%) spP95781[MUTX_STRMU_MUTATOR MUTT PROTEIN (7.8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE) (8-OXO-DGTPASE) (DGTP PYROPHOSPHOHYDROLASE) db BAA11250.1 (D78162) MutX [Streptococcus mutans] Length = 159
SeqID 1693	SA-307.1	Contig126 (20359-20697 m)	45	Identities = 46/150 (30%), Positives = 73/150 (48%), Gaps = 16/150 (10%) db BAB07445.1 (AP001519) unknown conserved protein in others [Bacillus halodurans] Length = 152
SeqID 1694	SA-308.1	Contig126 (19077-20287 m)	76	Identities = 243/393 (61%), Positives = 303/393 (76%), Gaps = 8/393 (2%) gb AAD00285.1 (U78604) putative membrane protein [Streptococcus mutans] Length = 395
SeqID 1695	SA-308.1	Contig126 (17861-19102 m)	49	Identities = 133/347 (38%), Positives = 207/347 (59%), Gaps = 5/347 (1%) gb AAA25160.1 (L16975) ORF1 [Lactococcus lactis] Length = 349
SeqID 1696	SA-31.1	Contig137 (11471-11818 p)	No Hits found	
SeqID 1697	SA-311.1	Contig126 (16069-17751 m)	82	Identities = 395/559 (70%), Positives = 485/559 (82%), Gaps = 8/559 (1%) gb AAA25161.1 (L16975) alpha-acetolactate synthase [Lactococcus lactis] Length = 554
SeqID 1698	SA-312.1	Contig126 (15336-16055 m)	72	Identities = 139/239 (58%), Positives = 188/239 (77%), Gaps = 3/239 (1%) gb AAB37482.1 (S82499) alpha-acetolactate decarboxylase, AIdB [Lactococcus lactis, ssp. lactis, NCDO2118, Peptide, 236 aa] gb AAB81923.1 (U92974) AIdB [Lactococcus lactis] Length = 236
SeqID 1699	SA-313.2	Contig126 (13827-15282 p)	82	Identities = 393/550 (71%), Positives = 462/550 (83%), ems CAA46282.1 (X65164) fibronectin-binding protein-like protein A [Streptococcus gordonii] Length = 550

SeqID 1700	SA-314.2	Contig126 (12285-13233 m)	54	Identities = 112/295 (37%), Positives = 184/295 (61%), Gaps = 1/295 (0%) ptiJF162240 conserved hypothetical protein VC1101 [imported] - Vibrio cholerae (group O1 strain N16981) gb AAAF94280.1 (AEQ04191) conserved hypothetical protein [Vibrio cholerae] Length = 321
SeqID 1701	SA-315.1	Contig126 (11389-12252 m)	63	Identities = 117/290 (40%), Positives = 186/290 (63%), Gaps = 9/290 (3%) ptiJF83165 probable permease of ABC transporter PA3837 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAAG07224.1 (AEQ04801.2) (AEQ04801) probable permease of ABC transporter [Pseudomonas aeruginosa] Length = 296
SeqID 1702	SA-316.1	Contig126 (10628-11389 m)	60	Identities = 116/254 (45%), Positives = 167/254 (65%) gb AAAF86540.1 (AF162894_1) (AF162894) ABC transporter [Enterococcus gallinarum] Length = 269
SeqID 1703	SA-318.1	Contig126 (8670-10331 m)	64	Identities = 237/555 (42%), Positives = 363/555 (64%), Gaps = 2/555 (0%) dbj BAB06117.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 555
SeqID 1704	SA-319.1	Contig126 (7825-8613 m)	63	Identities = 155/262 (59%), Positives = 189/262 (71%), Gaps = 4/262 (1%) gb AAAF62859.1 (AF157484_1) (AF157484) tributyrin esterase [Lactococcus lactis subsp. lactis] Length = 258
SeqID 1705	SA-32.1	Contig137 (11161-11478 p)	No Hits found	
SeqID 1706	SA-320.1	Contig126 (7025-7684 m)	No Hits found	
SeqID 1707	SA-321.1	Contig126 (6333-6878 p)	21	Identities = 30/60 (50%), Positives = 39/60 (65%), Gaps = 4/60 (5%) ptiJF72654 hypothetical protein APE0666 - Aeropyrum pernix (strain K1) dbj BA479638.1 (AP0000060) 102aa long hypothetical protein [Aeropyrum pernix] Length = 102

SeqID 1708	SA-322.1	Contig126 (6116-6787 m)	58	<p>Identities = 103/220 (46%), Positives = 141/220 (63%), Gaps = 3/220 (1%) sp P7012 IRPIA_METH_PROBABLE_RIBOSE_5-PHOSPHATE ISOMERASE (PHOSPHORIBOSYLTRANSFERASE) [D88555] orf2 [Methanobacterium thermoautotrophicum] (strain Delta H) dbj BA413846.1 gb AA885114.1 (AE000842) ribose 5-phosphate isomerase [Methanobacterium thermoautotrophicum] Length = 226</p>
SeqID 1709	SA-323.1	Contig126 (4848-6059 m)	79	<p>Identities = 275/408 (67%), Positives = 325/408 (79%), Gaps = 7/408 (1%) sp O32808 DEOB_LACLC PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE) gb AAC45496.1 (U80410) phosphopentomutase [Lactococcus lactis subsp. cremoris] Length = 411</p>
SeqID 1710	SA-324.1	Contig126 (4390-4800 m)	55	<p>Identities = 73/130 (56%), Positives = 93/130 (71%) sp P52147 ARC2_ECOLI_ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER) gb AAB06628.1 (U36947) ArsC [Plasmid R46] Length = 141</p>
SeqID 1711	SA-325.1	Contig126 (3542-4351 m)	74	<p>Identities = 149/272 (54%), Positives = 201/272 (73%), Gaps = 3/272 (1%) dbj BA805250.1 (AP001512) purine nucleoside phosphorylase [Bacillus halodurans] Length = 272</p>
SeqID 1712	SA-326.1	Contig126 (2284-3540 m)	50	<p>Identities = 121/410 (29%), Positives = 215/410 (51%), Gaps = 19/410 (4%) gb AAD53928.1 (AF179611_12 (AF179611) chloride channel protein [Zymomonas mobilis] Length = 425</p>
SeqID 1713	SA-327.1	Contig126 (1590-2300 m)	82	<p>Identities = 177/216 (81%), Positives = 197/216 (90%) sp Q56037 DEOD_STRITR_PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE) (PNP) gb AAC44007.1 (U40830) deoD [Streptococcus thermophilus] prf1 J209356A deoD gene [Streptococcus thermophilus] Length = 216</p>
SeqID 1714	SA-328.1	Contig126 (814-1581 m)	No Hits found	

SeqID 1715	SA-329.1	Contig126 (169-789 p)	99	<p>Identities = 262/262 (100%), Positives = 262/262 (100%) pir T44638 capsular polysaccharide biosynthesis protein cpsY [Imported] - Streptococcus agalactiae emb CAB36980.1 (Y17218) CpsY protein [Streptococcus agalactiae] emb CAB36982.2 (Y17241) CpsY protein [Streptococcus agalactiae] gb AAD53064.1 (AF163833_1 (AF163833) CpsY [Streptococcus agalactiae] Length = 307</p>
SeqID 1716	SA-330.2	Contig132 (27403-27660 p)	No Hits found	
SeqID 1717	SA-331.2	Contig132 (26320-27393 p)	69	<p>Identities = 212/347 (61%), Positives = 261/347 (75%), Gaps = 3/347 (0%) emb CAA04376.1 (AJ000883) purK [Lactococcus lactis] Length = 349</p>
SeqID 1718	SA-333.1	Contig132 (25842-26333 p)	58	<p>Identities = 102/158 (64%), Positives = 129/158 (81%) emb CAA04375.1 (AJ000883) purE [Lactococcus lactis] Length = 161</p>
SeqID 1719	SA-334.1	Contig132 (24299-25561 p)	68	<p>Identities = 239/419 (57%), Positives = 300/419 (71%), Gaps = 7/419 (1%) sp Q2ZF4 PUR2_LACLA PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (GARS) (RIBONUCLEOTIDE SYNTHETASE) (FLYNN) RIBONUCLEOTIDE SYNTHETASE (FLYNN) RIBONUCLEOTIDE SYNTHETASE emb CAA04374.1 (AJ000883) purD [Lactococcus lactis] Length = 412</p>
SeqID 1720	SA-335.1	Contig132 (23212-24015 m)	41	<p>Identities = 66/258 (25%), Positives = 119/258 (45%), Gaps = 9/258 (3%) sp P26833 YNGB_CLOPE HYPOTHETICAL 31.2 KDA PROTEIN IN NAGH 5 REGION (ORFB) pir S43902 hypothetical protein B - Clostridium perfringens gb AA23257.1 (M81878) unknown [Clostridium perfringens] Length = 279</p>
SeqID 1721	SA-336.1	Contig132 (22212-23189 p)	55	<p>Identities = 133/299 (44%), Positives = 188/299 (62%), Gaps = 12/99 (0%) pir S41858 hypothetical protein Thermococcus bacterium saccharolyticum Length = 320</p>

SeqID 1722	SA-337.1	Contig132 (21323-22204 p)	37	<p>Identities = 78/160 (48%), Positives = 110/160 (68%) sp P26832 NGA_CLOPE_HYPOTHETICAL_PROTEIN_IN_NAGH 5_REGION_ORFA_prl S43901 hypothetical protein A - Clostridium perfringens (fragment) gb AA23256.1 (M81878) unknown [Clostridium perfringens] Length = 182</p>
SeqID 1723	SA-338.1	Contig132 (20389-21306 p)	58	<p>Identities = 162/225 (72%), Positives = 191/225 (84%) emb CAA69950.1 (Y08695) putative acylneuraminate lyase [Clostridium tertium] Length = 226</p>
SeqID 1724	SA-339.1	Contig132 (19703-20392 p)	32	<p>Identities = 40/148 (27%), Positives = 74/148 (49%), Gaps = 4/148 (2%) db JBA05827.1 (AP001514) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 214</p>
SeqID 1725	SA-34.1	Contig137 (10492-10787 p)	40	<p>Identities = 30/91 (32%), Positives = 50/91 (53%), Gaps = 6/91 (6%) gb AAAF3773.1 (AF154006.1) (AF154006) surface protein PspC [Streptococcus pneumoniae] Length = 678</p>
SeqID 1726	SA-340.1	Contig132 (19267-19710 p)	43	<p>Identities = 48/151 (31%), Positives = 66/151 (42%), Gaps = 5/151 (3%) gb AAAC44392.1 (U43526) ORF-1 [Streptococcus pneumoniae] Length = 150</p>
SeqID 1727	SA-342.1	Contig132 (18424-19254 p)	56	<p>Identities = 94/262 (35%), Positives = 158/262 (59%), Gaps = 1/262 (0%) prl F72379 sugar ABC transporter, permease protein Thermotoga maritima (strain MSB9) gb AAD35515.1 (AE001721.14) (AE001721) sugar ABC transporter, permease protein [Thermotoga maritima] Length = 271</p>
SeqID 1728	SA-343.1	Contig132 (17527-18414 p)	51	<p>Identities = 106/289 (36%), Positives = 168/289 (57%), Gaps = 6/289 (2%) db BAB05584.1 (AP001513) sugar transport system (permease) (binding protein dependent transporter) [Bacillus halodurans] Length = 309</p>
SeqID 1729	SA-344.1	Contig132 (16123-17439 p)	20	<p>Identities = 54/187 (28%), Positives = 90/187 (47%), Gaps = 14/187 (7%) db JF59796 sugar-binding protein homolog yscO - Bacillus subtilis emb CAB12516.1 (Z59107) similar to sugar- binding protein [Bacillus subtilis] Length = 412</p>

SeqID 1730	SA-345.1	Contig132 (15378-16076 p)	62	Identities = 107/226 (47%), Positives = 148/226 (65%), Gaps = 6/226 (2%) prijC70180 conserved hypothetical protein B80644 - Lyme disease spirochete gb AA068999.1 (AE001166) conserved hypothetical protein [Borrelia burgdorferi] Length = 232
SeqID 1731	SA-347.1	Contig132 (13827-15131 p)	97	Identities = 434/434 (100%), Positives = 434/434 (100%) gb AAG18476.1 (AF151359) group B streptococcal surface immunogenic protein [Streptococcus agalactiae] gb AAG18477.1 (AF151361) group B streptococcal surface immunogenic protein [Streptococcus agalactiae] Length = 434
SeqID 1732	SA-348.1	Contig132 (12781-13680 p)	62	Identities = 163/274 (59%), Positives = 196/274 (71%), Gaps = 11/274 (4%) gb AAC46072.1 (U50357) zoon A endopeptidase [Streptococcus zooepidemicus] Length = 285
SeqID 1733	SA-351.1	Contig132 (11041-12688 p)	74	Identities = 310/515 (60%), Positives = 390/515 (75%), Gaps = 4/515 (0%) db BAB04352.1 (AP001509) phosphoribosylaminimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Bacillus halodurans] Length = 511
SeqID 1734	SA-352.1	Contig132 (10269-11021 p)	44	Identities = 65/263 (24%), Positives = 117/263 (43%), Gaps = 34/263 (12%) prijH69779 antibiotic resistance protein homolog ydFB - Bacillus subtilis db BAA19369.1 (AB001488) SIMILAR TO BACILLUS CEREBUS ZWITTERMICIN A-RESISTANCE GENE [Bacillus subtilis] emb CAB12342.1 (Z99106) similar to antibiotic resistance protein [Bacillus subtilis] Length = 261
SeqID 1735	SA-353.1	Contig132 (9698-10246 p)	61	Identities = 137/152 (90%), Positives = 140/152 (91%), Gaps = 2/152 (1%) gb AAF08602.1 U70775_1 (U70775) phosphoribosylglycinamide formyltransferase homolog [Streptococcus pyogenes] Length = 151

SeqID 1736	SA-356.1	Contig132 (8508-9530 p)	85	<p>Identities = 257/339 (75%), Positives = 293/339 (85%), Gaps = 4/339 (1%) gb AAC16901.1 (AF018634) phosphoribosylformylglycinamide cyclo-ligase [Lactococcus lactis subsp. cremoris] Length = 340</p>
SeqID 1737	SA-357.1	Contig132 (7026-6480 p)	83	<p>Identities = 343/470 (72%), Positives = 406/470 (85%), Gaps = 6/470 (1%) pfl T51702 amidophosphoribosyltransferase (EC 2.4.2.14) [imported] - Lactococcus lactis gb AAD72627.1 (U64311) phosphoribosylpyrophosphate amidotransferase [Lactococcus lactis] Length = 506</p>
SeqID 1738	SA-36.1	Contig137 (6548-10369 p)	No Hits found	
SeqID 1739	SA-361.1	Contig132 (4533-5015 m)	39	<p>Identities = 39/137 (28%), Positives = 63/137 (45%), Gaps = 7/137 (5%) pfl 2119294A YFW1 gene [Saccharomyces cerevisiae] Length = 605</p>
SeqID 1740	SA-363.1	Contig132 (3046-6792 p)	25	<p>Identities = 198/746 (26%), Positives = 330/746 (43%), Gaps = 103/746 (13%) emb CAC12194.1 (AL445066) phosphoribosylformylglycinamide synthase related protein [Thermoplasma acidophilum] Length = 759</p>
SeqID 1741	SA-364.2	Contig132 (2240-2944 p)	84	<p>Identities = 183/235 (77%), Positives = 206/235 (86%) sp Q07296 PUR7_STRPN PHOSPHORIBOSYLAMINOIMIDAZOLE- SUCCINOCARBOXAMIDE SYNTHASE (SAICAR SYNTHETASE) pfl A36941 phosphoribosylaminoimidazole succinocarboxamide synthase (EC 6.3.2.6) - Streptococcus pneumoniae gb AA03540.1 (L15190) SAICAR synthetase [Streptococcus pneumoniae] gb AA069512.1 (M35180) SAICAR synthetase [Streptococcus pneumoniae] Length = 235</p>
SeqID 1742	SA-366.2	Contig139 (35877-38139 m)	85	<p>Identities = 560/755 (74%), Positives = 648/755 (85%), Gaps = 12/755 (1%) gb AAD01782.1 (AF023421) CbpE [Lactococcus lactis] Length = 748</p>

SeqID 1743	SA-367.1	Contig139 (35236-35591 m)	29	Identities = 31/101 (30%), Positives = 48/101 (48%), Gaps = 2/101 (1%) pifJ(A70315) APA4 hydrolase - Aquifex aeolicus gb AAC06510.1 (AE000676) APA4 hydrolase [Aquifex aeolicus] Length = 134
SeqID 1744	SA-368.1	Contig139 (34870-35172 m)	No Hits found	Identities = 63/288 (21%), Positives = 129/288 (43%), Gaps = 27/288 (9%) refNP_053160.1 pXO2-05 [Bacillus anthracis] gb AAE13610.1 (AF188935_7 (AF188935) pXO2-05 [Bacillus anthracis] Length = 282
SeqID 1745	SA-371.1	Contig137 (8461-8485 p)	37	Identities = 72/9629 (78%), Positives = 821/9629 (87%), Gaps = 1/929 (0%) sp Q9ZHB3 SYL_STRPN ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE-TRNA LIGASE) (ILERS) gb AAC95446.1 (AF068901) isoleucine-TRNA synthetase [Streptococcus pneumoniae] Length = 930
SeqID 1746	SA-370.1	Contig139 (31961-34753 p)	87	Identities = 132/227 (58%), Positives = 179/227 (78%), Gaps = 2/227 (0%) gb AAC95445.1 (AF068901) cell division protein DivIVA [Streptococcus pneumoniae] Length = 262
SeqID 1747	SA-371.1	Contig139 (30906-31676 p)	68	Identities = 101/255 (39%), Positives = 162/255 (62%) gb AAC95444.1 (AF068901) YmhH [Streptococcus pneumoniae] Length = 261
SeqID 1748	SA-372.1	Contig139 (30108-30896 p)	60	Identities = 34/83 (40%), Positives = 54/83 (64%) emb CAA75619.1 (Y15422) hypothetical protein [Lactococcus lactis subsp. cremoris] Length = 91
SeqID 1749	SA-373.1	Contig139 (29852-30106 p)	59	Identities = 86/200 (43%), Positives = 120/200 (60%), Gaps = 25/200 (12%) gb AAC95442.1 (AF068901) YmfF [Streptococcus pneumoniae] Length = 179
SeqID 1750	SA-374.1	Contig139 (29244-29849 p)	57	Identities = 140/223 (62%), Positives = 177/223 (78%) gb AAC95441.1 (AF068901) YmhE [Streptococcus pneumoniae] Length = 223
SeqID 1751	SA-375.1	Contig139 (28558-29232 p)	76	Identities = 327/426 (76%), Positives = 363/426 (84%), Gaps = 7/426 (1%) gb AAC95440.1 (AF068901) cell division protein FtsZ [Streptococcus pneumoniae] Length = 419
SeqID 1752	SA-376.1	Contig139 (27272-28552 p)	84	

SeqID 1753	SA-377.1	Contig139 (25877-27250 p)	80	Identities = 293/458 (63%), Positives = 368/458 (79%), Gaps = 1/458 (0%) gb AAC95439.1 (AF068901) cell division protein FtsA [Streptococcus pneumoniae] Length = 457
SeqID 1754	SA-379.1	Contig139 (24468-25604 p)	55	Identities = 123/396 (31%), Positives = 210/396 (52%), Gaps = 38/396 (9%) gb AAC95451.1 (AF068902) cell division protein DvlB [Streptococcus pneumoniae] Length = 399
SeqID 1755	SA-380.1	Contig139 (23388-24464 p)	80	Identities = 248/358 (69%), Positives = 293/358 (81%), Gaps = 1/358 (0%) d bj BAB16029.1 (AB030845) MurG [Streptococcus pyogenes] Length = 360
SeqID 1756	SA-381.1	Contig139 (22030-23385 p)	84	Identities = 340/449 (75%), Positives = 392/449 (86%) gb AAC95449.1 (AF068902) D-glutamic acid adding enzyme MurD [Streptococcus pneumoniae] Length = 450
SeqID 1757	SA-382.1	Contig139 (21655-21900 p)	No Hits found	
SeqID 1758	SA-384.1	Contig139 (19769-21610 p)	84	Identities = 457/609 (75%), Positives = 536/609 (87%), Gaps = 2/609 (0%) sp O07631 TYPA_BACSU GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG pr E9872 GTP-binding translation elongation factor homolog ylaG - Bacillus subtilis emb CAB09712.1 (Z97025) product highly similar to elongation factor EF-G [Bacillus subtilis] emb CAB13350.1 (Z99111) similar to GTP-binding elongation factor [Bacillus subtilis] Length = 612
SeqID 1759	SA-385.1	Contig139 (19157-19537 p)	55	Identities = 51/124 (41%), Positives = 71/124 (57%), Gaps = 1/124 (0%) sp P54510 YQHL_BACSU HYPOTHETICAL 14.6 KD PROTEIN IN GCVT-SPOIIIA INTERGENIC REGION pr IC69959 glpE protein homolog yqHl - Bacillus subtilis d bj BAA12549.1 (D84432) yqHl [Bacillus subtilis] emb CAB14385.1 (Z99116) similar to hypothetical proteins [Bacillus subtilis] Length = 126

SeqID 1760	SA-387.1	Contig139 (18177-19145 p)	64	Identities = 145/315 (46%), Positives = 209/315 (66%), Gaps = 2/315 (0%) dbj BA05144.1 (AP001512) glucose kinase [Bacillus halodurans] Length = 330
SeqID 1761	SA-388.1	Contig139 (17971-18180 p)	84	Identities = 53/67 (79%), Positives = 62/67 (92%) dbj BA036473.1 (AB036428) hypothetical 8.3 kDa protein [Streptococcus mutans] Length = 68
SeqID 1762	SA-389.1	Contig139 (17421-17867 m)	57	Identities = 57/123 (46%), Positives = 85/123 (69%) dbj BA06471.1 (AB036428) type IV prelin peptidase homologue [Streptococcus mutans] Length = 218
SeqID 1763	SA-39.1	Contig137 (7426-8382 m)	No Hits found	Identities = 95/202 (47%), Positives = 134/202 (66%) dbj BA05417.1 (AP001512) endonuclease III (DNA repair) [Bacillus halodurans] Length = 218
SeqID 1764	SA-390.1	Contig139 (16788-17420 p)	61	Identities = 88/384 (22%), Positives = 159/384 (40%), Gaps = 24/384 (6%) pir JA69832 probable acid-CoA ligase (EC 6.2.1.-) ynfT [similarity] - Bacillus subtilis emb CAA74543.1 (Y14084) hypothetical protein [Bacillus subtilis] emb CAB12876.1 (Z99109) similar to long-chain fatty-acid-CoA ligase [Bacillus subtilis] Length = 479
SeqID 1765	SA-391.1	Contig139 (15458-16675 p)	38	
SeqID 1766	SA-392.1	Contig139 (14410-15453 p)	45	Identities = 96/340 (28%), Positives = 160/340 (46%), Gaps = 21/340 (6%) emb CAC11722.1 (AL445064) acetyl-CoA acetyltransferase related protein [Thermoplasma acidophilum] Length = 388
SeqID 1767	SA-393.1	Contig139 (13834-14349 p)	No Hits found	
SeqID 1768	SA-394.1	Contig139 (12717-13709 m)	55	Identities = 132/316 (41%), Positives = 201/316 (62%), Gaps = 2/316 (0%) dbj BA05467.1 (AP001513) biotin synthase [Bacillus halodurans] Length = 333

SeqID 1769	SA-395.1	Contig139 (12177-12716 m)	58	Identities = 69/168 (41%), Positives = 105/168 (62%) pir B69832 biotin biosynthesis homolog ynfU - Bacillus subtilis emb CAA74544.1 (Y14084) hypothetical protein [Bacillus subtilis] emb CAB12877.1 (Z99109) similar to biotin biosynthesis [Bacillus subtilis] Length = 186
SeqID 1770	SA-396.1	Contig139 (11543-12109 p)	60	Identities = 102/191 (53%), Positives = 134/191 (69%), Gaps = 4/191 (2%) sp Q02003 TRPG_LACUA ANTHRANILATE SYNTHASE COMPONENT II (GLUTAMINE AMIDO-TRANSFERASE) pir S35125 anthranilate synthase (EC 4.1.3.27) beta chain - Lactococcus lactis subsp. lactis gb AA25224.1 (M87483) anthranilate synthase beta subunit [Lactococcus lactis] Length = 198
SeqID 1771	SA-397.1	Contig139 (9673-11415 p)	68	Identities = 280/582 (48%), Positives = 400/582 (68%), Gaps = 6/582 (1%) dbj BAB06054.1 (AP001515) ABC transporter (ATP-binding protein) [Bacillus halodurans] Length = 599
SeqID 1772	SA-398.1	Contig139 (7941-9686 p)	69	Identities = 284/575 (49%), Positives = 406/575 (70%), Gaps = 2/575 (0%) dbj BAB06055.1 (AP001515) ABC transporter (ATP-binding protein) [Bacillus halodurans] Length = 585
SeqID 1773	SA-399.1	Contig139 (7161-7745 p)	34	Identities = 46/154 (29%), Positives = 68/154 (43%), Gaps = 36/154 (23%) gb AAE38806.1 (AF155139) VanZf [Paenibacillus popilliae] Length = 205
SeqID 1774	SA-4.1	Contig137 (39841-40488 p)	No Hits found	
SeqID 1775	SA-40.1	Contig137 (7185-7433 p)	No Hits found	
SeqID 1776	SA-400.1	Contig139 (6106-7230 p)	67	Identities = 206/349 (59%), Positives = 257/349 (73%), Gaps = 5/349 (1%) dbj BAB06225.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 362
SeqID 1777	SA-401.2	Contig139 (5495-6073 p)	29	Identities = 46/89 (51%), Positives = 62/89 (68%), Gaps = 1/89 (1%) pir F70023 hypothetical protein ynfD - Bacillus subtilis emb CAB15221.1 (Z99120) ynfD [Bacillus subtilis] Length = 102

SeqID 1778	SA-402.2	Contig139 (4092-5426 p)	58	Identities = 155/463 (33%), Positives = 262/463 (56%) Gaps = 33/463 (7%) pjlG70015 conserved hypothetical protein yunD - Bacillus subtilis emb CAB15227.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] Length = 462
SeqID 1779	SA-403.1	Contig139 (2944-4017 p)	55	Identities = 125/344 (36%), Positives = 199/344 (57%) Gaps = 21/344 (6%) pjlA69875 hypothetical protein ybL - Bacillus subtilis emb CAB11358.1 (Z38682) YbL protein [Bacillus subtilis] emb CAB13378.1 (Z99111) ybL [Bacillus subtilis] Length = 350
SeqID 1780	SA-405.1	Contig139 (2469-2954 p)	57	Identities = 56/149 (37%), Positives = 94/149 (62%) spP57643COAD_BUCAL PHOSPHOPANTETHEINE ADENYLTRANSFERASE (PANTETHEINE-PHOSPHATE ADENYLTRANSFERASE) (PPAT) (DEPHOSPHO-COA PYROPHOSPHORYLASE) dbj BAB13272.1 (AP001119) lipopolysaccharide core biosynthesis protein kdtB [Buchnera sp. APS] Length = 165
SeqID 1781	SA-407.1	Contig139 (2149-2472 p)	No Hits found	
SeqID 1782	SA-409.1	Contig139 (1418-2170 p)	46	Identities = 80/180 (44%), Positives = 118/180 (65%) Gaps = 3/180 (1%) dbj BAB06309.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 189
SeqID 1783	SA-41.1	Contig137 (7095-7170 p)	No Hits found	
SeqID 1784	SA-410.1	Contig139 (1051-1419 m)	31	Identities = 30/97 (30%), Positives = 51/97 (51%), Gaps = 3/97 (3%) gb AAD56628.1 AF165216.3 (AF165216) Bta [Streptococcus pneumoniae] Length = 115
SeqID 1785	SA-411.1	Contig139 (5-1006 p)	86	Identities = 267/328 (81%), Positives = 290/328 (88%) spP44339ASNA_HAEIN ASPARTATE--AMMONIA LIGASE (ASPARAGINE SYNTHETASE A) pjlH64077 aspartate--ammonia ligase (EC 6.3.1.1) - Haemophilus influenzae (strain Rd KW20) gb AAC22222.1 (U32738) aspartate--ammonia ligase (asna) [Haemophilus influenzae Rd] Length = 330

SeqID 1786	SA-412.2	Contig134 (36525-37172 m)	75	Identities = 125/212 (59%), Positives = 165/212 (78%) gb AAE81675.1 AF232889.4 (AF232889) SLO (Streptococcus mutans) Length = 217
SeqID 1787	SA-413.1	Contig134 (36796-36485 p)	62	Identities = 100/229 (43%), Positives = 145/229 (62%) sp P45113 MTN_HAEIN_MTA/SAH_NUCLEOSIDASE [INCLUDES: 5-METHYLTHIOADENOSINE NUCLEOSIDASE : S-ADENOSYLHOMOCYSTEINE NUCLEOSIDASE] pi C64169 pfs protein - Haemophilus influenzae (strain Rd KW20) gb AAC22869.1 (U32801) pfs protein (pfs) [Haemophilus influenzae Rd] Length = 229
SeqID 1788	SA-414.1	Contig134 (35517-35786 p)	No Hits found	Identities = 92/181 (50%), Positives = 125/181 (68%), Gaps = 4/181 (2%) sp P54570 YQKG_BACSU_HYPOTHETICAL_21.0 KDA PROTEIN IN GLN-Q/ANSR_INTERGENIC REGION pi A69967 conserved hypothetical protein yqkg - Bacillus subtilis emb BAA12639.1 (D84432) Yqkg [Bacillus subtilis] emb CAB14293.1 (Z99116) similar to hypothetical proteins [Bacillus subtilis] Length = 185
SeqID 1789	SA-415.1	Contig134 (34963-35517 p)	62	Identities = 238/453 (52%), Positives = 322/453 (70%), Gaps = 1/453 (0%) db JBAB03784.1 (AP001507) UDP-N-acetylglucosamine pyrophosphorylase [Bacillus halodurans] Length = 455
SeqID 1790	SA-416.1	Contig134 (33563-34942 p)	68	Identities = 48/144 (31%), Positives = 83/144 (56%), Gaps = 10/144 (6%) db JBAB04569.1 (AP001510) unknown conserved protein in others [Bacillus halodurans] Length = 148
SeqID 1791	SA-417.1	Contig134 (32906-33319 p)	58	Identities = 41/127 (32%), Positives = 63/127 (49%), Gaps = 11/127 (8%) pi E69798 conserved hypothetical protein yeth - Bacillus subtilis emb CAB12535.1 (Z99107) similar to hypothetical proteins [Bacillus subtilis] Length = 120
SeqID 1792	SA-418.1	Contig134 (32516-32893 p)	48	Identities = 133/320 (41%), Positives = 193/320 (59%), Gaps = 4/320 (1%) db JBAB06422.1 (AP001516) unknown conserved protein [Bacillus halodurans] Length = 329
SeqID 1793	SA-419.1	Contig134 (31471-32427 p)	60	

SeqID 1794	SA-42.1	Contig137 (6439-6649 p)	No Hits found	
SeqID 1795	SA-420.1	Contig134 (31220-31474 p)	50	Identities = 27/90 (30%), Positives = 49/90 (54%), Gaps = 7/90 (7%) pir T35570 hypothetical protein SC6G4.19c SC6G4.19c - Streptomyces coelicolor emb CAA20397.1 (AL031317) SC6G4.19c, unknown, len: 190 aa; contains Pro-Ser- rich domain at N-terminus [Streptomyces coelicolor A3(2)] Length = 190
SeqID 1796	SA-421.1	Contig134 (31045-31359 m)	No Hits found	
SeqID 1797	SA-422.1	Contig134 (31017-31256 p)	No Hits found	
SeqID 1798	SA-423.1	Contig134 (30787-31020 p)	No Hits found	
SeqID 1799	SA-424.1	Contig134 (30080-30778 p)	52	Identities = 82/239 (34%), Positives = 125/239 (51%), Gaps = 15/239 (6%) pir T44434 3-oxoacyl-Hacyl-carrier-protein reductase (EC 1.1.1.100) [imported] - Moritella marina db JBA485256.1 (AB021978) 3-oxoacyl-Hacyl carrier protein reductase homolog [Moritella marina] Length = 244
SeqID 1800	SA-425.1	Contig134 (29851-30087 p)	No Hits found	
SeqID 1801	SA-426.1	Contig134 (29501-29761 p)	No Hits found	
SeqID 1802	SA-427.1	Contig134 (28815-29315 p)	33	Identities = 35/153 (22%), Positives = 64/153 (40%), Gaps = 5/153 (3%) pir T35964 hypothetical protein SC9C7.13c - Streptomyces coelicolor emb CAA22725.1 (AL035161) hypothetical protein SC9C7.13c [Streptomyces coelicolor A3(2)] Length = 179
SeqID 1803	SA-428.1	Contig134 (28120-28575 p)	44	Identities = 30/138 (21%), Positives = 66/138 (48%) db JBA05950.1 (AP001514) unknown conserved protein in others [Bacillus halodurans] Length = 482
SeqID 1804	SA-429.1	Contig134 (27217-28119 p)	55	Identities = 126/320 (39%), Positives = 180/320 (55%), Gaps = 18/320 (5%) db JBA05950.1 (AP001514) unknown conserved protein in others [Bacillus halodurans] Length = 482

SeqID 1805	SA-430.1	Contig134 (24924-27023 p)	44	Identities = 19/697 (28%), Positives = 322/697 (45%), Gaps = 58/697 (8%) dbj BA05949.1 (AP001514) unknown [Bacillus halodurans] Length = 1091
SeqID 1806	SA-431.1	Contig134 (23373-24857 p)	29	Identities = 7/1359 (19%), Positives = 148/359 (40%), Gaps = 49/359 (13%) sp Q45535 COTH_BACSU INNER SPORE COAT PROTEIN H. pil IE69605 spore coat protein (inner) coH - Bacillus subtilis. emb CA807793.1 (Z33767) ywH [Bacillus subtilis] emb CAB15623.1 (Z99122) spore coat protein (inner) [Bacillus subtilis] Length = 362
SeqID 1807	SA-432.1	Contig134 (22742-23419 p)	No Hits found	
SeqID 1808	SA-433.1	Contig134 (22079-22690 p)	No Hits found	
SeqID 1809	SA-434.2	Contig134 (20268-21631 p)	55	Identities = 162/436 (37%), Positives = 248/436 (56%), Gaps = 13/436 (2%) pil IC69596 branched-chain amino acid transporter braB - Bacillus subtilis gb AAC00400.1 (AF008220) branch-chain amino acid transporter [Bacillus subtilis] emb CAB14938.1 (Z99119) branched-chain amino acid transporter [Bacillus subtilis] Length = 445
SeqID 1810	SA-435.1	Contig134 (18101-20098 p)	72	Identities = 395/667 (59%), Positives = 501/667 (74%), Gaps = 12/667 (1%) sp P37468 SYM_BACSU METHIONYL-TRNA SYNTHETASE (METHIONINE-TRNA LIGASE) (METRS) pil IS6607 methionine-TRNA ligase (EC 6.1.1.10) metS - Bacillus subtilis dbj BA05273.1 (D26185) methionyl-TRNA synthetase [Bacillus subtilis] emb CAB11814.1 (Z99104) methionyl-TRNA synthetase [Bacillus subtilis] Length = 664
SeqID 1811	SA-436.1	Contig134 (17083-17958 m)	69	Identities = 163/282 (57%), Positives = 205/282 (71%), Gaps = 1/282 (0%) sp P45134 TEHB_HAEIN TELLURITE RESISTANCE PROTEIN TEHB HOMOLOG pil H64113 hemagglutinin hag1 homolog - Haemophilus influenzae (strain Rd KVV20) gb AAC22923.1 (U32807) tellurite resistance protein (tehB) [Haemophilus influenzae Rd] Length = 286

SeqID 1812	SA-437.1	Contig134 (16203-16925 p)	No Hits found	
SeqID 1813	SA-438.1	Contig134 (14677-15894 m)	19	Identities = 60/197 (30%), Positives = 83/197 (41%), Gaps = 12/197 (6%) sp P17334 PTCC_ECOLI PTS SYSTEM, CELLOBIOSE-SPECIFIC IIC COMPONENT (IIC-CEL) (CELLOBIOSE-PERMEASE IIC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, C COMPONENT) p A64933 celB protein - Escherichia coli (strain K-12) gb AAC74807.1 (AE000268) PEP-dependent phosphotransferase enzyme II for cellobiose, arbutin, and salicin [Escherichia coli K12] Length = 482
SeqID 1814	SA-439.1	Contig134 (13851-14636 m)	33	Identities = 53/240 (22%), Positives = 102/240 (42%), Gaps = 24/240 (10%) db JAB07204.1 (AP001518) unknown [Lactococcus lactis] Length = 307
SeqID 1815	SA-44.1	Contig137 (5697-6446 p)	No Hits found	Identities = 218/275 (79%), Positives = 246/275 (89%) sp P21998 EXOA_STRPN EXODEOXYRIBONUCLEASE p A32301 exodeoxyribonuclease (EC 3.1.11.1) exoA - Streptococcus pneumoniae gb AA26679.1 (J04234) exodeoxyribonuclease [Streptococcus pneumoniae] Length = 275
SeqID 1816	SA-441.1	Contig134 (12947-13774 m)	87	
SeqID 1817	SA-442.1	Contig134 (12550-12806 p)	58	Identities = 56/107 (52%), Positives = 74/107 (68%), Gaps = 1/107 (0%) db JAB07204.1 (AP001518) arsenate reductase [Bacillus halodurans] Length = 119
SeqID 1818	SA-443.1	Contig134 (12072-12549 p)	57	Identities = 75/156 (48%), Positives = 99/156 (63%), Gaps = 9/156 (5%) p A182390 methylated-DNA-protein-cysteine S-methyltransferase (EC 2.1.1.63) VCA1017 [similarity] - Vibrio cholerae (group O1 strain N16961) gb AAAF6913.1 (AE004427) methylated-DNA-protein-cysteine S-methyltransferase [Vibrio cholerae] Length = 157

SeqID 1819	SA-445.1	Contig134 (10835-12016 p)	42	<p>Identities = 102/313 (32%), Positives = 168/313 (53%), Gaps = 21/313 (6%) spIQ58424ISERA_METJIA D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) pir JA64427 phosphoglycerate dehydrogenase (EC 1.1.1.95) - Methanococcus jannaschii gb AAB99020.1 (U87544) phosphoglycerate dehydrogenase (serA) [Methanococcus jannaschii] Length = 524</p>
SeqID 1820	SA-446.1	Contig134 (10213-10773 p)	41	<p>Identities = 45/170 (26%), Positives = 78/170 (45%), Gaps = 13/170 (7%) pir G81269 probable acetyltransferase CJ1715 [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73701.1 (AL139079) putative acetyltransferase [Campylobacter jejuni] Length = 176</p>
SeqID 1821	SA-447.1	Contig134 (9065-10156 p)	67	<p>Identities = 169/363 (46%), Positives = 252/363 (69%), Gaps = 8/363 (2%) gb AAFI3453.1 AF204962.1 (AF204962) phosphoserine aminotransferase [Bacillus alcalophilus] Length = 361</p>
SeqID 1822	SA-448.1	Contig134 (8297-8932 m)	54	<p>Identities = 80/203 (39%), Positives = 116/203 (56%), Gaps = 7/203 (3%) ref XP_005810.1 CGI-32 protein [Homo sapiens] Length = 307</p>
SeqID 1823	SA-45.1	Contig137 (5361-5807 p)	No Hits found	<p>Identities = 141/287 (49%), Positives = 190/287 (66%), Gaps = 2/287 (0%) db JBAB03768.1 (AP001507) unknown conserved protein [Bacillus halodurans] Length = 289</p>
SeqID 1824	SA-450.1	Contig134 (7155-8027 p)	65	<p>Identities = 45/116 (38%), Positives = 62/116 (52%), Gaps = 8/116 (6%) db JBAB03765.1 (AP001507) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 116</p>
SeqID 1825	SA-451.1	Contig134 (6832-7158 p)	56	
SeqID 1826	SA-452.1	Contig134 (5938-6801 p)	41	<p>Identities = 82/219 (37%), Positives = 124/219 (56%), Gaps = 3/219 (1%) db JBAB03763.1 (AP001507) DNA polymerase III delta subunit [Bacillus halodurans] Length = 328</p>

SeqID 1827	SA-453.1	Contig134 (5283-5918 p)	59	<p>Identities = 112/210 (53%), Positives = 148/210 (70%), Gaps = 12/10 (0%) <i>dbj BA003761.1 </i> (AP001507) thymidylate kinase <i>[Bacillus halodurans]</i> Length = 210</p>
SeqID 1828	SA-454.1	Contig134 (4535-5194 p)	51	<p>Identities = 73/166 (43%), Positives = 116/166 (69%), Gaps = 2/166 (1%) <i>pir J172290</i> conserved hypothetical protein - <i>Thermotoga maritima</i> (strain MSB8) <i>gb AAD36216.1 </i> (AE001771_9 (AE001771) conserved hypothetical protein [Thermotoga maritima]) Length = 215</p>
SeqID 1829	SA-455.1	Contig134 (3806-4516 p)	75	<p>Identities = 135/233 (57%), Positives = 180/233 (76%) <i>pir J135757</i> probable branched chain amino acid transport ATP- binding protein - <i>Streptomyces coelicolor</i> <i>emb CAB52068.1 </i> (AL109732) putative branched chain amino acid transport ATP-binding protein [Streptomyces coelicolor A3(2)] Length = 238</p>
SeqID 1830	SA-456.1	Contig134 (3042-3806 p)	74	<p>Identities = 136/273 (49%), Positives = 190/273 (68%), Gaps = 21/273 (7%) <i>pir J172290</i> branched chain amino acid ABC transporter, ATP-binding protein - <i>Thermotoga maritima</i> (strain MSB8) <i>gb AAD36214.1 </i> (AE001771_7 (AE001771) branched chain amino acid ABC transporter, ATP-binding protein [Thermotoga maritima]) Length = 284</p>
SeqID 1831	SA-457.1	Contig134 (2088-3041 p)	60	<p>Identities = 121/343 (35%), Positives = 195/343 (56%), Gaps = 36/343 (10%) <i>pir J172290</i> branched chain amino acid ABC transporter, permease protein - <i>Thermotoga maritima</i> (strain MSB8) <i>gb AAD36213.1 </i> (AE001771_6 (AE001771) branched chain amino acid ABC transporter, permease protein [Thermotoga maritima]) Length = 359</p>

SeqID 1832	SA-468.2	Contig134 (1216-2085 p)	64	Identities = 140/295 (47%), Positives = 200/295 (67%), Gaps = 7/295 (2%) pir D72290 branched chain amino acid ABC transporter, perimease protein - Thermotoga maritima (strain MSB8) gb AAD36212.1 AE001771_5 (AE001771) branched chain amino acid ABC transporter, perimease protein [Thermotoga maritima] Length = 299
SeqID 1833	SA-46.1	Contig137 (4933-5361 p)	No Hits found	Identities = 114/360 (31%), Positives = 182/360 (49%), Gaps = 27/360 (7%) pir C72290 branched chain amino acid ABC transporter, periplasmic amino acid-binding protein - Thermotoga maritima (strain MSB8) gb AAD36211.1 AE001771_4 (AE001771) branched chain amino acid ABC transporter, periplasmic amino acid-binding protein [Thermotoga maritima] Length = 370
SeqID 1834	SA-460.2	Contig134 (1-1110 p)	49	Identities = 30/102 (29%), Positives = 60/102 (58%) gb AAD05186.1 AF110185 unknown [Burkholderia pseudomallei] Length = 163
SeqID 1835	SA-462.1	Contig135 (65101-65484 m)	40	Identities = 224/324 (69%), Positives = 276/324 (85%), Gaps = 1/324 (0%) gb AAAF98271.1 AF197933_1 (AF197933) beta-ketoacyl-ACP synthase III [Streptococcus pneumoniae] Length = 324
SeqID 1836	SA-463.1	Contig135 (64130-65101 m)	83	Identities = 64/74 (86%), Positives = 67/74 (90%) gb AAAF98272.1 AF197933_2 (AF197933) acyl carrier protein [Streptococcus pneumoniae] Length = 74
SeqID 1837	SA-464.1	Contig135 (63848-64072 m)	71	Identities = 257/318 (80%), Positives = 277/318 (86%), Gaps = 1/318 (0%) gb AAAF98273.1 AF197933_3 (AF197933) trans-2-enoyl-ACP reductase II [Streptococcus pneumoniae] Length = 324
SeqID 1838	SA-465.1	Contig135 (62734-63693 m)	85	

SeqID 1839	SA-466.1	Contig135 (61788-62714 m)	77	<p>Identities = 204/306 (66%), Positives = 242/306 (78%), Gaps = 1/306 (0%) gb AAAF98274.1 AF197933.4 (AF197933) malonyl-CoA:ACP transacylase, MCAT [Streptococcus pneumoniae] Length = 306</p>
SeqID 1840	SA-467.1	Contig135 (61045-61779 m)	84	<p>Identities = 184/243 (75%), Positives = 212/243 (86%) gb AAAF98275.1 AF197933.5 (AF197933) beta-ketacyl-A:ACP reductase [Streptococcus pneumoniae] Length = 243</p>
SeqID 1841	SA-468.1	Contig135 (59797-61029 m)	90	<p>Identities = 340/410 (82%), Positives = 375/410 (90%) gb AAAF98276.1 AF197933.6 (AF197933) beta-ketacyl-A:ACP synthase II [Streptococcus pneumoniae] Length = 411</p>
SeqID 1842	SA-469.1	Contig135 (59295-59795 m)	58	<p>Identities = 103/169 (60%), Positives = 127/169 (74%), Gaps = 11/169 (6%) gb AAAF98277.1 AF197933.7 (AF197933) biotin carboxyl carrier protein [Streptococcus pneumoniae] Length = 161</p>
SeqID 1843	SA-47.1	Contig137 (2969-4462 p)	73	<p>Identities = 278/497 (55%), Positives = 367/497 (72%), Gaps = 1/497 (0%) p J JH0206 hypothetical 57.4K protein - Enterococcus faecalis plasmid pAM-beta-1 gb AAAB94754.1 (AF039139) replication protein E [Cloning vector pL252] gb AAAB96788.1 (AF041239) replication protein E [Cloning vector pL253] gb AAC38603.1 (AF007787) RepE [Enterococcus faecalis] Length = 496</p>
SeqID 1844	SA-470.1	Contig135 (58876-59288 m)	91	<p>Identities = 130/140 (92%), Positives = 135/140 (95%) gb AAAF98278.1 AF197933.8 (AF197933) beta-hydroxyacyl-A:ACP dehydratase [Streptococcus pneumoniae] Length = 140</p>
SeqID 1845	SA-471.1	Contig135 (57465-58838 m)	85	<p>Identities = 361/451 (80%), Positives = 405/451 (89%) gb AAAF98279.1 AF197933.9 (AF197933) acetyl-CoA carboxylase biotin carboxylase subunit [Streptococcus pneumoniae] Length = 455</p>

SeqID 1846	SA-472.1	Contig135 (56584-57459 m)	83	<p>Identities = 221/285 (77%), Positives = 248/285 (86%), Gaps = 1/285 (0%) gblAAAF98280.1(AF-97933_10 (AF197933) acetyl-CoA carboxylase beta subunit [Streptococcus pneumoniae] Length = 288</p>
SeqID 1847	SA-473.1	Contig135 (55818-56591 m)	83	<p>Identities = 186/254 (73%), Positives = 222/254 (87%) gblAAAF98281.1(AF197933_11 (AF197933) acetyl-CoA carboxylase alpha subunit [Streptococcus pneumoniae] Length = 255</p>
SeqID 1848	SA-474.1	Contig135 (54716-55264 m)	45	<p>Identities = 76/142 (53%), Positives = 99/142 (69%) dbj BAA88824.1 (AB016077) sakacin A production response regulator [Streptococcus mutans] Length = 149</p>
SeqID 1849	SA-475.1	Contig135 (53393-54670 p)	74	<p>Identities = 262/425 (61%), Positives = 322/425 (75%), Gaps = 1/425 (0%) sblp P37464 SYS_BACSU SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) pfl S86043 serine--tRNA ligase (EC 6.1.1.11) - Bacillus subtilis dbj BAA05249.1 (D26185) seryl-tRNA synthetase [Bacillus subtilis] emb CAB11789.1 (Z99104) seryl-tRNA synthetase [Bacillus subtilis] Length = 425</p>
SeqID 1850	SA-477.1	Contig135 (52035-53102 m)	40	<p>Identities = 72/330 (21%), Positives = 143/330 (42%), Gaps = 32/330 (9%) emb CAA07406.1 (AJ006986) transmembrane protein [Streptococcus pneumoniae] Length = 332</p>
SeqID 1851	SA-478.1	Contig135 (51635-51997 p)	75	<p>Identities = 88/112 (78%), Positives = 96/112 (85%) gblAAD46488.1(AF130465_4 (AF130465) unknown [Streptococcus salivarius] Length = 124</p>
SeqID 1852	SA-48.1	Contig137 (2759-2871 m)	No Hits found	Identities = 247/303 (81%), Positives = 276/303 (90%) gblAAD46487.1(AF130465_3 (AF130465) mannose-specific phosphotransferase system component IID [Streptococcus salivarius] Length = 303
SeqID 1853	SA-480.1	Contig135 (50605-51516 p)	90	
SeqID 1854	SA-481.1	Contig135 (49778-50590 p)	84	<p>Identities = 209/271 (77%), Positives = 233/271 (85%), Gaps = 1/271 (0%) gblAAD46486.1(AF130465_2 (AF130465) mannose-specific phosphotransferase system component IIC [Streptococcus salivarius] Length = 271</p>

SeqID 1855	SA-483.1	Contig135 (48735-49745 p)	89	Identities = 287/336 (85%), Positives = 306/336 (90%), Gaps = 6/336 (1%) gb AA046485.1 AF130465_1 (AF130465) mannose-specific phosphotransferase system component IAB [Streptococcus salivarius] Length = 330
SeqID 1856	SA-484.1	Contig135 (47620-48432 p)	50	Identities = 89/267 (33%), Positives = 139/267 (51%), Gaps = 3/267 (1%) dbj BAB06825.1 (AP001517) unknown conserved protein [Bacillus halodurans] Length = 269
SeqID 1857	SA-485.1	Contig135 (46947-47531 m)	No Hits found	
SeqID 1858	SA-486.1	Contig135 (46246-46773 m)	44	Identities = 52/189 (27%), Positives = 92/189 (48%), Gaps = 12/189 (6%) pir C71375 conserved hypothetical integral membrane protein TP0333 - syphilis spirochete gb AAC65028.1 (AE001188) conserved hypothetical integral membrane protein [Treponema pallidum] Length = 203
SeqID 1859	SA-487.1	Contig135 (45206-45931 p)	No Hits found	
SeqID 1860	SA-488.1	Contig135 (44722-46143 m)	58	Identities = 193/471 (40%), Positives = 286/471 (59%), Gaps = 42/471 (8%) pir B62096 conserved hypothetical protein VC2278 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95422.1 (AE004299) conserved hypothetical protein [Vibrio cholerae] Length = 430
SeqID 1861	SA-489.1	Contig135 (44130-44573 m)	53	Identities = 68/149 (45%), Positives = 101/149 (67%), Gaps = 1/149 (0%) dbj BAB04264.1 (AP001508) unknown conserved protein [Bacillus halodurans] Length = 157
SeqID 1862	SA-492	Contig137 (2519-2611 p)	No Hits found	
SeqID 1863	SA-490.1	Contig135 (43616-44137 m)	49	Identities = 56/163 (34%), Positives = 94/163 (57%), Gaps = 1/163 (0%) pir D72360 conserved hypothetical protein - Thermococcus maritima (strain MSBB) gb AAD35662.1 AE001732.7 (AE001732) conserved hypothetical protein [Thermococcus maritima] Length = 179

SeqID 1864	SA-491.1	Contig135 (42300-43607 m)	40	Identities = 108/324 (33%), Positives = 178/324 (54%), Gaps = 33/324 (10%) sp Q02115 LYTR_BACSU MEMBRANE-BOUND PROTEIN LYTR. pir A47679 lyt divergen expression attenuator Lytr - Bacillus subtilis gb AA22578.1 (M87645) membrane bound protein [Bacillus subtilis] emb CAB15582.1 (Z99122) membrane-bound protein [Bacillus subtilis] Length = 306
SeqID 1865	SA-493.1	Contig135 (41940-42236 p)	No Hits found	Identities = 74/137 (54%), Positives = 95/137 (69%), Gaps = 2/137 (1%) db BAC04908.1 (AP001511) Hit-like protein involved in cell-cycle regulation [Bacillus halodurans] Length = 142
SeqID 1866	SA-494.1	Contig135 (41524-41943 p)	65	
SeqID 1867	SA-495.1	Contig135 (40685-41272 m)	No Hits found	Identities = 381/652 (58%), Positives = 485/652 (73%), Gaps = 19/652 (2%) sp O34580 PCRA_BACSU ATP-DEPENDENT DNA HELICASE PCRA. pir E69794 ATP-dependent DNA helicase homolog yerF - Bacillus subtilis emb CAA75552.1 (Y15254) PcrA protein [Bacillus subtilis] emb CAB12481.1 (Z99107) similar to ATP-dependent DNA helicase [Bacillus subtilis] Length = 739
SeqID 1869	SA-498.1	Contig135 (37777-38163 p)	53	Identities = 61/87 (70%), Positives = 71/87 (81%) gb AAA88579.1 (M14339) unknown [Streptococcus pneumoniae] Length = 93
SeqID 1870	SA-499.1	Contig135 (36427-37644 p)	62	Identities = 208/423 (49%), Positives = 293/423 (69%), Gaps = 11/423 (2%) sp P41008 PYRP_BACCL URACIL PERMEASE (URACIL TRANSPORTER) pir S38893 uracil transport protein - Bacillus caldolyticus emb CAA53697.1 (X76083) uracil permease [Bacillus caldolyticus] Length = 432
SeqID 1871	SA-5.1	Contig137 (39630-39841 p)	No Hits found	
SeqID 1872	SA-50.1	Contig137 (2617-2736 p)	No Hits found	

SeqID 1873	SA-500.1	Contig135 (34376-35722 m)	69	Identities = 256/443 (57%), Positives = 333/443 (74%), Gaps = 4/443 (0%) spjP44917Y883_HAEN HYPOTHETICAL PROTEIN HI0883 pirJH64099 probable amino acid transport protein HI0883 sodium-dependent - Haemophilus influenzae (strain Rd KW20) gb AAC22541.1 (U32770) amino acid carrier protein, putative [Haemophilus influenzae Rd] Length = 456
SeqID 1874	SA-501.1	Contig135 (33077-34312 m)	43	Identities = 118/282 (41%), Positives = 181/282 (63%) spjP46348YEAB_BACSU HYPOTHETICAL 31.8 KD PROTEIN IN GABP-GUAA INTERGENIC REGION (ORFX) pirJH69791 cation efflux system membrane protein homolog yeaB - Bacillus subtilis gb AA662307.1 (U51115) YeaB [Bacillus subtilis] emb CAB12451.1 (Z99107) alternate gene name: ydxT~similar to cation efflux system membrane protein [Bacillus subtilis] Length = 290
SeqID 1875	SA-502.1	Contig135 (32528-32918 m)	49	Identities = 34/110 (30%), Positives = 67/110 (60%), Gaps = 1/110 (0%) pirJH71191 hypothetical protein PH1801 - Pyrococcus horikoshii dbj BAA30920.1 (AP000007) 109aa long hypothetical protein [Pyrococcus horikoshii] Length = 109
SeqID 1876	SA-503.1	Contig135 (31850-32545 m)	53	Identities = 80/226 (35%), Positives = 136/226 (59%), Gaps = 1/226 (0%) pirJH69983 conserved hypothetical protein ysbB - Bacillus subtilis emb CAA98613.1 (Z75208) hypothetical protein [Bacillus subtilis] emb CAB14850.1 (Z39118) similar to hypothetical proteins [Bacillus subtilis] Length = 231
SeqID 1877	SA-504.1	Contig135 (31153-31782 m)	42	Identities = 44/194 (22%), Positives = 90/194 (45%), Gaps = 13/194 (6%) emb CAA76857.1 (V17797) hypothetical protein [Enterococcus faecalis] Length = 247
SeqID 1878	SA-505.1	Contig135 (30605-30751 p)	No Hits found	
SeqID 1879	SA-506.1	Contig135 (30121-30657 m)	No Hits found	
SeqID 1880	SA-507.1	Contig135 (29390-29749 m)	No Hits found	

SeqID 1881	SA-508.2	Contig135 (28209-28997 m)	53	Identities = 124/246 (50%), Positives = 161/246 (65%), Gaps = 22/246 (9%) pir[C28551] hypothetical protein 3 - Streptococcus mutans (strain GS-5) (fragment) gb AA88865.1 (M18954) unknown protein [Streptococcus mutans] Length = 228
SeqID 1882	SA-509.2	Contig135 (73687-74551 p)	66	Identities = 150/285 (52%), Positives = 198/285 (68%), Gaps = 5/285 (1%) gb AAK04462.1 AE006273.8 (AE006273) pseudouridine synthase [Lactococcus lactis subsp. lactis] Length = 293
SeqID 1883	SA-511.1	Contig137 (2184-2513 p)	No Hits found	
SeqID 1884	SA-510.1	Contig135 (72831-73670 p)	61	Identities = 120/267 (44%), Positives = 174/267 (64%), Gaps = 3/267 (1%) sp O31612 JBN_BACSU HYPOTHETICAL 30.0 KDA PROTEIN IN MECA-TENA INTERGENIC REGION pir F69844 conserved hypothetical protein yj6N - Bacillus subtilis emb CAB13018.1 (Z99110) similar to hypothetical proteins [Bacillus subtilis] Length = 266
SeqID 1885	SA-511.1	Contig135 (72188-72859 p)	69	Identities = 115/208 (55%), Positives = 159/208 (76%), Gaps = 3/208 (1%) db p BA005668.1 (AP001516) GTP pyrophosphokinase [Bacillus halodurans] Length = 211
SeqID 1886	SA-512.1	Contig135 (71505-72078 m)	46	Identities = 63/184 (34%), Positives = 99/184 (53%), Gaps = 10/184 (5%) pir C69844 hypothetical protein yj6K - Bacillus subtilis emb CAB13015.1 (Z99110) yj6K [Bacillus subtilis] Length = 190

SeqID 1887	SA-513.1	Contig135 (70355-71329 m)	69	<p>Identities = 166/319 (52%), Positives = 231/319 (72%), Gaps = 4/319 (1%) <i>slpP1413KPRS_BACSU RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE) (PRPP SYNTHETASE)</i> <i>prlJKBRS ribose-phosphate pyrophosphokinase (EC 2.7.6.1) prs - Bacillus subtilis</i> <i>pdbJDKRJB Chain B, Crystal Structures Of Bacillus Subtilis Phosphoribosylpyrophosphate Synthetase; Molecular Basis Of Allosteric Inhibition And Activation. pdbJDKRJA Chain A, Crystal Structures Of Bacillus Subtilis Phosphoribosylpyrophosphate Synthetase; Molecular Basis Of Allosteric Inhibition And Activation. pdbJDKRJB Chain B, Crystal Structures Of Bacillus Subtilis Phosphoribosylpyrophosphate Synthetase; Molecular Basis Of Allosteric Inhibition And Activation. pdbJDKRJA Chain A, Crystal Structures Of Bacillus Subtilis Phosphoribosylpyrophosphate Synthetase; Molecular Basis Of Allosteric Inhibition And Activation. embICAA34523.1] (X'16518) PRPP synthetase (AA</i></p>
SeqID 1888	SA-514.1	Contig135 (69920-70354 m)	55	<p>Identities = 63/118 (53%), Positives = 81/118 (68%), Gaps = 1/118 (0%) <i>gblAAG01802.1(AF276772_1 (AF276772) cysteine desulfurase Nifs [Methanosarcina thermophila]</i> Length = 404</p>
SeqID 1889	SA-515.1	Contig135 (69318-69647 m)	No Hits found	
SeqID 1890	SA-517.1	Contig135 (67303-68555 p)	69	<p>Identities = 223/448 (49%), Positives = 313/448 (69%) <i>slpP94417AK3_BACSU PROBABLE ASPARTOKINASE (ASPARTATE KINASE) <i>prlJAG9763 homoserine dehydrogenase homolog ycm - Bacillus subtilis</i> <i>djbJBA009011.1 (D50453) homologue of aspartokinase 2 alpha and beta subunits LysC of B. subtilis [Bacillus subtilis]</i> <i>embICAB12187.1 (Z99106) similar to homoserine dehydrogenase [Bacillus subtilis]</i> Length = 454</i></p>

SeqID 1891	SA-518.1	Contig135 (66559-67209 m)	42	<p>Identities = 59/190 (31%), Positives = 93/190 (48%), Gaps = 10/190 (5%) <i>gbljAB2498</i> CbbY family protein-VCA0102 [imported] - <i>Vibrio cholerae</i> (group O1 strain N16981) <i>gbljAAF90016.1</i> [AC004353] CbbY family protein [<i>Vibrio cholerae</i>] Length = 219</p>
SeqID 1892	SA-519.3	Contig135 (65631-66422 m)	64	<p>Identities = 139/248 (56%), Positives = 185/248 (74%) <i>dbj BAB16033.1</i> [AB030809] <i>Pseudomonas putida</i> enoyl-CoA hydratase II homologue [<i>Streptococcus pyogenes</i>] Length = 248</p>
SeqID 1893	SA-52.1	Contig137 (1679-2173 p)	No Hits found	
SeqID 1894	SA-520.2	Contig116 (395-688 m)	42	<p>Identities = 24/86 (27%), Positives = 43/86 (49%), Gaps = 6/86 (6%) <i>gbljAAD33114.1</i> [AF094574.4] (AF094574) negative regulator of translation [<i>Haemophilus influenzae</i>] Length = 98</p>
SeqID 1895	SA-523.2	Contig116 (1354-4734 m)	73	<p>Identities = 767/1103 (69%), Positives = 836/1103 (75%), Gaps = 58/1103 (5%) <i>gbljAAD39085.1</i> [AF091393.1] (AF091393) surface protein R28 [<i>Streptococcus pyogenes</i>] Length = 1260</p>
SeqID 1896	SA-524.1	Contig116 (4977-6170 p)	45	<p>Identities = 187/187 (100%), Positives = 187/187 (100%) <i>gbljAAG09971.1</i> [AF248037.6] (AF248037) unknown [<i>Streptococcus agalactiae</i>] Length = 189</p>
SeqID 1897	SA-528.1	Contig116 (6365-6889 m)	97	<p>Identities = 174/174 (100%), Positives = 174/174 (100%) <i>gbljAAG09969.1</i> [AF248037.4] (AF248037) unknown [<i>Streptococcus agalactiae</i>] Length = 174</p>
SeqID 1898	SA-527.2	Contig116 (7021-7599 p)	90	<p>Identities = 177/198 (89%), Positives = 180/198 (90%), Gaps = 11/198 (5%) <i>gbljAAG09968.1</i> [AF248037.3] (AF248037) cation efflux system protein [<i>Streptococcus agalactiae</i>] Length = 287</p>
SeqID 1899	SA-528.2	Contig116 (7971-8354 p)	92	<p>Identities = 125/128 (97%), Positives = 128/128 (99%) <i>gbljAAG09967.1</i> [AF248037.2] (AF248037) aldose reductase [<i>Streptococcus agalactiae</i>] Length = 280</p>
SeqID 1900	SA-529.1	Contig116 (8355-8825 p)	96	<p>Identities = 152/156 (97%), Positives = 152/156 (97%), Gaps = 4/156 (2%) <i>gbljAAG09967.1</i> [AF248037.2] (AF248037) aldose reductase [<i>Streptococcus agalactiae</i>] Length = 280</p>

SeqID 1901	SA-53.1	Contig137 (1454-1842 p)	No Hits found	
SeqID 1902	SA-530.1	Contig116 (8935-9390 p)	58	Identities = 90/90 (100%), Positives = 90/90 (100%) gb AA09956.1 AF248037_1 (AF248037) alcohol dehydrogenase [Streptococcus agalactiae] Length = 96
SeqID 1903	SA-531.1	Contig116 (9315-9971 p)	65	Identities = 114/231 (49%), Positives = 161/231 (69%), Gaps = 6/231 (2%) gb AA020655.1 (AE005134) alcohol dehydrogenase; Adh2 [Halobacterium sp. NRC-1] Length = 347
SeqID 1904	SA-532.1	Contig116 (9987-10376 p)	64	Identities = 53/123 (43%), Positives = 84/123 (68%) pir B69970 transcription regulator MerR family homolog yraB - Bacillus subtilis emb CA63468.1 (X92868) mercuric resistance operon regulatory protein [Bacillus subtilis] emb CAB14842.1 (Z99117) similar to transcriptional regulator (MerR family) [Bacillus subtilis] Length = 140
SeqID 1905	SA-533.1	Contig116 (10386-10781 p)	54	Identities = 55/131 (41%), Positives = 73/131 (54%), Gaps = 8/131 (6%) pir B72308 hypothetical protein - Thermotoga maritima (strain MS88) gb AAD36075.1 AE001782.2 (AE001782) hypothetical protein [Thermotoga maritima] Length = 135
SeqID 1906	SA-534.1	Contig116 (10905-11122 p)	48	Identities = 33/93 (35%), Positives = 59/93 (62%), Gaps = 1/93 (1%) pir T29425 4-carboxymuconolactone decarboxylase homolog - Streptomyces coelicolor emb CAA20070.1 (AL031155) 3-oxoadipate enol-lactone hydrolase/4- carboxymuconolactone decarboxylase [Streptomyces coelicolor A3(2)] Length = 449
SeqID 1907	SA-535.1	Contig116 (11209-11493 p)	No Hits found	

SeqID 1908	SA-536.1	Contig116 (11732-12223 p)	42	<p>Identities = 39/149 (26%), Positives = 71/149 (47%), Gaps = 4/149 (2%) pirJH63035 probable transcription regulator PA4878 [imported] - Pseudomonas aeruginosa (strain PAO1) gbJAG08283.1 AE004901.5 (AE004901) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 270</p>
SeqID 1909	SA-537.1	Contig116 (12267-12656 m)	52	<p>Identities = 42/130 (32%), Positives = 71/130 (54%), Gaps = 3/130 (2%) pirJG69153 conserved hypothetical protein MTH413 - Methanobacterium thermoautotrophicum (strain Delta H) gbJAA84919.1 (AE000825) conserved protein [Methanobacterium thermoautotrophicum] Length = 130</p>
SeqID 1910	SA-538.1	Contig116 (12669-15636 m)	22	<p>Identities = 141/566 (24%), Positives = 242/566 (41%), Gaps = 52/566 (9%) pirJIT31094 surface antigen BspA - Bacteroides forsythus gbJAA82625.1 (AF054892) surface antigen BspA [Bacteroides forsythus] Length = 1081</p>
SeqID 1911	SA-54.1	Contig137 (321-1361 p)	53	<p>Identities = 102/413 (24%), Positives = 189/413 (45%), Gaps = 76/413 (18%) spiP55340 ECSB_BACSU PROTEIN ECSB pirJG69619 ABC transporter (membrane protein) ecsB - Bacillus subtilis embJCA61075.1 (X87807) hypothetical EcsB protein [Bacillus subtilis] embJCA474408.1 (Y14077) Hypothetical protein [Bacillus subtilis] embJCA812845.1 (Z99109) ABC transporter (membrane protein) [Bacillus subtilis] Length = 408</p>
SeqID 1912	SA-540.1	Contig116 (15899-18067 m)	79	<p>Identities = 475/727 (65%), Positives = 565/727 (80%), Gaps = 19/727 (2%) spiP78027 RIR1_MYCPN RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (RIBONUCLEOTIDE REDUCTASE) pirIS73938 ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain nrDE - Mycoplasma pneumoniae (strain ATCC 29342) gbJAA96160.1 (AE000050) ribonucleoside-diphosphate reductase alpha chain-MPN324(new), 513(Himmelmreich et al., 1996) [Mycoplasma pneumoniae] Length = 721</p>

SeqID 1913	SA-541.1	Contig116 (18069-18470 m)	76	<p>Identities = 76/127 (59%), Positives = 105/127 (81%), Gaps = 1/127 (0%) sp P47472 NRD1_MYCGE-NRDI PROTEIN p I D64225 hypothetical protein MG230 - Mycoplasma genitalium gb AAC71451.1 (U39702) nrd1 protein (nrd) [Mycoplasma genitalium] Length = 153</p>
SeqID 1914	SA-542.1	Contig116 (18483-19493 m)	87	<p>Identities = 259/335 (77%), Positives = 299/335 (88%) sp P75461 IR2_MYCPN RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE BETA CHAIN (RIBONUCLEOTIDE REDUCTASE) p I S73840 ribonucleotide reductase 2 - Mycoplasma pneumoniae strain ATCC 29342 gb AAB96162.1 (AE000050) ribonucleoside-diphosphate reductase beta chain [Mycoplasma pneumoniae] Length = 339</p>
SeqID 1915	SA-544.1	Contig116 (20046-20954 m)	56	<p>Identities = 105/309 (33%), Positives = 173/309 (55%), Gaps = 21/309 (6%) p I T00087 rhamnosyltransferase - Streptococcus mutans db JBAAC32090.1 (AB010970) rhamnosyltransferase [Streptococcus mutans] Length = 311</p>
SeqID 1916	SA-545.2	Contig116 (21204-21404 p)	No Hits found	
SeqID 1917	SA-546.1	Contig116 (24213-24722 p)	No Hits found	
SeqID 1918	SA-547.1	Contig116 (21164-24883 m)	53	<p>Identities = 46/1194 (38%), Positives = 666/1194 (55%), Gaps = 74/1194 (6%) gb AAB17762.1 (U56908) SCPB [Streptococcus agalactiae] Length = 1150</p>
SeqID 1919	SA-548.1	Contig116 (25055-25481 m)	60	<p>Identities = 65/143 (45%), Positives = 93/143 (64%), Gaps = 5/143 (3%) p I F83632 conserved hypothetical protein PA0115 [imported] - Pseudomonas aeruginosa (strain PAC1) gb AAG03505.1 (AE004449) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 150</p>
SeqID 1920	SA-549.1	Contig116 (25515-26279 m)	32	<p>Identities = 48/180 (26%), Positives = 84/180 (46%), Gaps = 4/180 (2%) p I F82497 uridine phosphorylase VCA0134 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF56047.1 (AE004354) uridine phosphorylase [Vibrio cholerae] Length = 243</p>

SeqID 1921	SA-55.1	Contig137 (2-319 p)	77	<p>Identities = 64/104 (61%), Positives = 82/104 (78%) sp P55339 ECOA_BACSU ABC-TYPE TRANSPORTER ATP-BINDING PROTEIN EC5A_prl F69619 ABC transporter (ATP-binding protein) ec5a - Bacillus subtilis emb CAA61074.1 (X87807) putative ATP-binding protein of ABC-type [Bacillus subtilis] emb CAA74409.1 (Y14077) Hypothetical protein [Bacillus subtilis] emb CAB12844.1 (Z99109) ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 247</p>
SeqID 1922	SA-550.1	Contig116 (26546-27901 m)	64	<p>Identities = 216/448 (48%), Positives = 297/448 (66%), Gaps = 4/448 (0%) prl F69808 RNA methyltransferase homolog yfjO - Bacillus subtilis emb CAB12631.1 (Z99108) similar to RNA methyltransferase [Bacillus subtilis] dbj BAA24300.1 (D78509) yfjO [Bacillus subtilis] Length = 466</p>
SeqID 1923	SA-551.1	Contig116 (28095-28776 p)	50	<p>Identities = 73/263 (27%), Positives = 140/263 (52%), Gaps = 9/263 (3%) dbj BAB04643.1 (AP001510) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 266</p>
SeqID 1924	SA-552.1	Contig116 (28860-29393 p)	68	<p>Identities = 96/175 (54%), Positives = 122/175 (68%) dbj BAB04659.1 (AP001510) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 175</p>
SeqID 1925	SA-554.1	Contig121 (35263-36249 p)	60	<p>Identities = 142/331 (42%), Positives = 204/331 (60%), Gaps = 2/331 (0%) gb AAFF61315.1 (U96166) unknown [Streptococcus cristatus] Length = 442</p>
SeqID 1926	SA-555.1	Contig121 (33762-35270 p)	19	<p>Identities = 66/194 (34%), Positives = 98/194 (50%), Gaps = 9/194 (4%) dbj BAA94320.1 (AB033763) hypothetical protein [Staphylococcus aureus] Length = 255</p>

SeqID 1927	SA-557.1	Contig121 (31361-33748 p)	63	<p>Identities = 336/794 (42%), Positives = 507/794 (63%), Gaps = 29/794 (3%)</p> <p>sp P28366 SECA-BAGSU-PROTEIN TRANSLOCASE SECA SUBUNIT pr JQ0647 preprotein translocase secA - Bacillus subtilis db BA001122.1 (D10279) secA protein [Bacillus subtilis] gb AAC44957.1 (U56901) involved in protein export [Bacillus subtilis] emb CAB15547.1 (Z95122) translocase binding subunit (ATPase) [Bacillus subtilis]</p> <p>Length = 841</p>
SeqID 1928	SA-558.1	Contig121 (30364-31374 p)	No Hits found	
SeqID 1929	SA-559.1	Contig121 (28826-30385 p)	No Hits found	
SeqID 1930	SA-56.1	Contig131 (56872-57270 p)	No Hits found	
SeqID 1931	SA-560.1	Contig121 (27275-28819 p)	No Hits found	
SeqID 1932	SA-561.1	Contig121 (26046-27275 p)	50	<p>Identities = 105/422 (24%), Positives = 213/422 (49%), Gaps = 49/422 (11%)</p> <p>pr JC82917 preprotein translocase UUU250 [imported] - Ureaplasma urealyticum gb AAF30659.1 AE002122.28 (AE002122) preprotein translocase [Ureaplasma urealyticum]</p> <p>Length = 471</p>
SeqID 1933	SA-562.1	Contig121 (24726-25922 p)	10	<p>Identities = 30/78 (38%), Positives = 42/78 (53%)</p> <p>gb AAF61315.1 (U96166) unknown [Streptococcus cristatus]</p> <p>Length = 442</p>
SeqID 1934	SA-563.1	Contig121 (23780-24665 p)	43	<p>Identities = 88/228 (38%), Positives = 136/228 (59%), Gaps = 10/228 (4%)</p> <p>gb AAC44016.1 (U40830) Epsi [Streptococcus thermophilus] pr J2209356K epsi gene [Streptococcus thermophilus]</p> <p>Length = 324</p>
SeqID 1935	SA-565.1	Contig121 (22613-23797 p)	35	<p>Identities = 91/256 (35%), Positives = 146/256 (56%), Gaps = 8/256 (3%)</p> <p>gb AAF28363.1 AF224467.2 (AF224467) putative glycosyl transferase [Haemophilus ducreyi]</p> <p>Length = 269</p>
SeqID 1936	SA-566.1	Contig121 (21382-22623 p)	37	<p>Identities = 103/259 (39%), Positives = 156/259 (59%), Gaps = 3/259 (1%)</p> <p>gb AAF28363.1 AF224467.2 (AF224467) putative glycosyl transferase [Haemophilus ducreyi]</p> <p>Length = 269</p>

SeqID 1937	SA-567.1	Contig121 (20180-21385 p)	38	Identities = 94/263 (35%), Positives = 158/263 (59%), Gaps = 4/263 (1%) gb AAAF28363.1 AF-224467_2 (AF-224467) putative glycosyl transferase [Haemophilus ducreyi] Length = 269
SeqID 1938	SA-568.1	Contig121 (19164-20171 p)	33	Identities = 68/286 (23%), Positives = 122/286 (41%), Gaps = 18/286 (6%) sp P37749 YFEG_ECOLI_HYPOTHETICAL_37.8_KD PROTEIN IN GND-RFC INTERGENIC REGION (GALF TRANSFERASE) pir J96845 probable nucleotide sugar synthetase - Escherichia coli gb AAB88405.1 (U09876) putative GalF transferase [Escherichia coli] gb AAC31634.1 (U03041) nucleotide sugar synthetase [Escherichia coli] db JBA116876.1 (D90841) ORF_ID:0351 10~similar to [SwissProt Accession Number P37749] [Escherichia coli] db JBA116888.1 (D90842) ORF_ID:0351 10; similar to [SwissProt Accession Number P37749] [Escherichia coli] gb AAC75095.1 (AE000294) putative GalF transferase [Escherichia coli K12] Length = 330
SeqID 1939	SA-569.1	Contig121 (16766-18616 m)	42	Identities = 180/657 (27%), Positives = 283/657 (42%), Gaps = 31/657 (4%) emb CAB65343.1 (AJ007010) liver stage antigen-3 [Plasmodium falciparum] Length = 1766
SeqID 1940	SA-57.1	Contig131 (56480-56863 p)	No Hits found	
SeqID 1941	SA-570.1	Contig121 (15272-15448 m)	No Hits found	
SeqID 1942	SA-571.1	Contig121 (14901-18633 p)	61	Identities = 668/1314 (50%), Positives = 812/1314 (60%), Gaps = 60/1314 (4%) db JBA167453.1 (AB029393) streptococcal hemagglutinin [Streptococcus gordonii] Length = 2178
SeqID 1943	SA-572.1	Contig121 (13022-14518 m)	59	Identities = 201/493 (40%), Positives = 302/493 (60%), Gaps = 5/493 (1%) pir JIS43609 rofa protein - Streptococcus pyogenes Length = 497

SeqID 1944	SA-573.1	Contig121 (10034-12925 p)	94	Identities = 579/667 (86%), Positives = 635/667 (94%), Gaps = 1/667 (0%) spQ34986 UVRB_STRPN EXONUCLEASE ABC SUBUNIT B pirJ442385 exonuclease ABC chain B - Streptococcus pneumoniae plasmid pSB470 gb AA27020.1 (M60215) yvs402 protein [Streptococcus pneumoniae] Length = 668
SeqID 1945	SA-574.1	Contig121 (10034-10873 p)	29	Identities = 58/190 (30%), Positives = 96/190 (50%), Gaps = 11/190 (5%) pirJ134651 probable transmembrane protein - Streptomyces coelicolor emb CAA22372.1 (AL034448) putative transmembrane protein [Streptomyces coelicolor A3(2)] Length = 307
SeqID 1946	SA-575.1	Contig121 (7587-9770 m)	21	Identities = 103/195 (53%), Positives = 156/195 (79%), Gaps = 4/195 (2%) gb AAAF16724.1 (AF141644_1) (AF141644) putative integral membrane protein [Lactococcus lactis] Length = 191
SeqID 1947	SA-576.1	Contig121 (6947-7587 m)	77	Identities = 147/240 (61%), Positives = 192/240 (79%) refNP_069514.1 glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus] pirJH69334 glutamine transport protein glnQ - Archaeoglobus fulgidus gb AA89056.1 (AE001058) glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus] Length = 242
SeqID 1948	SA-577.1	Contig121 (6348-6707 m)	No Hits found	
SeqID 1949	SA-578.1	Contig121 (6098-6256 p)	No Hits found	
SeqID 1950	SA-579.1	Contig121 (4759-6072 p)	77	Identities = 287/435 (66%), Positives = 345/435 (79%), Gaps = 7/435 (1%) spP20964 OBG_BACSU SPOOB-ASSOCIATED GTP-BINDING PROTEIN pirJ32804 GTP-binding protein obg - Bacillus subtilis gb AA22505.1 (M24537) GTP-binding protein [Bacillus subtilis] emb CAB14752.1 (Z99118) GTPase activity [Bacillus subtilis] Length = 428

SeqID 1951	SA-581.1	Contig131 (55941-55345 p)	22	<p>Identities = 25/79 (31%), Positives = 31/79 (38%)</p> <p>spP04929jHRPX_PLALO HISTIDINE-RICH GLYCOPROTEIN PRECURSOR prj KGZQHL histidine-rich glycoprotein precursor Plasmodium lophurae emb CAA28598.1 (X01489) histidine-rich protein [Plasmodium lophurae] prj 1101401A protein, His rich [Plasmodium sp.] Length = 351</p>
SeqID 1952	SA-582.1	Contig121 (3151-4392 m)	73	<p>Identities = 24/71 (41%), Positives = 31/41 (75%)</p> <p>sp Q9X4A7 PEPS_STRTR AMINOPEPTIDASE PEPS gb AAD28348.1 AF102860.2 (AF102860) aminopeptidase Peps [Streptococcus thermophilus] Length = 413</p>
SeqID 1953	SA-583.1	Contig121 (2613-2852 m)	No Hits found	
SeqID 1954	SA-584.1	Contig121 (2539-3117 p)	34	<p>Identities = 41/152 (26%), Positives = 75/152 (48%), Gaps = 4/152 (2%) emb CAB88235.1 (AL353012) hypothetical serine- rich repeat protein [Schizosaccharomyces pombe] Length = 451</p>
SeqID 1955	SA-585.2	Contig121 (387-2429 p)	38	<p>Identities = 173/492 (35%), Positives = 270/492 (54%), Gaps = 38/492 (7%) gb AAK04264.1 AE006254_5 (AE006254) amidase [Lactococcus lactis subsp. lactis] Length = 499</p>
SeqID 1956	SA-586.2	Contig121 (3-302 p)	57	<p>Identities = 39/89 (43%), Positives = 57/89 (63%), Gaps = 4/89 (4%) dbj BAB06992.1 (AP001518) 16S pseudouridylylate synthase [Bacillus halodurans] Length = 238</p>
SeqID 1957	SA-589.2	Contig122 (32148-33029 m)	86	<p>Identities = 230/291 (79%), Positives = 257/291 (88%)</p> <p>sp Q07211 SCRK_STRMU FRUCTOKINASE dbj BAA02467.1 (D13175) fructokinase [Streptococcus mutans] Length = 293</p>
SeqID 1958	SA-59.1	Contig131 (55843-55980 m)	No Hits found	
SeqID 1959	SA-590.1	Contig122 (31083-32030 m)	82	<p>Identities = 232/312 (74%), Positives = 262/312 (83%)</p> <p>sp Q89935 IMANA_STRMU MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) dbj BAA0402.1 (D16594) Mannosephosphate isomerase [Streptococcus mutans] Length = 316</p>

SeqID 1960	SA-591.1	Contig122 (28446-30974 m)	75	<p>Identities = 503/843 (59%), Positives = 643/843 (75%), Gaps = 16/843 (4%) sp P47847 SECA USMO PREPROTEIN-TRANSLOCASE SECA SUBUNIT gp AA50286.1 (L32090) secA [Listeria monocytogenes] Length = 836</p>
SeqID 1961	SA-592.1	Contig122 (27313-28320 m)	54	<p>Identities = 122/348 (35%), Positives = 188/348 (53%), Gaps = 32/348 (9%) pf J81871 2-dehydro-3-deoxyphosphonate aldolase (EC 4.1.2.15) MMA2180 [imported] - Neisseria meningitidis (group A strain Z2491) emb CA85392.1 (AL182758) phospho-2-dehydro-3-deoxyphosphonate aldolase [Neisseria meningitidis] Length = 351</p>
SeqID 1962	SA-593.1	Contig122 (26929-27288 m)	73	<p>Identities = 61/120 (50%), Positives = 91/120 (75%), Gaps = 1/120 (0%) gp AA6322706.1 (AF276617) acyl carrier protein synthase, AcpS [Streptococcus pneumoniae] Length = 120</p>
SeqID 1963	SA-594.1	Contig122 (25632-26932 m)	72	<p>Identities = 227/366 (62%), Positives = 270/366 (73%) gp AAD51027.1 AF171873.1 (AF171873) alanine racemase [Streptococcus pneumoniae] Length = 367</p>
SeqID 1964	SA-597.1	Contig122 (24201-25739 m)	66	<p>Identities = 249/530 (46%), Positives = 341/530 (63%), Gaps = 18/530 (3%) gp AAB52378.1 (U31811) immunogenic secreted protein precursor [Streptococcus pyogenes] Length = 534</p>
SeqID 1965	SA-598.1	Contig122 (22106-24121 m)	84	<p>Identities = 483/671 (71%), Positives = 568/671 (83%) sp Q54900 REGG_STRPN ATP-DEPENDENT DNA HELICASE REGG pf J1016 helicase recG homolog - Streptococcus pneumoniae emb CAA90280.1 (Z49888) MmsA [Streptococcus pneumoniae] pf J2209420A mmsA gene [Streptococcus pneumoniae] Length = 671</p>
SeqID 1966	SA-599.1	Contig122 (20901-21821 m)	72	<p>Identities = 173/300 (57%), Positives = 224/300 (74%) db BAB07646.1 (AP001520) aryl-alcohol dehydrogenase [Bacillus halodurans] Length = 305</p>

SeqID 1967	SA-6.1	Contig137 (39066-39299 p) -----	42	Identities = 31/81 (38%), Positives = 43/81 (52%), Gaps = 18/81 (22%) sp P43813 DNLL-HAEN DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+]) pir D64182 DNA ligase (NAD+) (EC 6.5.1.2) - Haemophilus influenzae (strain Rd_KW20) gb AAC22753.1 (U32789) DNA ligase (lig) [Haemophilus influenzae Rd] Length = 679
SeqID 1968	SA-60.1	Contig131 (65778-66306 p)	31	Identities = 42/95 (44%), Positives = 56/95 (58%), Gaps = 4/95 (4%) ref XP_001738.1 megakaryocyte stimulating factor [Homo sapiens] Length = 1385
SeqID 1969	SA-600.1	Contig122 (19925-20803 m)	56	Identities = 114/279 (40%), Positives = 171/279 (60%), Gaps = 3/279 (1%) sp P28244 YDIB_ECOLI HYPOTHETICAL 31.2 KDA PROTEIN IN LPP-AROD INTERGENIC REGION pir D64927 probable shikimate 5-dehydrogenase (EC 1.1.1.25) ydib - Escherichia coli dbj BA15449.1 (D90811) Shikimate 5-dehydrogenase (EC 1.1.1.25) [Escherichia coli] gb AAC74762.1 (AE000264) putative oxidoreductase [Escherichia coli K12] Length = 288
SeqID 1970	SA-601.1	Contig122 (18928-19690 p)	64	Identities = 158/319 (49%), Positives = 214/319 (66%), Gaps = 4/319 (1%) dbj BAB05343.1 (AP001512) L-asparaginase [Bacillus halodurans] Length = 322
SeqID 1971	SA-602.1	Contig122 (17477-18659 m)	30	Identities = 99/281 (31%), Positives = 141/281 (49%), Gaps = 31/281 (11%) pir IC59862 conserved hypothetical protein ykRA - Bacillus subtilis emb CAB13328.1 (Z99111) similar to hypothetical proteins [Bacillus subtilis] gb AAC24929.1 (AF012285) unknown [Bacillus subtilis] Length = 257
SeqID 1972	SA-603.2	Contig122 (16969-17421 p)	55	Identities = 62/141 (43%), Positives = 93/141 (64%) dbj BAB06903.1 (AP001518) BH3184-unknown conserved protein [Bacillus halodurans] Length = 147

SeqID 1973	SA-604.2	Contig122 (15490-16701 m)	79	<p>Identities = 250/404 (61%), Positives = 328/404 (80%), Gaps = 1/404 (0%) sp P1348 YFBQ_HAEIN PROBABLE AMINOTRANSFERASE H0286 gb AAC21948.1 (U32714) aminotransferase [Haemophilus influenzae Rd] Length = 404</p>
SeqID 1974	SA-605.1	Contig122 (14579-15364 m)	62	<p>Identities = 129/257 (50%), Positives = 181/257 (70%), Gaps = 3/257 (1%) db JBA08181.1 (AP001515) transcriptional pleiotropic repressor [Bacillus halodurans] Length = 259</p>
SeqID 1975	SA-606.1	Contig122 (13964-14512 m)	69	<p>Identities = 101/183 (55%), Positives = 133/183 (72%) pir J070008 pyrazinamidase/nicotinamidase homolog yueJ - Bacillus subtilis emb CAB15164.1 (Z99120) similar to pyrazinamidase/nicotinamidase [Bacillus subtilis] Length = 183</p>
SeqID 1976	SA-607.1	Contig122 (12952-13917 p)	51	<p>Identities = 151/321 (47%), Positives = 196/321 (61%), Gaps = 36/321 (11%) pir J075610 probable 3-hydroxyacyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1) gb AAF12219.1 AE001862.45 (AE001862) 3-hydroxyacyl-CoA dehydrogenase, putative [Deinococcus radiodurans] Length = 347</p>
SeqID 1977	SA-608.1	Contig122 (12134-12646 m)	64	<p>Identities = 88/210 (41%), Positives = 141/210 (66%), Gaps = 3/210 (1%) pir J06969 conserved hypothetical protein yqzB - Bacillus subtilis emb CAB14454.1 (Z99116) similar to hypothetical proteins [Bacillus subtilis] emb CAB14467.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 212</p>
SeqID 1978	SA-609.1	Contig122 (11293-12123 m)	65	<p>Identities = 129/264 (47%), Positives = 186/264 (69%), Gaps = 1/264 (0%) db JBA05032.1 (AP001511) unknown conserved protein [Bacillus halodurans] Length = 270</p>
SeqID 1979	SA-611.1	Contig122 (6635-11280 m)	73	<p>Identities = 495/670 (56%), Positives = 648/670 (73%), Gaps = 4/670 (0%) sp P22983 PODK_CLOS PYRUVATE, PHOSPHATE DIKINASE (PYRUVATE, ORTHOPHOSPHATE DIKINASE) Length = 874</p>

SeqID 1980	SA-612.1	--Contig122(8195-8497 m)	61	<p>Identities = 42/96 (43%), Positives = 64/96 (65%) dbj BAB04384.1 AP001509 glutamyl-RNA (Gln) amidotransferase subunit C [Bacillus halodurans] Length = 96</p>
SeqID 1981	SA-613.1	Contig122 (6728-8195 m)	73	<p>Identities = 285/485 (58%), Positives = 365/485 (74%), Gaps = 2/485 (0%) sp Q06491 GATA_BACSU GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (GLU-ADT SUBUNIT A) pri B69795 glutamyl-RNA(Gln) amidotransferase (EC 2.6.-.-) chain A [validated] - Bacillus subtilis emb CAB12488.1 (Z99107) alternate gene name: yedB--similar to amidase [Bacillus subtilis] Length = 485</p>
SeqID 1982	SA-614.1	Contig122 (5287-6729 m)	74	<p>Identities = 309/476 (64%), Positives = 381/476 (74%), Gaps = 1/476 (0%) sp Q92X0 GATB_BACHD GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B (GLU-ADT SUBUNIT B) pri T44293 hypothetical protein yerN [imported] - Bacillus halodurans dbj BA75312.1 AB011836 similar to B subtilis yerN gene[87 identity] [Bacillus halodurans] dbj BAB04386.1 AP001509 glutamyl-RNA (Gln) amidotransferase subunit B [Bacillus halodurans] Length = 476</p>
SeqID 1983	SA-615.1	Contig122 (4243-6157 m)	54	<p>Identities = 102/292 (34%), Positives = 169/292 (56%), Gaps = 3/292 (1%) pri T30575 hypothetical protein - Bacillus megaterium (fragment) emb CAA04271.1 AJ000733) hypothetical protein [Bacillus megaterium] Length = 296</p>
SeqID 1984	SA-616.1	Contig122 (3599-4126 m)	42	<p>Identities = 52/153 (33%), Positives = 88/153 (56%) sp P54452 YOEK_BACSU HYPOTHETICAL 20.1 KD PROTEIN IN NUCB-AROD INTERGENIC REGION pri C68951 conserved hypothetical protein yoeG - Bacillus subtilis dbj BAA12443.1 (D84432) YoeG [Bacillus subtilis] emb CAB14510.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 172</p>

SeqID 1985	SA-617.1	Contig122 (2481-3599 m)	73	<p>Identities = 219/373 (58%), Positives = 280/373 (74%), Gaps = 8/373 (2%) spIP54453YQEH_BACSU HYPOTHETICAL 41.0 KD PROTEIN IN NUCB-AROD INTERGENIC REGION pir E69951 conserved hypothetical protein yqeH - Bacillus subtilis dbj BA12444.1 (D84432) YqeH [Bacillus subtilis] emb CAB14508.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 366</p>
SeqID 1986	SA-618.1	Contig122 (2071-2388 m)	56	<p>Identities = 49/97 (50%), Positives = 67/97 (68%), Gaps = 2/97 (2%) spIP54454YQEI_BACSU HYPOTHETICAL 10.8 KD PROTEIN IN AROD-COMER INTERGENIC REGION pir E69951 dihydrodipicolinate reductase homolog yqeI - Bacillus subtilis dbj BA12448.1 (D84432) YqeI [Bacillus subtilis] emb CAB14507.1 (Z99117) similar to dihydrodipicolinate reductase [Bacillus subtilis] Length = 96</p>
SeqID 1987	SA-620.1	Contig131 (55074-55907 m)	44	<p>Identities = 77/263 (29%), Positives = 126/263 (47%), Gaps = 34/263 (12%) gp AAC48867.1 (U40453) integrase [Streptococcus pyogenes phage T12] Length = 362</p>
SeqID 1988	SA-620.1	Contig122 (1309-1941 m)	59	<p>Identities = 85/187 (45%), Positives = 134/187 (71%) spIP54455INADD_BACSU PROBABLE NICOTINATE-NUCLEOTIDE ADENYLTRANSFERASE (DEAMIDO-NAD(+)-PYROPHOSPHORYLASE) (DEAMIDO-NAD(+)-DIPHOSPHORYLASE) (NICOTINATE MONONUCLEOTIDE ADENYLTRANSFERASE) (NAMIN ADENYLTRANSFERASE) pir F69951 conserved hypothetical protein yqeJ - Bacillus subtilis dbj BA12447.1 (D84432) YqeJ [Bacillus subtilis] emb CAB14506.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 189</p>

SeqID 1989	SA-621.1	Contig122 (725-1312 m)	55	<p>Identities = 79/180 (43%), Positives = 116/180 (63%) sp P54466 YOEK_BACSU HYPOTHETICAL 21.3 KD PROTEIN- IN ARD-COMER INTERGENIC REGION. pir IG89951 conserved hypothetical protein yoeK - Bacillus subtilis dbj BA112448.1 (D84432) yoeK [Bacillus subtilis] emb CAB14505.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] Length = 186</p>
SeqID 1990	SA-622.1	Contig122 (140-692 m)	42	<p>Identities = 46/175 (26%), Positives = 81/175 (46%), Gaps = 12/175 (6%) gb AAG19496.1 (AE005041) Vng1100c [Halobacterium sp. NRC-1] Length = 183</p>
SeqID 1991	SA-623.2	Contig129 (30428-31114 m)	52	<p>Identities = 80/214 (37%), Positives = 122/214 (56%), Gaps = 32/214 (15%) gb AAC95438.1 (AF068901) unknown [Streptococcus pneumoniae] Length = 234</p>
SeqID 1992	SA-624.1	Contig129 (31243-32463 m)	74	<p>Identities = 220/398 (55%), Positives = 306/398 (76%), Gaps = 3/398 (0%) gb AAF36228.1 (AF168363.4) (AF168363) oxalate-formate antiporter [Lactococcus lactis] Length = 421</p>
SeqID 1993	SA-625.1	Contig129 (32650-34017 m)	76	<p>Identities = 313/453 (69%), Positives = 375/453 (82%) gb AAC95436.1 (AF068901) D-Ala-D-Ala adding enzyme [Streptococcus pneumoniae] Length = 457</p>
SeqID 1994	SA-626.1	Contig129 (34164-35210 m)	81	<p>Identities = 243/346 (70%), Positives = 289/346 (83%) sp O5463 DDL_STRPN D-ALANINE--D-ALANINE LIGASE (D- ALANYLALANINE SYNTHETASE) (D-ALA-D-ALA LIGASE) gb AAC95435.1 (AF068901) D-Ala-D-Ala ligase [Streptococcus pneumoniae] Length = 347</p>
SeqID 1995	SA-627.1	Contig129 (35351-35947 m)	94	<p>Identities = 181/198 (91%), Positives = 189/198 (95%) sp P9603 RECR_STRTR RECOMBINATION PROTEIN RECR gb AAC44615.1 (U58210) RecM [Streptococcus thermophilus] Length = 198</p>
SeqID 1996	SA-628.1	Contig129 (35962-38004 m)	69	<p>Identities = 346/698 (49%), Positives = 482/698 (68%), Gaps = 17/698 (2%) gb AAC44614.1 (U58210) penicillin-binding protein 2b [Streptococcus thermophilus] Length = 704</p>

SeqID 1997	SA-629.1	Contig129 (38136-38828 m)	95	<p>Identities = 219/230 (95%), Positives = 226/230 (98%) emb CAB51328.1(AJ131895) phosphoglyceromutase [Streptococcus pneumoniae] Length = 230</p>
SeqID 1998	SA-63.1	Contig131 (54046-54684 m)	16	<p>Identities = 30/100 (30%), Positives = 43/100 (43%), Gaps = 217/100 (21%) gb AAAG10259.1(AF264920_1) (AF264920) DS06238.4-like protein [Drosophila yakuba] Length = 213</p>
SeqID 1999	SA-630.1	Contig129 (39006-39763 m)	77	<p>Identities = 164/252 (65%), Positives = 202/252 (80%) sp P50918 TPIS_LACLA TRIOSEPHOSPHATE ISOMERASE (TIM) gb AAC43266.1 U07640 triosephosphate isomerase [Lactococcus lactis] Length = 252</p>
SeqID 2000	SA-632.1	Contig129 (40284-40760 p)	45	<p>Identities = 48/145 (33%), Positives = 73/145 (50%), Gaps = 6/145 (4%) pii T39903 serine-rich protein - fission yeast (Schizosaccharomyces pombe) emb CA422127.1 (AL033534) hypothetical serine-rich secreted protein [Schizosaccharomyces pombe] Length = 534</p>
SeqID 2001	SA-633.1	Contig129 (39844-41140 m)	94	<p>Identities = 384/398 (96%), Positives = 396/398 (99%) sp P33170 EFITU_STOR ELONGATION FACTOR TU (EF-TU) pii F60663 translation elongation factor EF-Tu - Streptococcus oralis Length = 398</p>
SeqID 2002	SA-635.1	Contig129 (41492-42709 m)	53	<p>Identities = 149/423 (35%), Positives = 229/423 (53%), Gaps = 41/423 (9%) sp Q47866 FTSW_ENTHR PROBABLE CELL DIVISION PROTEIN FTSW gb AAB39929.1 U68049 putative cell division protein ftsW [Enterococcus hirae] Length = 397</p>
SeqID 2003	SA-636.1	Contig129 (42866-45661 m)	59	<p>Identities = 362/945 (38%), Positives = 559/945 (58%), Gaps = 65/945 (6%) sp Q32483 CAPP_RHOA PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC) dbj BA21835.1 D88668 phosphoenolpyruvate carboxylase [Rhodospseudomonas palustris] Length = 936</p>
SeqID 2004	SA-637.1	Contig129 (45870-47669 p)	80	<p>Identities = 443/519 (85%), Positives = 489/519 (93%) dbj BAB16034.1 (AB030810) Bacillus licheniformis P2-peptidase homologue [Streptococcus pyogenes] Length = 519</p>

SeqID 2005 SeqID 2006	SA-638.1 SA-639.1	Contig129 (47728-48117 m) Contig129 (48101-48571 m)	No Hits found No Hits found	
SeqID 2007	SA-64.1	Contig131 (53290-53961 m)	61	Identities = 102/221 (46%), Positives = 145/217 (65%) emb CAC07978.1 A0278983 COP protein [Ralstonia metallidurans] Length = 228
SeqID 2008	SA-640.1	Contig129 (48875-49630 p)	32	Identities = 64/210 (30%), Positives = 95/210 (44%), Gaps = 15/210 (7%) emb CA472266.1 (Y11477) endolysin [Bacteriophage Bastille] Length = 364
SeqID 2009	SA-641.1	Contig129 (49663-50280 m)	36	Identities = 39/156 (24%), Positives = 83/156 (52%), Gaps = 13/156 (8%) gb AAG20117.1 (AE005090) NADH dehydrogenase/oxidoreductase-like protein; NoA [Halobacterium sp. NRC-1] Length = 303
SeqID 2010	SA-642.1	Contig129 (50575-51048 p)	59	Identities = 61/164 (37%), Positives = 96/164 (58%), Gaps = 13/164 (7%) sp P36922 EBSC_ENTFA EBSC PROTEIN prf CA49939 ebSC protein - Enterococcus faecalis gb AAC36853.1 (L23802) regulatory protein [Enterococcus faecalis] Length = 164
SeqID 2011	SA-643.1	Contig129 (51058-51711 p)	42	Identities = 65/191 (34%), Positives = 93/191 (48%), Gaps = 13/191 (6%) prf G72260 phosphoglycerate mutase - Thermotoga maritima (strain MS98) gb AAD36444.1 AE001791.6 (AE001791) phosphoglycerate mutase [Thermotoga maritima] Length = 201
SeqID 2012	SA-644.1	Contig129 (51747-52649 m)	34	Identities = 69/232 (29%), Positives = 108/232 (45%), Gaps = 9/232 (3%) prf E56814 conserved hypothetical protein ynfB - Bacillus subtilis dbj BA020111.1 (D98418) YnfB [Bacillus subtilis] emb CAB12552.1 (Z99107) similar to hypothetical proteins [Bacillus subtilis] emb CAB12562.1 (Z99108) similar to hypothetical proteins [Bacillus subtilis] Length = 235

SeqID 2013	SA-646.1	Contig129 (52812-54314 p)	70	<p>Identities = 318/491 (64%), Positives = 391/491 (78%), Gaps = --T149TT(0%) sp P37477 SYK_BACSU6.7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRs) prj B66111 lysine--rRNA ligase (EC 6.1.1.6) [ysS - Bacillus subtilis dbj BA05316.1 (D26185) [ysy-rRNA thymithetase [Bacillus subtilis] emb CAB11858.1 (Z99104) [ysyl-rRNA synthetase [Bacillus subtilis] Length = 499</p> <p>Identities = 103/151 (68%), Positives = 120/151 (79%) sp P11998 RISB_BACSU6.7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHETASE (DMRL SYNTHASE) (LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN) prj A26708 riboflavin synthase (EC 2.5.1.9) complex beta chain ribH [validated] - Bacillus subtilis pdb 1RVV1 Chain 1, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV2 Chain 2, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV3 Chain 3, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV4 Chain 4, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV5 Chain A, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV6 Chain B, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV7 Chain C, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV8 Chain D, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV9 Chain E, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS pdb 1RVV10 Chain F, SynthaseRIBOFLAVIN SYNTHASE COMPLEX OF BACILLUS SUBTILIS</p>
SeqID 2014	SA-647.1	Contig129 (54389-54859 m)	69	

SeqID 2015	SA-648.1	Contig129 (54874-56067 m)	72	<p>Identities = 230/395 (58%), Positives = 307/395 (77%) sp P50855 GCH2_ACTPL RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBA [INCLUDES: GTP CYCLOHYDROLASE II ; 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP SYNTHASE)] pflJ150848 GTP cyclohydrolase II (EC 3.5.4.25) / 3, 4-dihydroxy-2-butanone 4-phosphate synthase (EC 5.4.99.-) [validated] - pleuropneumoniae gb AA486524.1 (U27202) GTP cyclohydrolase III / 3,4-dihydroxy-2-butanone 4-phosphate synthase [Actinobacillus pleuropneumoniae] Length = 401</p>
SeqID 2016	SA-649.1	Contig129 (56065-56735 m)	67	<p>Identities = 98/216 (45%), Positives = 147/216 (67%), Gaps = 2/216 (0%) db JBAB05274.1 (AP001512) riboflavin synthase alpha subunit [Bacillus halodurans] Length = 215</p>
SeqID 2017	SA-651.1	Contig131 (51942-53309 m)	49	<p>Identities = 114/466 (24%), Positives = 227/466 (48%), Gaps = 42/466 (9%) db JBAB04092.1 (AP001508) two-component sensor histidine kinase [Bacillus halodurans] Length = 459</p>
SeqID 2018	SA-651.1	Contig129 (56716-57825 m)	66	<p>Identities = 180/353 (50%), Positives = 257/353 (71%) sp P50853 RIBD_ACTPL RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBD [INCLUDES: DIAMINOHYDROXYPHOSPHORIBOSYLAMINOPYRIMIDINE DEAMINASE (RIBOFLAVIN-SPECIFIC DEAMINASE); 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL REDUCTASE (HTP REDUCTASE)] Length = 376</p>
SeqID 2019	SA-653.1	Contig129 (53685-53894 p)	61	<p>Identities = 192/436 (44%), Positives = 274/436 (62%), Gaps = 14/436 (3%) pflJ052733 manganese transport protein XF1015 [imported] - Xylella fastidiosa (strain 945c) gb AAAF5825.1 AE003939_4 (AE003939) manganese transport protein [Xylella fastidiosa] Length = 472</p>

SeqID 2020	SA-654.2	Contig129 (59996-60805 m)	40	Identities = 63/215 (29%), Positives = 108/215 (49%), Gaps = 13/215 (6%) pifH75355 hypothetical protein - <i>Dennococcus radiodurans</i> (strain R1) gb AAAF11325.1 AE002018.7 (AE002018) hypothetical protein [Dennococcus radiodurans] Length = 250
SeqID 2021	SA-655.2	Contig129 (60917-61129 m)	53	Identities = 28/64 (43%), Positives = 41/64 (63%) sp O63371 Y352. TREPA HYPOTHETICAL PROTEIN TP0352 pifH71333 hypothetical protein TP0352 - <i>Syphilis spirochete</i> gb AAC65352.1 (AE001215) T. pallidum predicted coding region TP0352 [Treponema pallidum] Length = 85
SeqID 2022	SA-656.2	Contig129 (61256-62542 m)	62	Identities = 201/407 (49%), Positives = 277/407 (67%), Gaps = 2/407 (0%) pifH69979 proteinase homolog yrnO - <i>Bacillus subtilis</i> emb CAB14676.1 (Z59117) similar to protease [Bacillus subtilis] Length = 422
SeqID 2023	SA-657.1	Contig129 (62672-63598 m)	50	Identities = 92/304 (30%), Positives = 161/304 (52%), Gaps = 5/304 (1%) pifH69979 proteinase homolog yrnN - <i>Bacillus subtilis</i> emb CAB14677.1 (Z59117) similar to protease [Bacillus subtilis] Length = 309
SeqID 2024	SA-658.2	Contig133 (43969-46162 m)	46	Identities = 294/409 (71%), Positives = 342/409 (82%), Gaps = 7/409 (1%) gb AACD0281.1 (U78600) putative pteG protein [Streptococcus mutans] Length = 409
SeqID 2025	SA-659.1	Contig133 (43486-43767 p)	No Hits found	
SeqID 2026	SA-66.1	Contig131 (51118-51453 m)	48	Identities = 45/76 (59%), Positives = 54/76 (70%) pifH44087 hypothetical protein [imported] - <i>Staphylococcus aureus</i> (fragment) Length = 151
SeqID 2027	SA-660.1	Contig133 (43100-43915 m)	No Hits found	
SeqID 2028	SA-661.1	Contig133 (42071-42823 m)	71	Identities = 135/242 (55%), Positives = 183/242 (74%) emb CAC10170.1 (AJ276301) response regulator [Streptococcus pneumoniae] Length = 245
SeqID 2029	SA-662.1	Contig133 (41703-42002 m)	65	Identities = 44/88 (50%), Positives = 65/88 (73%) emb CAC10175.1 (AJ278302) histidine kinase [Streptococcus pneumoniae] Length = 446

SeqID 2030	SA-663.1	Contig133 (40732-41580 m)	55	Identities = 105/291 (36%), Positives = 161/291 (55%), Gaps = 18/291 (6%) emb CAB88481.1 (AL353816) putative ABC transport system ATP-binding protein [Streptomyces coelicolor A3(2)] Length = 289
SeqID 2031	SA-664.1	Contig133 (39572-40726 m)	No Hits found	
SeqID 2032	SA-665.2	Contig133 (39693-39929 p)	No Hits found	
SeqID 2033	SA-666.1	Contig133 (38309-39376 m)	36	Identities = 78/262 (29%), Positives = 129/262 (48%), Gaps = 29/262 (11%) gb AAE71283.1 AF253562.7 (AF253562) racemase [Enterococcus faecalis] Length = 711
SeqID 2034	SA-667.1	Contig133 (37637-38014 m)	No Hits found	
SeqID 2035	SA-668.1	Contig133 (37144-37584 p)	No Hits found	
SeqID 2036	SA-669.1	Contig133 (37128-37619 m)	55	Identities = 49/164 (29%), Positives = 96/164 (57%), Gaps = 8/164 (4%) sp P37081 PTRB_KLEPN PTS SYSTEM, SORBOSE-SPECIFIC IIB COMPONENT (EIIB-SOR) (SORBOSE-PERMEASE IIB COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, B COMPONENT) (EIIB-SOR) pr J560186 phosphotransferase system enzyme II component B, sorbose-specific - Klebsiella pneumoniae emb CAA48858.1 (X66059) EIIB-B Sor PTS [Klebsiella pneumoniae] pr J2022173D sorB gene [Klebsiella pneumoniae] Length = 164
SeqID 2037	SA-67.1	Contig133 (50330-51832 p)	74	Identities = 303/506 (59%), Positives = 389/506 (75%), Gaps = 6/506 (1%) sp P44023 YFCC_HAEIN HYPOTHEICAL PROTEIN H10594 pr JEB4010 hypothetical protein H10594 - Haemophilus influenzae (strain Rd KW20) gb AAC22251.1 (U32741) conserved hypothetical transmembrane protein [Haemophilus influenzae Rd] Length = 509
SeqID 2038	SA-670.1	Contig133 (36303-37112 m)	48	Identities = 70/251 (27%), Positives = 132/251 (51%), Gaps = 6/251 (2%) gb AAC44860.1 (U65015) PTS permease for mannose subunit IIPMan [Vibrio furnissii] Length = 258

SeqID 2039	SA-671.1	Contig133 (35479-36306 m)	54	<p>Identities = 94/280 (33%), Positives = 156/280 (55%), Gaps = 13/280 (4%) sp P08188 PTND_ECOLI PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) (MANNOSE-PERMEASE IID COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, D COMPONENT) (EI-M-MAN) pir V06CMM phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IID - Escherichia coli gb AA24445.1 (J02689) mannose permease subunit I-M-MAN [Escherichia coli] db BAA15631.1 (D90026) PTS system, Mannose-specific IID component (EIID-MAN) (Mannose-permease IID component) (Phosphotransferase enzyme II, D component) (EI-M-MAN), [Escherichia coli] gb AAC74889.1 (AE000276) PTS enzyme IID, mannose-specific [Escherichia coli K12] Length = 286</p>
SeqID 2040	SA-672.1	Contig133 (33692-35341 m)	24	<p>Identities = 84/258 (32%), Positives = 138/258 (52%), Gaps = 23/258 (8%) db BAB05628.1 (AP001513) two-component sensor histidine kinase [Bacillus halodurans] Length = 597</p>
SeqID 2041	SA-673.1	Contig133 (32915-33688 m)	56	<p>Identities = 86/252 (34%), Positives = 147/252 (58%), Gaps = 17/252 (6%) emb CA854580.1 (AJ006398) response regulator [Streptococcus pneumoniae] gb AAF31452.1 (AF221126_1 (AF221126) putative response regulator [Streptococcus pneumoniae] Length = 245</p>
SeqID 2042	SA-674.1	Contig133 (31866-32906 m)	53	<p>Identities = 114/331 (34%), Positives = 184/331 (55%), Gaps = 3/331 (0%) gb AAD18094.2 (U75349) periplasmic-iron-binding protein B1A [Brachyspira hyodysenteriae] Length = 336</p>
SeqID 2043	SA-675.1	Contig133 (31147-31644 p)	46	<p>Identities = 55/150 (36%), Positives = 84/150 (55%), Gaps = 2/150 (1%) pir F75336 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF11472.1 (AE002031_1 (AE002031) conserved hypothetical protein [Deinococcus radiodurans] Length = 190</p>

SeqID 2044	SA-676.1	Contig133 (30110-31147 p)	70	<p>Identities = 212/345 (61%), Positives = 268/345 (77%), Gaps = 1/345 (0%) prfj[C69830 glucanase homolog yHc - Bacillus subtilis emb CA474526.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CA812860.1 (Z99109) similar to glucanase [Bacillus subtilis] Length = 346</p>
SeqID 2045	SA-677.1	Contig133 (29644-30099 p)	80	<p>Identities = 103/142 (72%), Positives = 123/142 (86%) emb CAB70606.1 (Y18363) ribonucleotide reductase-like (Nrd-like) protein [Streptococcus dysgalactiae subsp. equisimilis] Length = 142</p>
SeqID 2046	SA-678.1	Contig133 (27085-29487 p)	61	<p>Identities = 398/694 (57%), Positives = 493/694 (70%), Gaps = 30/694 (4%) emb CAB70615.1 (AJ133440) cyclo-nucleotide phosphodiesterase, putative [Streptococcus dysgalactiae subsp. equisimilis] Length = 693</p>
SeqID 2047	SA-68.1	Contig131 (49259-50185 p)	65	<p>Identities = 162/313 (51%), Positives = 207/313 (65%), Gaps = 7/313 (2%) sp Q6171 ARCC_GLOPE CARBAMATE KINASE emb CAA66387.1 (X97788) carbamate kinase [Clostridium perfringens] Length = 314</p>
SeqID 2048	SA-680.1	Contig133 (24609-26825 m)	93	<p>Identities = 647/739 (87%), Positives = 698/739 (93%), Gaps = 1/739 (0%) sp Q54089 REL_A_STREQ PUTATIVE GTP PYROPHOSPHOKINASE (ATP:GTP 3-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE) (P)PPGPP SYNTHETASE (STRINGENT RESPONSE-LIKE PROTEIN) prfj[S39975 stringent response-like protein - Streptococcus equisimilis emb CAA51353.1 (X72832) stringent response-like protein [Streptococcus equisimilis] prfj[2009358E stringent response-like protein [Streptococcus equisimilis] Length = 739</p>
SeqID 2049	SA-681.1	Contig133 (24156-24599 m)	83	<p>Identities = 104/145 (71%), Positives = 128/145 (88%) prfj[S39974 hypothetical protein - Streptococcus equisimilis emb CAA51352.1 (X72832) ORF-1 [Streptococcus equisimilis] prfj[2009358D rel upstream ORF [Streptococcus equisimilis] Length = 147</p>

SeqID 2050	SA-682.1	Contig133 (22976-23901 m)	70	Identities = 180/304 (59%), Positives = 227/304 (74%), Gaps = 4/304 (1%) pir T46757 lipoprotein-imb [validated] - Streptococcus agalactiae gb AA13796.1 (AF062533) Lmb [Streptococcus agalactiae] Length = 306
SeqID 2051	SA-686.1	Contig133 (21506-22951 m)	55	Identities = 213/463 (46%), Positives = 277/463 (59%), Gaps = 41/463 (8%) pir T46758 hypothetical 92.4K protein - Streptococcus agalactiae gb AAD13797.1 (AF062533) unknown [Streptococcus agalactiae] Length = 822
SeqID 2052	SA-687.1	Contig133 (20370-21608 m)	24	Identities = 66/253 (26%), Positives = 101/253 (39%), Gaps = 64/253 (25%) pir T46758 hypothetical 92.4K protein - Streptococcus agalactiae gb AAD13797.1 (AF062533) unknown [Streptococcus agalactiae] Length = 822
SeqID 2053	SA-688.2	Contig133 (19312-20088 p)	68	Identities = 139/255 (54%), Positives = 189/255 (73%), Gaps = 6/255 (2%) gb AAA25174.1 (M35375) lactose repressor (lacR, alt.) Lactococcus lactis gb AAA25176.1 (M60447) repressor protein [Lactococcus lactis] gb AAA25186.1 (M60673) lacR [Lactococcus lactis] Length = 261
SeqID 2054	SA-689.2	Contig139 (185493-186197 p)	59	Identities = 99/228 (43%), Positives = 149/228 (64%), Gaps = 3/228 (1%) pir I40084 gtrR protein - Bacillus brevis emb CAA55264.1 (X78502) gtrR [Brevibacillus brevis] Length = 242
SeqID 2055	SA-68.1	Contig131 (48249-49247 p)	87	Identities = 264/332 (79%), Positives = 292/332 (87%) emb CAB75986.1 (A272085) ornithine carbamoyltransferase [Staphylococcus aureus] emb CAB75987.1 (A272086) ornithine carbamoyltransferase Otc8850 [Staphylococcus aureus] Length = 333
SeqID 2056	SA-690.1	Contig139 (183328-185271 p)	77	Identities = 412/638 (64%), Positives = 506/638 (79%), Gaps = 7/638 (1%) cb JBAB06860.1 (AP001517) thronyl-tRNA synthetase 1 [Bacillus halodurans] Length = 645
SeqID 2057	SA-691.1	Contig139 (181537-182871 p)	52	Identities = 189/290 (65%), Positives = 234/290 (80%) emb CAA72250.1 (Y11463) ORF5 [Streptococcus pneumoniae] Length = 290

SeqID 2058	SA-692.1	Contig139 (180537-181535 p)53-----	Identities = 120/350 (34%), Positives = 180/350 (51%), Gaps = 29/350 (8%) gb AAAG19110.1 (AE005009) Vng600c- [Halobacterium sp. NRC-1] Length = 361
SeqID 2059	SA-693.1	Contig139 (179026-180492 p)	76	Identities = 305/483 (63%), Positives = 378/483 (78%) gb AAC35010.1 (AF055987) intracellular α -amylase [Streptococcus mutans] Length = 486
SeqID 2060	SA-694.2	Contig139 (177890-178894 p)	94	Identities = 304/332 (91%), Positives = 320/332 (95%) dbj BAAB8121.3 (AB028599) catalibolite control protein A [Streptococcus bovis] Length = 334
SeqID 2061	SA-696.2	Contig139 (176595-177680 m)	81	Identities = 257/359 (71%), Positives = 304/359 (84%) gb AAC46293.1 (AF014480) PepQ [Streptococcus mutans] Length = 359
SeqID 2062	SA-697.1	Contig139 (174747-176537 p)	42	Identities = 148/586 (25%), Positives = 252/586 (42%), Gaps = 77/586 (13%) emb CAB66297.1 (AL136519) beta-N-acetylglucosaminidase [Streptomyces coelicolor A3(2)] Length = 615
SeqID 2063	SA-698.1	Contig139 (173973-174731 p)	No Hits found	Identities = 197/271 (72%), Positives = 228/271 (83%) sp P44481Y048_HAEIN PUTATIVE OXIDOREDUCTASE HI0048 pir B84045 D-arabinitol 2-dehydrogenase homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21726.1 (U32690) oxidoreductase [Haemophilus influenzae Rd] Length = 285
SeqID 2064	SA-699.1	Contig139 (172927-173766 p)	76	Identities = 118/427 (27%), Positives = 199/427 (45%), Gaps = 25/427 (5%) dbj BAB06435.1 (AP001516) two-component sensor histidine Kinase [Bacillus halodurans] Length = 437
SeqID 2065	SA-7.1	Contig137 (38846-39100 m)	No Hits found	Identities = 203/343 (59%), Positives = 261/343 (75%) dbj BAB04425.1 (AP001509) D-mannosate dehydratase [Bacillus halodurans] Length = 345
SeqID 2066	SA-70.1	Contig131 (46851-48146 m)	44	
SeqID 2067	SA-700.1	Contig139 (171757-172803 p)	73	

SeqID 2068	SA-701.1	Contig139 (170339-171739 p)	62	<p>Identities = 215/465 (46%), Positives = 295/465 (63%), Gaps = 7/465 (1%) dbj BA04424.1 (AP001509) uronate isomerase [Bacillus halodurans] Length = 472</p>
SeqID 2069	SA-702.1	Contig139 (169705-170322 p)	51	<p>Identities = 92/199 (46%), Positives = 124/199 (62%), Gaps = 6/199 (3%) pri F72422 KHG-KDPG bifunctional aldolase TM0066 [similarity] - Thermotoga maritima (strain MSB8) gb AAD35160.1 AE001693.8 (AE001693) 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Thermotoga maritima] Length = 205</p>
SeqID 2070	SA-704.1	Contig139 (168917-169588 p)	50	<p>Identities = 67/225 (29%), Positives = 119/225 (52%), Gaps = 17/225 (7%) sp P42239 YCBG_BACSU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GLTP-CWLJ INTERGENIC REGION (ORF6) pri B69753 transcription regulator GntR family homolog ycbG - Bacillus subtilis dbj BAA06471.1 (D30808) homologue of protein A which gene locates upstream pyruvate dehydrogenase gene cluster [Bacillus subtilis] emb CAB12044.1 (Z99105) similar to transcriptional regulator (GntR family) [Bacillus subtilis] Length = 233</p>

SeqID 2071	SA-705.1	Contig139 (167089-168888 p)	57	<p>Identities = 255/599 (42%), Positives = 356/599 (59%), Gaps = 25/599 (4%) gbIAAF65327.1 (AF234293) GUSA, hexaHis tagged [Binary vector pCambia-1201] gbIAAF65330.1 (AF234294) GUSA, hexaHis tagged [Binary vector pCambia-1281Z] gbIAAF65334.1 (AF234295) GUSA, hexaHis tagged [Binary vector pCambia-1281Z] gbIAAF65342.1 (AF234297) GUSA, hexaHis tagged [Binary vector pCambia-1301] gbIAAF65372.1 (AF234306) GUSA, hexaHis tagged [Binary vector pCambia-1381Z] gbIAAF65380.1 (AF234312) GUSA, hexaHis tagged [Binary vector pCambia-1391Z] gbIAAF65397.1 (AF234314) GUSA, hexaHis tagged [Binary vector pCambia-2201] gbIAAF65404.1 (AF234316) GUSA, hexaHis tagged [Binary vector pCambia-2301] Length = 620</p>
SeqID 2072	SA-706.1	Contig139 (166047-167072 p)	49	<p>Identities = 115/342 (33%), Positives = 179/342 (51%), Gaps = 19/342 (4%) pirJ[G72422 2-keto-3-deoxygluconate kinase - Thermotoga maritima (strain MSB8)] gbAAD35161.1(AE001693.7 (AE001693) 2-keto-3-deoxygluconate kinase [Thermotoga maritima] Length = 339</p>
SeqID 2073	SA-707.1	Contig139 (164430-165980 p)	33	<p>Identities = 107/443 (24%), Positives = 180/443 (40%), Gaps = 37/443 (8%) spIP944881YNAJ_BACSU HYPOTHETICAL SYMPORTER IN GLNA-XYNB INTERGENIC REGION pirJAg9688 H⁺-symporter homolog ynaJ - Bacillus subtilis gbIAAB41090.1 (U66480) YnaJ [Bacillus subtilis] emb(CAB13541.1 (Z99113) similar to H⁺-symporter [Bacillus subtilis] Length = 463</p>
SeqID 2074	SA-708.2	Contig139 (163229-164224 p)	68	<p>Identities = 165/329 (50%), Positives = 230/329 (69%), Gaps = 1/329 (0%) gbIAAB17653.1 (U31175) D-specific D-2-hydroxyacid dehydrogenase [Staphylococcus aureus] Length = 330</p>
SeqID 2075	SA-71.1	Contig131 (46021-46854 m)	54	<p>Identities = 100/305 (32%), Positives = 152/305 (49%), Gaps = 31/305 (10%) dbj(BA08434.1 (AP001516) two-component response regulator [Bacillus halodurans] Length = 312</p>

SeqID 2076	SA-710.2	Contig139 (162160-163218 p)	55	<p>Identities = 127/332 (38%), Positives = 202/332 (60%), Gaps = 1/332 (0%) pir E71373 probable regulatory protein (pfoS/R) - syphilis spirochete gb AAC65034.1 (AE001189) regulatory protein (pfoS/R) [Treponema pallidum] Length = 350</p> <p>Identities = 88/282 (31%), Positives = 152/282 (53%), Gaps = 5/282 (1%) sp P39592 YWB_L_BACSU HYPOTHETICAL TRANSCRIPTION REGULATOR YWB1_pir J539679 transcription regulator homolog ywb1 - Bacillus subtilis emb CA51580.1 (X73124) [pa-24d [Bacillus subtilis] emb CA51587.1 (Z95123) alternate gene name: ipa-24d-similar to transcriptional regulator (LysR family) [Bacillus subtilis] Length = 301</p>
SeqID 2077	SA-712.1	Contig139 (161083-161987 m)	50	
SeqID 2078	SA-713.1	Contig139 (160228-161046 p)	No Hits found	
SeqID 2079	SA-714.1	Contig139 (159291-160064 p)	70	<p>Identities = 128/253 (50%), Positives = 187/253 (73%) sp P73707 YBBM_ECOLI HYPOTHETICAL 28.2 KD PROTEIN IN USHA-TESA INTERGENIC REGION Length = 259</p>
SeqID 2080	SA-715.1	Contig139 (158638-159294 p)	63	<p>Identities = 95/202 (47%), Positives = 142/202 (70%), Gaps = 2/202 (0%) sp P77279 YBBL_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBBL_pir A64780 probable ABC transport protein ybbL - Escherichia coli gb AA040244.1 (U82864) hypothetical protein [Escherichia coli] gb AAC73592.1 (AE000155) putative ATP-binding component of a transport system [Escherichia coli K12] Length = 225</p>
SeqID 2081	SA-716.1	Contig139 (157783-158421 m)	59	<p>Identities = 91/211 (43%), Positives = 131/211 (61%), Gaps = 7/211 (3%) sp P06486 DEDA_ECOLI DEDA PROTEIN (DSG-1 PROTEIN) pir JXMECAD dedA protein - Escherichia coli gb AA023964.1 (M68935) dedA [Escherichia coli] gb AAC75377.1 (AE000320) orf, hypothetical protein [Escherichia coli K12] db JBA016174.1 (D90863) dedA protein [Escherichia coli] Length = 219</p>

SeqID 2082	SA-717.2	Contig139 (156980-157705 p)	50	Identities = 103/200 (51%), Positives = 136/200 (67%), Gaps = 4/200 (2%) spIQ03158 NUCE_STRPN DNA-ENTRY NUCLEASE (COMPETENCE-SPECIFIC NUCLEASE) p[IS]10641 endA protein - Streptococcus pneumoniae emb[CA38734.1] (X54225) membrane nuclease [Streptococcus pneumoniae] Length = 274
SeqID 2083	SA-719.1	Contig125 (39398-40735 m)	40	Identities = 151/266 (56%), Positives = 189/266 (71%), Gaps = 15/266 (5%) p[IS]572385 hypothetical protein 9 - Enterococcus faecalis plasmid pAD1 emb[CAA66668.1] (X96977) orf9 [Enterococcus faecalis] Length = 278
SeqID 2084	SA-72.1	Contig131 (45077-45799 m)	72	Identities = 139/236 (58%), Positives = 178/236 (74%) gb AAD45529.1 AF162655_1 (AF162655) choline transporter [Streptococcus pneumoniae] Length = 242
SeqID 2085	SA-720.1	Contig125 (38800-39384 m)	24	Identities = 36/142 (25%), Positives = 62/142 (43%), Gaps = 7/142 (4%) p[IS]70463 hypothetical protein ad_1894 - Aquifex aeolicus gb AAC07706.1 (AE000762) putative protein [Aquifex aeolicus] Length = 237
SeqID 2086	SA-721.1	Contig125 (37843-38661 m)	53	Identities = 89/287 (33%), Positives = 157/287 (58%), Gaps = 15/287 (5%) gb AAF27301.1 AF154674_2 (AF154674) ParA [Lactococcus lactis subsp. lactis] gb AAF27325.1 (AF178424) ParA [Lactococcus lactis] Length = 262
SeqID 2087	SA-722.1	Contig125 (37566-37846 m)	No Hits found	
SeqID 2088	SA-723.1	Contig125 (37172-37561 m)	40	Identities = 33/93 (35%), Positives = 53/93 (56%), Gaps = 2/93 (2%) r[INP_038304.1] ORF4 [Streptococcus thermophilus bacteriophage 7201] gb AAF26503.1 AF118440_1 (AF145054) ORF4 [Streptococcus thermophilus bacteriophage 7201] Length = 268
SeqID 2089	SA-725.1	Contig125 (36856-37167 m)	No Hits found	
SeqID 2090	SA-726.1	Contig125 (35394-36722 m)	No Hits found	
SeqID 2091	SA-727.1	Contig125 (34305-35003 m)	66	Identities = 105/222 (47%), Positives = 162/222 (72%), Gaps = 2/222 (0%) gb AAG28336.1 (U88582) SaD [Streptococcus mutans] Length = 222

SeqID 2092	SA-728.1	Contig125 (33542-34177 m)	26	Identities = 54/103 (52%), Positives = 70/103 (67%), Gaps = 2/103 (1%) gb AACG2337.1 (U8552) <i>SalE</i> (Streptococcus mutans) Length = 108
SeqID 2093	SA-729.1	Contig125 (31914-33509 p)	75	Identities = 346/521 (66%), Positives = 411/521 (78%), Gaps = 24/521 (4%) gb AAD17886.1 (AF100456) <i>hyaluronate-associated protein precursor</i> (Streptococcus equi) Length = 522
SeqID 2094	SA-73.1	Contig131 (44407-44805 p)	No Hits found	
SeqID 2095	SA-730.1	Contig125 (31012-31481 m)	83	Identities = 119/148 (80%), Positives = 136/148 (91%) gb AAC17173.1 (AF065141) unknown (Streptococcus mutans) Length = 356
SeqID 2096	SA-731.1	Contig125 (30392-31078 m)	89	Identities = 188/218 (86%), Positives = 205/218 (93%) gb AAC17173.1 (AF065141) unknown (Streptococcus mutans) Length = 356
SeqID 2097	SA-732.1	Contig125 (29462-30349 p)	52	Identities = 96/320 (30%), Positives = 172/320 (53%), Gaps = 16/320 (5%) sp P42422 YXDK_BACSU HYPOTHETICAL SENSOR-LIKE HISTIDINE KINASE IN IDH 3 REGION pri JH70073 two-component sensor histidine kinase homolog yxkK - Bacillus subtilis db BAA03301.1 (D14399) hypothetcal protein [Bacillus subtilis] emb CAB16001.1 (Z39124) similar to two-component sensor histidine kinase [YxdJ] [Bacillus subtilis] Length = 325
SeqID 2098	SA-733.1	Contig125 (28746-29414 p)	55	Identities = 95/226 (42%), Positives = 136/226 (60%), Gaps = 10/226 (4%) pri D70032 two-component response regulator [YvcQ] homolog yrcP - Bacillus subtilis emb CAB08062.1 (Z394043) hypothetcal protein [Bacillus subtilis] emb CAB15477.1 (Z39121) similar to two-component response regulator [YvcQ] [Bacillus subtilis] Length = 237
SeqID 2099	SA-734.1	Contig125 (26819-28636 p)	45	Identities = 154/666 (23%), Positives = 300/666 (44%), Gaps = 40/666 (6%) gb AAF99895.1 (AF267498_5 (AF267498) permease ORF1 (Streptococcus mutans) Length = 640

SeqID 2100	SA-735.1	Contig125 (25927-26679 p)	68	Identities = 118/242 (48%), Positives = 175/242 (71%), Gaps = 1/242 (0%) gb AA096934.1 AF267498.4 (AF267498) ABC transporter Otx [Streptococcus mutans] Length = 246
SeqID 2101	SA-736.1	Contig125 (25443-25901 p)	56	Identities = 59/146 (40%), Positives = 87/146 (59%), Gaps = 3/146 (2%) gb AA08491.1 (U25181) nisin-resistance protein [Lactococcus lactis] Length = 318
SeqID 2102	SA-737.1	Contig125 (25003-25479 p)	52	Identities = 51/177 (28%), Positives = 104/177 (57%), Gaps = 5/177 (2%) gb AA08491.1 (U25181) nisin-resistance protein [Lactococcus lactis] Length = 318
SeqID 2103	SA-738.1	Contig125 (24286-24774 m)	No Hits found	
SeqID 2104	SA-739.1	Contig125 (23406-24254 p)	62	Identities = 123/230 (42%), Positives = 178/230 (60%), Gaps = 18/230 (6%) emb CAB98627.1 (AJ012388) hypothetical protein [Lactococcus lactis] Length = 286
SeqID 2105	SA-74.1	Contig131 (43560-45074 m)	80	Identities = 326/506 (64%), Positives = 410/506 (80%), Gaps = 1/506 (0%) pir T44634 choline transporter [imported] - Streptococcus pneumoniae gb AAD45530.1 AF626556_1 (AF626556) choline transporter [Streptococcus pneumoniae] Length = 506
SeqID 2106	SA-740.1	Contig125 (22530-23273 p)	No Hits found	
SeqID 2107	SA-741.1	Contig125 (21118-22452 p)	79	Identities = 29/1439 (66%), Positives = 353/439 (80%), Gaps = 10/439 (2%) sp P39815 GID_BACSU GID PROTEIN pir A69632 glucose-inhibited division protein gid - Bacillus subtilis emb CAA04423.1 (AJ000975) Gid protein [Bacillus subtilis] emb CAB13486.1 (Z99112) glucose-inhibited division protein [Bacillus subtilis] Length = 435
SeqID 2108	SA-742.1	Contig125 (20306-21004 p)	56	Identities = 83/229 (36%), Positives = 133/229 (57%), Gaps = 1/229 (0%) db BA04138.1 (AP001508) transcriptional regulator (GntR family) [Bacillus halodurans] Length = 240

SeqID 2109	SA-743.2	Contig125 (18531-20093 m)	86	Identities = 418/511 (81%), Positives = 467/511 (90%), Gaps = 3/511 (0%) gb AAK05584.1 AE006379_1 (AE006379) GMP synthase (EC 6.3.5.2) [Lactococcus lactis subsp. lactis] Length = 513
SeqID 2110	SA-744.2	Contig119 (32996-33796 m)	57	Identities = 113/251 (45%), Positives = 160/251 (63%), Gaps = 3/251 (1%) gb AAK04846.1 AE006308_6 (AE006308) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis] Length = 257
SeqID 2111	SA-745.1	Contig119 (32371-33006 m)	74	Identities = 126/211 (59%), Positives = 161/211 (75%) pir B9997 conserved hypothetical protein ymqJ - Bacillus subtilis gb AAC00285.1 (AF008220) ymqJ [Bacillus subtilis] emb CAB14968.1 (Z99119) similar to hypothetical proteins [Bacillus subtilis] Length = 213
SeqID 2112	SA-746.1	Contig119 (31405-31899 m)	60	Identities = 73/152 (48%), Positives = 99/152 (65%), Gaps = 3/152 (1%) db BAB06136.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 156
SeqID 2113	SA-747.1	Contig119 (30218-31369 m)	63	Identities = 164/370 (44%), Positives = 251/370 (67%), Gaps = 15/370 (4%) sp P32727 NUSA_BACSU N UTILIZATION SUBSTANCE PROTEIN A HOMOLOG emb CAB13533.1 (Z99112) nusa [Bacillus subtilis] Length = 371
SeqID 2114	SA-748.1	Contig119 (29800-30196 m)	65	Identities = 46/92 (50%), Positives = 67/92 (72%), Gaps = 1/92 (1%) sp P32726 YLXR_BACSU HYPOTHETICAL 10.4 KD PROTEIN IN NUSA-INFIB INTERGENIC REGION (ORF3) pir D36905 conserved hypothetical protein ykr - Bacillus subtilis emb CAA79232.1 (Z18631) ORF3 [Bacillus subtilis] emb CAB13534.1 (Z99112) alternate gene name: ymxB-similar to hypothetical proteins [Bacillus subtilis] Length = 91
SeqID 2115	SA-749.1	Contig119 (29605-29907 m)	67	Identities = 50/97 (51%), Positives = 69/97 (70%) sp P55768 YTXQ_ENTFC PROBABLE RIBOSOMAL PROTEIN IN INFIB 5 REGION Length = 103
SeqID 2116	SA-75.1	Contig131 (40941-43481 p)	38	Identities = 19/596 (3%), Positives = 324/596 (53%), Gaps = 31/596 (5%) db BAA24464.1 (D85082) YfX [Bacillus subtilis] Length = 610

SeqID 2117	SA-751.1	Contig119 (26802-29585 m)	98	<p>Identities = 926/927 (99%), Positives = 927/927 (99%) sp Q9ZF20 IF2_STRAG_TRANSLATION_INITIATION_FACTOR IF-2_emb CAA05919.1 (AJ003164) Initiation factor IF2 [Streptococcus agalactiae] emb CAC00489.1 (AJ251495) Initiation factor 2 [Streptococcus agalactiae] emb CAC00491.1 (AJ251496) Initiation factor 2 [Streptococcus agalactiae] Length = 927</p>
SeqID 2118	SA-752.1	Contig119 (26343-26711 m)	91	<p>Identities = 122/122 (100%), Positives = 122/122 (100%) emb CAA05920.1 (AJ003164) ribosome binding factor A [Streptococcus agalactiae] emb CAC00486.1 (AJ251493) ribosome binding factor A [Streptococcus agalactiae] emb CAC00488.1 (AJ251494) ribosome binding factor A [Streptococcus agalactiae] emb CAC00490.1 (AJ251495) ribosome binding factor A [Streptococcus agalactiae] emb CAC00492.1 (AJ251496) ribosome binding factor A [Streptococcus agalactiae] emb CAC00498.1 (AJ251499) ribosome binding factor A [Streptococcus agalactiae] Length = 122</p>
SeqID 2119	SA-753.1	Contig119 (25234-26259 p)	26	<p>Identities = 58/220 (26%), Positives = 90/220 (40%), Gaps = 8/220 (3%) sp Q01109 BAH_STRHY_ACETYL-HYDROLASE gb AA179277.1 (M64783) acetyl-hydrolase [Streptomyces hygroscopicus] Length = 299</p>
SeqID 2120	SA-754.1	Contig119 (24675-25091 m)	68	<p>Identities = 67/138 (48%), Positives = 99/138 (71%) gb AAG10085.1 AF296446_1 (AF296446) CopY [Streptococcus mutans] Length = 147</p>
SeqID 2121	SA-755.1	Contig119 (22428-24662 m)	76	<p>Identities = 44/0740 (59%), Positives = 57/1740 (76%), Gaps = 1/740 (0%) gb AAG10086.1 AF296446_2 (AF296446) CopA [Streptococcus mutans] Length = 742</p>
SeqID 2122	SA-757.1	Contig119 (22181-22387 m)	58	<p>Identities = 31/67 (46%), Positives = 43/67 (63%) gb AAG10087.1 AF296446_3 (AF296446) CopZ [Streptococcus mutans] Length = 67</p>

SeqID 2123	SA-758.1	Contig119 (21457-22071 m)	65	<p>Identities = 107/192 (55%), Positives = 137/192 (70%) sp O22216 YVGF_BAGSU-HYPOTHETICAL 21.7 KDA PROTEIN IN SSG-SEG INTERGENIC REGION pir JA7004 conserved hypothetical protein yvgT - Bacillus subtilis emb CAB15351.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] Length = 202</p>
SeqID 2124	SA-759.1	Contig119 (20630-21480 m)	66	<p>Identities = 138/238 (57%), Positives = 184/238 (76%) emb CAB94816.1 (AJ245582) hypothetical protein [Streptococcus thermophilus] Length = 240</p>
SeqID 2125	SA-76.1	Contig131 (40208-40957 p)	44	<p>Identities = 58/255 (22%), Positives = 115/255 (44%), Gaps = 26/255 (10%) ref NP_069699.1 carboxylesterase (est-1) [Archaeoglobus fulgidus] pir JA89358 carboxylesterase (est-1) homolog - Archaeoglobus fulgidus gb AA890371.1 (AE007044) carboxylesterase (est-1) [Archaeoglobus fulgidus] Length = 266</p>
SeqID 2126	SA-760.1	Contig119 (17875-20517 m)	83	<p>Identities = 655/879 (74%), Positives = 748/879 (84%), Gaps = 4/879 (0%) sp P13252 DPO1_STRPN DNA POLYMERASE I (POL1) pir JA32948 DNA-directed DNA polymerase (EC 2.7.7.7) - Streptococcus pneumoniae gb AA28954.1 (J04479) DNA polymerase I [Streptococcus pneumoniae] Length = 877</p>
SeqID 2127	SA-761.1	Contig119 (17405-17845 m)	58	<p>Identities = 72/134 (53%), Positives = 94/134 (69%), Gaps = 3/134 (2%) db JBAR05880.1 (AP001514) unknown conserved protein [Bacillus halodurans] Length = 137</p>
SeqID 2128	SA-762.1	Contig119 (16844-17323 m)	75	<p>Identities = 113/156 (72%), Positives = 135/156 (86%), Gaps = 1/156 (0%) gb AAB18795.1 (U76538) Fur-like protein [Streptococcus pyogenes] Length = 155</p>
SeqID 2129	SA-765.1	Contig119 (15128-16691 m)	11	<p>Identities = 41/146 (28%), Positives = 63/146 (43%), Gaps = 13/146 (8%) emb CA06650.1 (AJ005645) sdrC [Staphylococcus aureus] Length = 947</p>

SeqID 2130	SA-766.1	Contig119 (14327-15013 m)	--78--	Identities = 143/228 (62%), Positives = 183/228 (79%), Gaps = 1/228 (0%) emb CA54578.1 (AJ006397) response regulator [Streptococcus pneumoniae] Length = 232
SeqID 2131	SA-767.1	Contig119 (13288-14325 m)	---71	Identities = 190/343 (55%), Positives = 249/343 (72%) emb CA54579.1 (AJ006397) histidine kinase [Streptococcus pneumoniae] Length = 350
SeqID 2132	SA-768.2	Contig119 (12486-13274 p)	23	Identities = 35/119 (29%), Positives = 62/119 (51%), Gaps = 15/119 (12%) pir S32215 hypothetical protein 1 - Bacillus megaterium emb CAA79984.1 (Z21972) ORF 1 [Bacillus megaterium] Length = 226
SeqID 2133	SA-769.2	Contig119 (11205-12347 m)	80	Identities = 259/377 (71%), Positives = 320/377 (84%) sp O32053 GT_BACSU QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) pir B69722 queuine tRNA-ribosyltransferase (EC 2.4.2.29) - Bacillus subtilis emb CAB14731.1 (Z99118) tRNA-guanine transglycosylase [Bacillus subtilis] emb CAB75333.1 (Y15896) tRNA-guanine transglycosylase [Bacillus subtilis] Length = 381
SeqID 2134	SA-77.1	Contig131 (39724-40080 p)	68	Identities = 70/119 (58%), Positives = 89/119 (73%), Gaps = 1/119 (0%) sp O2009 YTRP_LACLA HYPOTHETICAL 13.3 KD PROTEIN IN TRPE 5 REGION pir S35123 hypothetical protein (trpe 5 region) - Lactococcus lactis subsp. lactis gb AA25222.1 (M87483) ORF 1 [Lactococcus lactis] Length = 119
SeqID 2135	SA-770.1	Contig119 (10787-11098 m)	59	Identities = 45/98 (45%), Positives = 65/98 (65%), Gaps = 3/98 (3%) pir T38499 hypothetical protein SPAC29B12.12 - fission yeast (Schizosaccharomyces pombe) emb CAB16256.1 (Z99164) hypothetical protein [Schizosaccharomyces pombe] Length = 113

SeqID 2136	SA-772.1	Contig119 (10241-10780 m)	53	<p>Identities = 62/173 (35%), Positives = 97/173 (55%), Gaps = 1/173 (0%) pri B69832 biotin biosynthesis homolog ynfU - Bacillus subtilis emb CAA74544.1 (Y14084) hypothetical protein [Bacillus subtilis] emb CAB12877.1 (Z99109) similar to biotin biosynthesis [Bacillus subtilis] Length = 186</p>
SeqID 2137	SA-773.1	Contig119 (9326-10102 m)	48	<p>Identities = 89/218 (40%), Positives = 129/218 (58%), Gaps = 4/218 (1%) pri F69830 conserved hypothetical protein ynfI - Bacillus subtilis emb CAA74530.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CAB12864.1 (Z99109) similar to hypothetical proteins [Bacillus subtilis] Length = 244</p>
SeqID 2138	SA-774.2	Contig119 (8820-9326 m)	62	<p>Identities = 71/154 (46%), Positives = 110/154 (71%) splP21335 YAAI_BACSU HYPOTHETICAL 17.8 KD PROTEIN IN SERS-DNAH INTERGENIC REGION pri S11690 conserved hypothetical protein yaaJ - Bacillus subtilis emb CAA36389.1 (X52144) ORF17 (AA 1-161) [Bacillus subtilis] db BAA05264.1 (D26185) unknown [Bacillus subtilis] emb CAB11794.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] pri 1617102A 17KD protein [Bacillus subtilis] Length = 161</p>
SeqID 2139	SA-776.1	Contig110 (3335-3646 p)	No Hits found	
SeqID 2140	SA-777.1	Contig110 (2062-2373 m)	27	<p>Identities = 25/35 (71%), Positives = 29/35 (82%) pri G81516 hypothetical protein CP0988 [improved] - Chlamydomonas reinhardtii (strain AR39) Length = 52</p>
SeqID 2141	SA-778.1	Contig131 (3258-3355 p)	No Hits found	
SeqID 2142	SA-779.1	Contig110 (1371-1676 m)	No Hits found	

SeqID 2143	SA-78.1	Contig131 (38025-39656 p)	48	Identities = 159/568 (27%), Positives = 265/568 (45%), Gaps = 82/568 (14%) sp P32399 YHGE_BACSU HYPOTHEICAL 84.1 KD PROTEIN IN HEMY-GLT INTERGENIC REGION (ORFB) p I H69832 phage infection protein homolog yHGE - Bacillus subtilis emb CAA74522.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CAB12856.1 (Z99109) alternate gene name: yxE~similar to phage infection protein [Bacillus subtilis] Length = 775
SeqID 2144	SA-780.1	Contig110 (499-846 m)	No Hits found	
SeqID 2145	SA-782.2	Contig139 (106281-108005 p)	46	Identities = 122/553 (22%), Positives = 265/553 (47%), Gaps = 12/553 (2%) db BA06924.1 (AP001518) BH3205~unknown conserved protein [Bacillus halodurans] Length = 561
SeqID 2146	SA-783.1	Contig139 (108099-108740 p)	64	Identities = 94/212 (44%), Positives = 137/212 (64%) p I E70860 probable serB2 protein - Mycobacterium tuberculosis (strain H37RV) emb CAA16127.1 (AL021287) serB2 [Mycobacterium tuberculosis] Length = 409
SeqID 2147	SA-784.1	Contig139 (108761-109246 m)	24	Identities = 24/77 (31%), Positives = 40/77 (51%) gb AAAG20030.1 (AE005083) isopentenyl pyrophosphate isomerase; Idi [Halobacterium 213] Length = 213
SeqID 2148	SA-785.1	Contig139 (109259-109714 m)	36	Identities = 32/116 (27%), Positives = 57/116 (48%), Gaps = 4/116 (3%) p I B70008 hypothetical protein yueI - Bacillus subtilis emb CAB15165.1 (Z99120) yueI [Bacillus subtilis] Length = 132
SeqID 2149	SA-786.1	Contig139 (109912-111219 p)	92	Identities = 396/435 (91%), Positives = 414/435 (95%), Gaps = 1/435 (0%) db JBA481815.1 (AB023913) enolase [Streptococcus intermedius] Length = 434
SeqID 2150	SA-787.1	Contig139 (111327-112391 m)	30	Identities = 62/236 (26%), Positives = 107/236 (45%), Gaps = 38/236 (16%) gb AAF20148.1 AF208390_1 (AF208390) actinin-like protein [Entamoeba histolytica] Length = 537

SeqID 2151	SA-788.1	Contig139 (112620-113903 p)	79	<p>Identities = 287/426 (67%), Positives = 346/426 (80%) sp Q9S400 ARO_A_STRPN_3-PHOSPHOSHIMIMATE 1- CARBOXYVINYLTTRANSFERASE [5- ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) gb AAD45819.1 AF169483_1 (AF169483) 5-enolpyruvylshikimate 3-phosphate synthase [Streptococcus pneumoniae] Length = 427</p>
SeqID 2152	SA-789.1	Contig139 (113896-114408 p)	56	<p>Identities = 65/164 (39%), Positives = 98/164 (59%), Gaps = 8/164 (4%) sp P43906 AROK_LACLA SHIKIMATE KINASE (SK pir S5281 shikimate kinase (EC 2.7.1.71) - Lactococcus lactis emb CAA55181.1 (X78413) shikimate kinase [Lactococcus lactis] Length = 162</p>
SeqID 2153	SA-79.1	Contig131 (37307-38101 p)	51	<p>Identities = 109/229 (47%), Positives = 165/229 (71%) gb AAC14610.1 (U95842) transmembrane protein Tmp7 [Lactococcus lactis] Length = 234</p>
SeqID 2154	SA-790.1	Contig139 (114432-115838 p)	43	<p>Identities = 143/409 (34%), Positives = 206/409 (49%), Gaps = 56/409 (13%) emb CAB76821.1 (AJ276231) PSR protein [Enterococcus faecalis] emb CAB76822.1 (AJ276232) PSR protein [Enterococcus faecalis] Length = 390</p>
SeqID 2155	SA-792.1	Contig139 (115939-117294 p)	63	<p>Identities = 198/452 (43%), Positives = 300/452 (65%) dbj BAB04406.1 (AP001509) RNA methyltransferase [Bacillus halodurans] Length = 458</p>
SeqID 2156	SA-793.1	Contig139 (117321-117623 p)	No Hits found	
SeqID 2157	SA-794.1	Contig139 (117741-118478 p)	58	<p>Identities = 112/245 (45%), Positives = 148/245 (59%), Gaps = 102/245 (4%) pir T09434 acid phosphatase (EC 3.1.3.2) [similarity] - Haemophilus influenzae (strains CCUG, Rd KW20) emb CAA68889.1 (Y07615) acid phosphatase [Haemophilus influenzae] Length = 235</p>

SeqID 2158	SA-795.1	Contig139 (118799-119317 p)	67	Identities = 93/173 (53%), Positives = 123/173 (70%), Gaps = 3/173 (1%) refNP_010829.1 Ydr540cp [Saccharomyces cerevisiae] pil[S62019 hypothetical protein YDR540C - yeast (Saccharomyces cerevisiae)] gb AAB64882.1 (U43834) Ydr540cp [Saccharomyces cerevisiae] Length = 179
SeqID 2159	SA-796.1	Contig139 (119446-119634 m)	No Hits found	
SeqID 2160	SA-797.1	Contig139 (119663-120118 m)	32	Identities = 29/95 (30%), Positives = 49/95 (51%), Gaps = 2/95 (2%) gb AAG09969.1 AF248037_4 (AF248037) unknown [Streptococcus agalactiae] Length = 174
SeqID 2161	SA-798.1	Contig139 (120154-120486 p)	34	Identities = 31/63 (49%), Positives = 44/63 (69%), Gaps = 2/63 (3%) gb AAG01392.1 AF208158_1 (AF208158) alpha-like protein 2 [Streptococcus agalactiae] Length = 785
SeqID 2162	SA-799.1	Contig139 (120607-121428 m)	92	Identities = 285/296 (96%), Positives = 287/296 (96%) pil T08011 probable transposase TnpA - Streptococcus pyogenes (fragment) gb AAB92607.1 (AF026542) TnpA [Streptococcus pyogenes] Length = 364
SeqID 2163	SA-8.1	Contig137 (36602-39009 p)	28	Identities = 123/560 (21%), Positives = 212/560 (36%), Gaps = 74/560 (13%) refNP_053169.1 pXO2-14 [Bacillus anthracis] gb AAF13619.1 AF188935_17 (AF188935) pXO2-14 [Bacillus anthracis] Length = 952
SeqID 2164	SA-80.1	Contig131 (36659-37198 m)	51	Identities = 47/181 (25%), Positives = 95/181 (51%), Gaps = 16/181 (8%) dbj BAB04438.1 (AP001509) transcriptional regulator [TetR/AcrR family] [Bacillus halodurans] Length = 188
SeqID 2165	SA-800.1	Contig139 (121476-121751 m)	61	Identities = 66/80 (82%), Positives = 68/80 (84%) pil T09011 probable transposase TnpA - Streptococcus pyogenes (fragment) gb AAB92607.1 (AF026542) TnpA [Streptococcus pyogenes] Length = 364

SeqID 2166	SA-801.1	Contig139 (121884-122021 p)	78	Identities = 36/49 (73%), Positives = 40/49 (81%) gb AAC398436.1 (L29324) unknown [Streptococcus pneumoniae] Length = 118
SeqID 2167	SA-803.1	Contig139 (122409-122756 m)	82	Identities = 93/98 (94%), Positives = 96/98 (97%) sp Q82849 HSL0_STRPY_33 KDA CHAPERONIN (HEAT SHOCK PROTEIN 33 HOMOLOG) (HSP93) gb AAC97154.1 (U49397) unknown [Streptococcus pyogenes] Length = 277
SeqID 2168	SA-804.1	Contig139 (122950-123369 m)	85	Identities = 104/135 (77%), Positives = 119/135 (88%) gb AAC97150.1 (U49397) MsmR [Streptococcus pyogenes] Length = 209
SeqID 2169	SA-805.1	Contig139 (123370-124158 m)	23	Identities = 59/72 (81%), Positives = 66/72 (90%) gb AAC97150.1 (U49397) MsmR [Streptococcus pyogenes] Length = 209
SeqID 2170	SA-806.1	Contig139 (124541-126205 p)	37	Identities = 141/1512 (27%), Positives = 222/1512 (42%), Gaps = 94/1512 (19%) pf IS52348 hypothetical protein 2 - Lactobacillus leichmannii emb CAA57459.1 (X81869) orf2 [Lactobacillus leichmannii] Length = 507
SeqID 2171	SA-807.1	Contig139 (126330-127217 p)	20	Identities = 45/141 (31%), Positives = 63/141 (43%), Gaps = 20/141 (14%) gb JBA04080.1 (AP001508) unknown [Bacillus halodurans] Length = 1661
SeqID 2172	SA-808.1	Contig139 (127219-128136 p)	46	Identities = 96/285 (36%), Positives = 150/285 (56%), Gaps = 10/285 (3%) gb AAC13546.1 (AF019629) putative fibrin-associated protein [Actinomyces naeslundii] Length = 365
SeqID 2173	SA-809.3	Contig139 (128192-128944 p)	36	Identities = 79/178 (44%), Positives = 112/178 (62%), Gaps = 71/178 (3%) gb AAC13546.1 (AF019629) putative fibrin-associated protein [Actinomyces naeslundii] Length = 365
SeqID 2174	SA-81.1	Contig131 (36277-36573 p)	66	Identities = 46/87 (47%), Positives = 69/87 (70%) ref NP_053020.1 hypothetical protein [Plasmid pNZ4000] gb AAD40361.1 (AF036485) hypothetical protein [Plasmid pNZ4000] gb AAF98302.1 (AF243383_3) (AF243383) unknown; Orf3 [Lactococcus lactis subsp. lactis] Length = 98

SeqID 2175	SA-810.3	Contig139 (128806-128955 p)	No Hits found	
SeqID 2176	SA-811.2	Contig123 (32704-32853 p)	85	Identities = 43/49 (87%), Positives = 46/49 (93%) sp O34102 RL33_LACLC 50S RIBOSOMAL PROTEIN L33 gb AA866692.1 (U89998) 50S ribosomal protein subunit L33 [Lactococcus lactis subsp. cremoris] Length = 49
SeqID 2177	SA-812.1	Contig123 (32506-32688 p)	55	Identities = 46/53 (86%), Positives = 49/53 (91%) sp O34102 RL32_LACLC 50S RIBOSOMAL PROTEIN L32 gb AA866691.1 (U89998) 50S ribosomal protein subunit L32 [Lactococcus lactis subsp. cremoris] Length = 58
SeqID 2178	SA-814.1	Contig123 (31008-32286 m)	84	Identities = 342/423 (80%), Positives = 377/423 (88%) sp P30053 SYH_STREQ HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) pf J530233 histidine-- trna ligase (EC 6.1.1.21) [validated] - Streptococcus equisimilis Length = 426
SeqID 2179	SA-817.1	Contig123 (29159-30913 m)	73	Identities = 339/586 (57%), Positives = 432/586 (72%), Gaps = 10/586 (1%) sp O32038 SYD_BAGSU ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pf D69591 aspartate--trna ligase (EC 6.1.1.12) asps - Bacillus subtilis emb CAB14714.1 (Z99118) aspartyl-RNA synthetase [Bacillus subtilis] Length = 592
SeqID 2180	SA-819.1	Contig123 (28225-29175 m)	57	Identities = 105/275 (38%), Positives = 182/275 (66%), Gaps = 11/275 (0%) emb CAB01834.1 (Z79580) putative ORF [Bacillus subtilis] emb CAA70630.1 (Y09476) Yit [Bacillus subtilis] emb CAB12952.1 (Z99109) alternate gene name: yuxA-similar to hypothetical proteins [Bacillus subtilis] Length = 280

SeqID 2181	SA-82.1	Contig131 (35422-36033 p)	77	<p>Identities = 139/201 (69%), Positives = 158/201 (77%), Gaps = 1/201 (0%) sp P21465 RS4_BACSU_30S_RIBOSOMAL_PROTEIN_S4 (BS4) pir J37146 ribosomal protein S4 - Bacillus subtilis gb AAZ27117.1 (M59358) ribosomal protein S4 [Bacillus subtilis] gb AAC00397.1 (AF008220) ribosomal protein S4 [Bacillus subtilis] emb CAB14944.1 (Z99119) ribosomal protein S4 (BS4) [Bacillus subtilis] Length = 200</p>
SeqID 2182	SA-820.1	Contig123 (27245-28117 m)	64	<p>Identities = 113/278 (40%), Positives = 192/278 (69%), Gaps = 1/278 (0%) db JBAB00397.1 (AP001512) unknown conserved protein [Bacillus halodurans] Length = 290</p>
SeqID 2183	SA-821.1	Contig123 (26910-27218 p)	43	<p>Identities = 27/88 (30%), Positives = 48/88 (53%), Gaps = 1/88 (1%) db JBAA11330.1 (D78257) BacB [Enterococcus faecalis] Length = 94</p>
SeqID 2184	SA-822.1	Contig123 (25131-26822 p)	80	<p>Identities = 377/566 (66%), Positives = 464/566 (81%), Gaps = 5/566 (0%) gb AAF68984.1 AF282249_3 (AF282249) ArgS [Lactococcus lactis subsp. lactis] Length = 564</p>
SeqID 2185	SA-823.1	Contig123 (24472-24918 m)	58	<p>Identities = 62/139 (44%), Positives = 89/139 (63%) sp Q54870 ARGR_STRPN_ARGININE_REPRESSOR pir B28667 hypothetical protein C - Streptococcus pneumoniae gb AAA88596.1 (M18729) unknown protein [Streptococcus pneumoniae] Length = 148</p>
SeqID 2186	SA-825.1	Contig123 (21839-24415 m)	81	<p>Identities = 593/858 (69%), Positives = 698/858 (81%), Gaps = 14/858 (1%) sp P10564 HEXA_STRPN_DNA_MISMATCH_REPAIR_PROTEIN_HEXA pir C28667 DNA mismatch repair protein hexA - Streptococcus pneumoniae gb AAA88597.1 (M18729) mismatch repair protein [Streptococcus pneumoniae] Length = 844</p>
SeqID 2187	SA-826.1	Contig123 (21579-21782 p)	76	<p>Identities = 48/63 (76%), Positives = 56/63 (88%) emb CAA71254.1 (Y10181) cold shock protein [Lactococcus lactis] emb CAA76695.1 (Y17215) cold shock protein B [Lactococcus lactis] Length = 66</p>

SeqID 2188	SA-828.1	Contig123 (19380-21359 m)	79	<p>Identities = 452/657 (68%), Positives = 543/657 (81%), Gaps = 8/657 (1%) sp P14160 HEXB_STRPN DNA MISMATCH REPAIR PROTEIN HEXB prf J433589 mismatch repair protein hexb [validated] - Streptococcus pneumoniae gb AA88800.1 (M29686) mismatch repair protein (Streptococcus pneumoniae) Length = 649</p>
SeqID 2189	SA-828.1	Contig123 (18116-19348 m)	55	<p>Identities = 145/401 (36%), Positives = 236/401 (58%), Gaps = 4/401 (0%) prf S58131 integral membrane protein LmrP - Lactococcus lactis emb CAA61918.1 (X89779) LmrP integral membrane protein [Lactococcus lactis] Length = 408</p>
SeqID 2190	SA-828.1	Contig123 (17524-18114 m)	61	<p>Identities = 86/201 (42%), Positives = 122/201 (59%), Gaps = 6/201 (2%) dbj BAB04943.1 (AP001511) holliday junction DNA helicase [Bacillus haecurans] Length = 203</p>
SeqID 2191	SA-831.1	Contig131 (34805-35092 p)	44	<p>Identities = 24/85 (28%), Positives = 45/85 (52%), Gaps = 8/85 (9%) sp P37468 VEG_BACSU VEG PROTEIN prf S66073 veg protein - Bacillus subtilis dbj BA405279.1 (D26185) unknown [Bacillus subtilis] emb CAB11820.1 (Z99104) veg [Bacillus subtilis] Length = 86</p>
SeqID 2192	SA-831.1	Contig123 (16850-17501 m)	63	<p>Identities = 87/176 (49%), Positives = 122/176 (68%), Gaps = 1/176 (0%) sp P05100 3MG1_ECOLI DNA-3-METHYLADENINE GLYCOSYLASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) (DNA-3-METHYLADENINE GLYCOSYLASE I) prf DGE01 3-methyladenine-DNA glycosylase (EC 3.2.2.-) - Escherichia coli emb CAA27472.1 (X03845) TAGI (aa 1-187) [Escherichia coli] gb AA24658.1 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] gb AAB18526.1 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] gb AAC76573.1 (AE000432) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli K12] Length = 187</p>

SeqID 2193	SA-832.1	Contig123 (15602-16861 m)	80	Identities = 292/417 (70%), Positives = 343/417 (82%), Gaps = 1/417 (0%) spIP54184/CINA_STRPN PUTATIVE COMPETENCE DAMAGE PROTEIN (EXPORTED PROTEIN 10) emb CAAB407.1.1 (Z34-303) CnA protein [Streptococcus pneumoniae] Length = 418
SeqID 2194	SA-833.1	Contig123 (14389-15528 m)	88	Identities = 340/340 (100%), Positives = 340/340 (100%) gb AAAG30537.1 AF307982.1 (AF307982) RecA [Streptococcus agalactiae] Length = 340
SeqID 2195	SA-834.1	Contig123 (13775-14185 m)	67	Identities = 61/127 (48%), Positives = 93/127 (73%) gb AAAF21893.1 AF103794.1 (AF103794) unknown [Listeria monocytogenes] Length = 131
SeqID 2196	SA-835.1	Contig123 (13307-13573 m)	70	Identities = 50/90 (55%), Positives = 67/90 (73%), Gaps = 1/90 (1%) db BAAG04987.1 (AP001511) unknown [Bacillus halodurens] Length = 90
SeqID 2197	SA-837.1	Contig123 (12888-13298 m)	68	Identities = 82/138 (59%), Positives = 109/138 (78%), Gaps = 1/138 (0%) spIQ34634 YRRK_BACSU HYPOTHETICAL 15.2 KDA PROTEIN IN UDK-ALAS INTERGENIC REGION pir ID9979 conserved hypothetical protein yrrk - Bacillus subtilis emb CAB14681.1 (Z99117) similar to hypothetical proteins [Bacillus subtilis] emb CAB14698.1 (Z99118) similar to hypothetical proteins [Bacillus subtilis] Length = 138
SeqID 2198	SA-838.1	Contig123 (12545-12862 m)	60	Identities = 50/95 (52%), Positives = 66/95 (68%), Gaps = 5/95 (5%) pir A65982 hypothetical protein yzB - Bacillus subtilis emb CAB14680.1 (Z99117) yzB [Bacillus subtilis] emb CAB14697.1 (Z99118) yzB [Bacillus subtilis] Length = 93
SeqID 2199	SA-839.2	Contig123 (10754-12295 m)	14	Identities = 39/172 (22%), Positives = 75/172 (42%), Gaps = 9/172 (5%) ref NP_066532.1 ABC transporter subunit [Naegleria gruberi] gb AAAG17810.1 AF288092.35 (AF288092) ABC transporter subunit [Naegleria gruberi] Length = 210

SeqID 2200	SA-84.1	Contig131 (33435-34793 p)	95	Identities = 398/452 (88%), Positives = 432/452 (95%), Gaps = 1/452 (0%) gplAAAF98347.1f (AF280763) DNA polymerase III delta prime subunit [Streptococcus pyogenes] Length = 455
SeqID 2201	SA-842.2	Contig112 (127-1845 p)	45	Identities = 193/426 (45%), Positives = 278/426 (64%), Gaps = 28/426 (6%) pirl[B82263] PTS system, trehalose-specific IIBC component VCO910 [imported] - Vibrio cholerae (group O1 strain N16861) gb AAAF94072.1f (AE004175) PTS system, trehalose-specific IIBC component [Vibrio cholerae] Length = 478
SeqID 2202	SA-843.1	Contig112 (2057-3692 p)	80	Identities = 380/547 (69%), Positives = 437/547 (79%), Gaps = 13/547 (2%) gplAAB65078.1f (U35633) dextran glucosidase DEXS [Streptococcus suis] Length = 542
SeqID 2203	SA-844.1	Contig112 (3912-5948 p)	53	Identities = 203/687 (29%), Positives = 362/697 (51%), Gaps = 34/697 (4%) dbj BAB03939.1f (AP001507) unknown conserved protein [Bacillus halodurans] Length = 701
SeqID 2204	SA-845.1	Contig112 (5951-6235 p)	50	Identities = 26/82 (31%), Positives = 52/82 (62%), Gaps = 2/82 (2%) dbj BAB03941.1f (AP001507) unknown conserved protein [Bacillus halodurans] Length = 89
SeqID 2205	SA-846.1	Contig112 (6248-7603 p)	64	Identities = 203/453 (44%), Positives = 293/453 (63%), Gaps = 22/453 (4%) pirl[T37086] probable integral membrane protein - Streptomyces coelicolor emb CAB52363.1f (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)] Length = 516
SeqID 2206	SA-847.1	Contig112 (7542-7700 m)	No Hits found	
SeqID 2207	SA-848.1	Contig112 (7606-8463 p)	54	Identities = 105/269 (39%), Positives = 158/269 (58%), Gaps = 4/269 (1%) sp O58094 TKTN_METJA PUTATIVE TRANSEPTOLASE N-TERMINAL SECTION (TK) pirl J64385 transketolase (EC 2.2.1.1) - Methanococcus jannaschii gb AA898676.1f (U67515) transketolase [Methanococcus jannaschii] Length = 274

SeqID 2208	SA-848.1	Contig112 (8460-9389 p)	50	<p>Identities = 99/310 (31%). Positives = 172/310 (54%). Gaps = 7/310 (2%). sp Q58092 TKTC_METUA PUTATIVE TRANSKETOLASE C-TERMINAL SECTION (TK) p I G64384 transketolase (EC 2.2.1.1) - Methanococcus jannaschii gb AAB98674.1 (U67515) transketolase [Methanococcus jannaschii] Length = 316</p>
SeqID 2209	SA-85.1	Contig131 (32943-33395 p)	67	<p>Identities = 80/149 (53%). Positives = 105/149 (69%). Gaps = 2/149 (1%). sp P02417 RL9_BACST 50S RIBOSOMAL PROTEIN L9 (BL17) p I R5BS7F ribosomal protein L9 - Bacillus stearothermophilus pdb 487D K Chain K, Seven Ribosomal Proteins Fitted To A Cryo-Electron Microscopic Map Of The Large 50s Subunit At 7.5 Angstroms Resolution pdb 1D1V Ribosomal Protein L9 Length = 149</p>
SeqID 2210	SA-850.1	Contig112 (9498-10757 p)	42	<p>Identities = 111/438 (25%). Positives = 195/438 (44%). Gaps = 51/438 (11%). p I G83576 hypothetical protein PA0545 [imported] - Pseudomonas aeruginosa gb AA03934.1 AE004491.1 (AE004491) hypothetical protein [Pseudomonas aeruginosa] Length = 434</p>
SeqID 2211	SA-851.1	Contig112 (10845-11114 p)	70	<p>Identities = 55/89 (61%). Positives = 71/89 (78%). sp P21473 RS15_BACSU 30S RIBOSOMAL PROTEIN S15 (BS18) p I F68700 ribosomal protein S15 (rpsO) - Bacillus subtilis emb CAB02960.1 (Z80835) ribosomal protein S15 [Bacillus subtilis] emb CAB13541.1 (Z99112) ribosomal protein S15 (BS18) [Bacillus subtilis] Length = 89</p>

SeqID 2212	SA-852.1	Contig112 (11495-13624 p)	74	<p>Identities = 431/708 (60%), Positives = 538/708 (75%), Gaps = 8/708 (1%) sp P50849 PNPA_BACSU POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) (VEGETATIVE PROTEIN 16) (VEG16) pf J070691 polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) alpha chain pnpA - Bacillus subtilis gbl AAC43595.1 U23668 polynucleotide phosphorylase [Bacillus subtilis] emb CAB13542.1 (Z99112) polynucleotide phosphorylase (PNPase) [Bacillus subtilis] prt J210369A polynucleotide phosphorylase [Bacillus subtilis] Length = 705</p>
SeqID 2213	SA-853.1	Contig112 (13626-14378 p)	No Hits found	
SeqID 2214	SA-854.1	Contig112 (14387-14871 p)	61	<p>Identities = 92/169 (54%), Positives = 125/169 (73%) emb CAB71304.1 (AJ130879) serine acetyltransferase [Clostridium sticklandii] Length = 191</p>
SeqID 2215	SA-855.1	Contig112 (14972-15163 p)	No Hits found	
SeqID 2216	SA-856.1	Contig112 (15232-16503 p)	70	<p>Identities = 246/467 (52%), Positives = 323/467 (68%), Gaps = 23/467 (4%) sp Q06752 SYC_BACSU CYSTEINYL-TRNA SYNTHETASE (CYSTEINE--TRNA LIGASE) (CYSRS) pf JC53402 cysteine--RNA ligase (EC 6.1.1.16) cysS - Bacillus subtilis gbl AA21798.1 (L14580) cysteinyl-HRNA synthetase [Bacillus subtilis] db BAA05328.1 (D26185) cysteinyl-RNA synthetase [Bacillus subtilis] emb CAA52167.1 (X73989) cysteine--RNA ligase [Bacillus subtilis] emb CAB11870.1 (Z99104) cysteinyl-RNA synthetase [Bacillus subtilis] Length = 466</p>
SeqID 2217	SA-857.1	Contig112 (16496-16882 p)	65	<p>Identities = 58/122 (47%), Positives = 87/122 (70%) pf J069742 conserved hypothetical protein yacZ - Bacillus subtilis emb CAB11871.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 143</p>

SeqID 2218	SA-858.1	Contig112 (16985-17740 p)	64	<p>Identities = 113/244 (46%), Positives = 163/244 (66%), Gaps = 6/244 (2%) sp Q06753 YACO_BAGSU-HYPOTHETICAL TRNA^{ARRNA} METHYLTRANSFERASE YACO pir S68124 conserved hypothetical protein yaco - Bacillus subtilis db BAA05329.1 (D26185) unknown [Bacillus subtilis] emb CAB11872.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 249</p>
SeqID 2219	SA-859.1	Contig112 (17737-18255 p)	52	<p>Identities = 66/147 (44%), Positives = 93/147 (62%), Gaps = 2/147 (1%) sp P37574 YACP_BACSU-HYPOTHETICAL 19.7 KD PROTEIN IN CYSS 3 REGION pir S66125 conserved hypothetical protein yacP - Bacillus subtilis db BAA05330.1 (D26185) unknown [Bacillus subtilis] emb CAB11873.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 170</p>
SeqID 2220	SA-86.1	Contig112 (31063-32937 p)	56	<p>Identities = 212/660 (32%), Positives = 376/660 (56%), Gaps = 14/660 (2%) db BAA07750.1 (AP001520) unknown conserved protein in B. subtilis [Bacillus halodurans] Length = 654</p>
SeqID 2221	SA-861.1	Contig112 (18348-19208 p)	53	<p>Identities = 100/284 (35%), Positives = 157/284 (55%), Gaps = 6/284 (2%) pir D69841 hypothetical protein yfH5 - Bacillus subtilis emb CAB01833.1 (Z79580) putative ORF [Bacillus subtilis] emb CAA70629.1 (Y06476) YfH5 [Bacillus subtilis] emb CAB12951.1 (Z99109) yfH5 [Bacillus subtilis] Length = 283</p>
SeqID 2222	SA-863.2	Contig112 (20193-21194 m)	35	<p>Identities = 73/255 (28%), Positives = 117/255 (45%), Gaps = 18/255 (7%) emb CAA50689.1 (X71844) putative transposase [Clostridium perfringens] Length = 350</p>
SeqID 2223	SA-864.3	Contig127 (33995-35254 p)	84	<p>Identities = 300/419 (71%), Positives = 359/419 (85%), Gaps = 1/419 (0%) gb AAK04483.1 AE0006275.7 (AE0006275) yfH5/-fH5 synthetase (EC 6.1.1) [Lactococcus lactis] subsp. [lactis] Length = 419</p>

SeqID 2224	SA-866.2	Contig127 (31587-33884 m)	75	Identities = 445/769 (57%), Positives = 562/769 (74%), Gaps = ---/9769 (4%) emb CAA05302.1 (AJ002291) penicillin-binding protein 1b [Streptococcus pneumoniae] gb AA04736.1 AF101781.1 (AF101781) penicillin-binding protein 1b [Streptococcus pneumoniae] Length = 821
SeqID 2225	SA-867.1	Contig127 (31366-31455 m)	No Hits found	
SeqID 2226	SA-868.1	Contig127 (27488-31063 m)	81	Identities = 814/1173 (69%), Positives = 978/1173 (82%), Gaps = 17/1173 (1%) emb CAB56706.1 (Y16468) DNA-dependent RNA polymerase subunit beta [Listeria monocytogenes] Length = 1184
SeqID 2227	SA-87.1	Contig131 (28966-30888 p)	78	Identities = 402/627 (64%), Positives = 503/627 (80%), Gaps = 5/627 (0%) db BAB07780.1 (AP001520) glucose-inhibited division protein [Bacillus halodurans] Length = 632
SeqID 2228	SA-872.1	Contig127 (23721-27371 m)	78	Identities = 935/990 (94%), Positives = 959/990 (96%), Gaps = 1/990 (0%) sp P95816 RPOC_STRPY DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT) emb CAA65249.1 (X96385) DNA-dependent RNA polymerase [Streptococcus pyogenes] Length = 989
SeqID 2229	SA-874.1	Contig127 (23242-23607 m)	59	Identities = 42/89 (42%), Positives = 75/89 (75%) gb AAC45308.1 (U81957) putative DNA binding protein [Streptococcus gordonii] Length = 122
SeqID 2230	SA-875.1	Contig127 (22098-23069 m)	74	Identities = 202/319 (63%), Positives = 254/319 (79%), Gaps = 1/319 (0%) gb AAC45310.1 (U81957) putative ABC transporter subunit ComYA [Streptococcus gordonii] Length = 319
SeqID 2231	SA-876.1	Contig127 (21161-22252 m)	59	Identities = 161/280 (57%), Positives = 218/280 (77%) gb AAC45311.1 (U81957) putative ABC transporter subunit ComYB [Streptococcus gordonii] Length = 282
SeqID 2232	SA-877.1	Contig127 (20835-21164 m)	58	Identities = 63/103 (61%), Positives = 85/103 (82%) gb AAC45312.1 (U81957) ComYC [Streptococcus gordonii] Length = 105

SeqID 2233	SA-878.1	Contig127 (20447-20860 m)	57	<p>Identities = 54/127 (42%), Positives = 83/127 (64%) gb AAC23740.1 (AF052207) competence protein [Streptococcus pneumoniae] Length = 134</p>
SeqID 2234	SA-879.1	Contig127 (20176-20421 m)	49	<p>Identities = 27/91 (29%), Positives = 50/91 (54%) emb CAA75316.1 (Y15043).hypothetical protein [Lactococcus lactis subsp. cremoris] Length = 128</p>
SeqID 2235	SA-880.1	Contig127 (19761-20222 m)	56	<p>Identities = 61/147 (41%), Positives = 98/147 (66%), Gaps = 3/147 (2%) emb CAA75315.1 (Y15043) homology to ComYD from Streptococcus gordonii, and ComGD from Bacillus subtilis [Lactococcus lactis subsp. cremoris] Length = 150</p>
SeqID 2236	SA-881.1	Contig127 (19412-19783 m)	No Hits found	
SeqID 2237	SA-882.1	Contig127 (18323-19297 m)	53	<p>Identities = 105/329 (31%), Positives = 177/329 (52%), Gaps = 17/329 (5%) sp P37876 YTX_K_BACSU HYPOTHETICAL 37.4 KD PROTEIN IN ACKA-SSPA INTERGENIC REGION pir G70003 hypothetical protein yxk - Bacillus subtilis gb AAC00317.1 (AF008220) Yxk [Bacillus subtilis] emb CAB14926.1 (Z99119) alternate gene name: ythI [Bacillus subtilis] Length = 329</p>
SeqID 2238	SA-883.1	Contig127 (17098-18291 m)	73	<p>Identities = 223/395 (56%), Positives = 293/395 (73%), Gaps = 3/395 (0%) sp P37877 ACKA_BACSU ACETATE KINASE (ACETOKINASE) pir B49835 acetate kinase (EC 2.7.2.1) ackA - Bacillus subtilis gb AAC36857.1 (L17320) acetate kinase [Bacillus subtilis] gb AAC00318.1 (AF008220) acetate kinase [Bacillus subtilis] emb CAB14925.1 (Z99119) acetate kinase [Bacillus subtilis] Length = 395</p>
SeqID 2239	SA-884.1	Contig127 (16741-16947 m)	70	<p>Identities = 39/64 (60%), Positives = 49/64 (75%) pir G75183 probable repressor protein PAB7155 - Pyrococcus abyssi (strain Orsay) emb CAB49550.1 (A248284) repressor protein, putative [Pyrococcus abyssi] Length = 73</p>
SeqID 2240	SA-885.2	Contig127 (16049-16510 m)	No Hits found	
SeqID 2241	SA-887.2	Contig139 (62447-62844 p)	No Hits found	

SeqID 2242	SA-889.1	Contig139 (52886-53620 m)	82	<p>Identities = 227/311 (72%), Positives = 269/311 (85%) spOQX9S0PYRD_STRPN DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODHASE) (DHOD) emb CAB51330.1 (AJ131985) dihydroorotate dehydrogenase (Streptococcus pneumoniae) Length = 311</p>
SeqID 2243	SA-889.1	Contig131 (28206-28617 p)	57	<p>Identities = 71/202 (35%), Positives = 120/202 (59%), Gaps = 5/202 (2%) spO32244YVBG_BACSU HYPOTHETICAL 22.6 KD PROTEIN IN OPUCA-ENO INTERGENIC REGION prj F70029 conserved hypothetical protein yvbG - Bacillus subtilis emb CAB15390.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] Length = 211</p>
SeqID 2244	SA-890.1	Contig139 (53807-55042 m)	72	<p>Identities = 237/410 (57%), Positives = 304/410 (73%) emb CAB89121.1 (AJ277485) beta-lactam resistance factor [Streptococcus pneumoniae] Length = 410</p>
SeqID 2245	SA-891.1	Contig139 (55061-56272 m)	70	<p>Identities = 204/410 (49%), Positives = 286/410 (69%), Gaps = 17/410 (4%) emb CAB89537.1 (AJ250766) MurM protein [Streptococcus pneumoniae] emb CAB89539.1 (AJ250767) MurM protein [Streptococcus pneumoniae] Length = 406</p>
SeqID 2246	SA-892.1	Contig139 (56285-57505 m)	60	<p>Identities = 165/410 (40%), Positives = 250/410 (60%), Gaps = 10/410 (2%) emb CAB89120.1 (AJ277484) beta-lactam resistance factor [Streptococcus pneumoniae] Length = 406</p>
SeqID 2247	SA-893.1	Contig139 (57505-58529 m)	68	<p>Identities = 127/269 (47%), Positives = 189/269 (70%), Gaps = 1/269 (0%) spPO9897YIDA_ECOLI HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION prj QCEGB hypothetical 29.7K protein. bpa-gyrb intergenic region - Escherichia coli (strain K-12) gb AAC76720.1 (AE000446) orf, hypothetical protein [Escherichia coli K12] Length = 270</p>
SeqID 2248	SA-894.1	Contig139 (58388-59704 m)	61	<p>Identities = 212/429 (49%), Positives = 287/429 (66%), Gaps = 5/429 (1%) db BA07537.1 (AP001520) unknown conserved protein [Bacillus halodurans] Length = 432</p>

SeqID 2249	SA-895.1	Contig139 (59768-60166 p)	No Hits found	
SeqID 2250	SA-896.1	Contig139 (60534-63194 p)	57	Identities = 378/886 (42%), Positives = 542/886 (60%), Gaps = 45/886 (5%) pir E59877 calcium-transporting ATPase homolog yj0B - Bacillus subtilis emb CA74269.1 (Y13937) putative PacI protein [Bacillus subtilis] emb CAB13439.1 (Z99112) similar to calcium-transporting ATPase [Bacillus subtilis] Length = 890
SeqID 2251	SA-897.1	Contig139 (63239-64099 m)	33	Identities = 60/221 (27%), Positives = 100/221 (45%), Gaps = 37/221 (16%) pir E75186 hypothetical protein PAB0011 - Pyrococcus abyssi (strain Orsay) emb CAB48940.1 (AJ248283) hypothetical protein [Pyrococcus abyssi] Length = 248
SeqID 2252	SA-898.1	Contig139 (64251-66182 p)	69	Identities = 315/644 (48%), Positives = 447/644 (68%), Gaps = 7/644 (1%) pir C69621 fructose-bisphosphatase (EC 3.1.3.11) - Bacillus subtilis dbj BAA11277.1 (D78193) yjyE [Bacillus subtilis] emb CAB16056.1 (Z99124) fructose-1,6-bisphosphatase [Bacillus subtilis] Length = 671
SeqID 2253	SA-899.1	Contig139 (66272-67396 p)	64	Identities = 177/371 (47%), Positives = 242/371 (64%), Gaps = 6/371 (1%) pir E59820 conserved hypothetical protein yhbA - Bacillus subtilis emb CAB07527.1 (Z93102) hypothetical 48.5 kd protein [Bacillus subtilis] emb CAB12719.1 (Z99108) alternate gene name: ygap~similar to hypothetical proteins [Bacillus subtilis] Length = 435
SeqID 2254	SA-9.1	Contig137 (36200-36682 p)	No Hits found	
SeqID 2255	SA-90.1	Contig131 (27053-28174 p)	72	Identities = 250/359 (69%), Positives = 292/359 (80%), Gaps = 6/359 (1%) dbj BAC04980.1 (AP001511) (5-methylaminomethyl)-2-thiouridylyl-methyltransferase [Bacillus halodurans] Length = 371

SeqID 2256	SA-901.1	Contig139 (67563-68563 p)	73	<p>Identities = 197/344 (57%), Positives = 255/344 (73%), Gaps = 2/344 (0%) spIP28367/RF2_BACSU PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) pir JN0146 translation releasing factor RF-2 - [Bacillus subtilis] gb AAC67534.1 (AF013188) release factor 2 [Bacillus subtilis] gb AAC67303.1 (AF017113) putative peptide chain release factor RF-2 [Bacillus subtilis] emb CAB15546.1 (Z99122) peptide chain release factor 2 [Bacillus subtilis] Length = 366</p>
SeqID 2257	SA-902.1	Contig139 (68562-69274 p)	76	<p>Identities = 138/228 (60%), Positives = 179/228 (77%) pir D69627 cell-division ATP-binding protein ftsE - Bacillus subtilis gb AAC67262.1 (AF017113) cell division ATP-binding protein [Bacillus subtilis] emb CAB15543.1 (Z99122) cell-division ATP-binding protein [Bacillus subtilis] Length = 228</p>
SeqID 2258	SA-904.1	Contig139 (69258-70187 p)	52	<p>Identities = 111/311 (35%), Positives = 181/311 (57%), Gaps = 31/311 (9%) sp O34876 FTSX_BACSU CELL DIVISION PROTEIN FTSX HOMOLOG pir G69627 cell-division protein ftsX - Bacillus subtilis gb AAC67264.1 (AF017113) cell division protein [Bacillus subtilis] emb CAB15542.1 (Z99122) cell-division protein [Bacillus subtilis] Length = 296</p>
SeqID 2259	SA-905.1	Contig139 (70240-70950 m)	41	<p>Identities = 65/185 (35%), Positives = 100/185 (53%), Gaps = 3/185 (1%) pir J475409 carboxymethylglutaminase-related protein - Deinococcus radiodurans (strain R1) gb AAF10898.1/AE001979.4 (AE001979) carboxymethylglutaminase-related protein [Deinococcus radiodurans] Length = 252</p>
SeqID 2260	SA-906.2	Contig139 (70947-71582 m)	48	<p>Identities = 83/197 (42%), Positives = 114/197 (57%), Gaps = 4/197 (2%) dbj BAB06539.1 (AP001516) BH2820-unknown conserved protein [Bacillus halodurans] Length = 211</p>

SeqID 2261	SA-907.2	Contig130 (21596-21796 p)	76	<p>Identities = 58/66 (84%), Positives = 60/66 (90%) -dbj BA23749.1 (AB009314) proton-translocating ATPase, c-subunit [Streptococcus bovis] Length = 67</p>
SeqID 2262	SA-908.2	Contig130 (21825-22545 p)	75	<p>Identities = 147/238 (61%), Positives = 180/238 (74%) dbj BA23750.1 (AB009314) proton-translocating ATPase, alpha subunit [Streptococcus bovis] Length = 239</p>
SeqID 2263	SA-909.1	Contig130 (22565-23060 p)	73	<p>Identities = 103/165 (62%), Positives = 130/165 (78%) sp P95785 ATPF_STRMU ATP SYNTHASE B CHAIN pir JC5737 membrane-bound proton-translocating ATPase (EC 3.6.1.-) b chain - Streptococcus mutans gb AAD13379.1 (U31170) ATPase, b subunit [Streptococcus mutans] Length = 165</p>
SeqID 2264	SA-91.1	Contig131 (26139-26807 m)	64	<p>Identities = 101/216 (46%), Positives = 155/216 (71%), Gaps = 2/216 (0%) dbj BAB06216.1 (AP001515) L-serine dehydratase beta subunit [Bacillus halodurans] Length = 220</p>
SeqID 2265	SA-910.1	Contig130 (23060-23596 p)	68	<p>Identities = 98/178 (55%), Positives = 127/178 (71%) sp O50156 ATPD_STRBO ATP SYNTHASE DELTA CHAIN dbj BA23752.1 (AB009314) proton-translocating ATPase, delta subunit [Streptococcus bovis] Length = 178</p>
SeqID 2266	SA-911.1	Contig130 (23812-25117 p)	98	<p>Identities = 480/501 (95%), Positives = 497/501 (98%) dbj BA23753.1 (AB009314) proton-translocating ATPase, alpha subunit [Streptococcus bovis] Length = 501</p>
SeqID 2267	SA-912.1	Contig130 (25133-26014 p)	93	<p>Identities = 254/293 (86%), Positives = 278/293 (94%), Gaps = 2/293 (0%) dbj BA23754.1 (AB009314) proton-translocating ATPase, gamma subunit [Streptococcus bovis] Length = 291</p>
SeqID 2268	SA-913.1	Contig130 (26088-27494 p)	92	<p>Identities = 434/466 (93%), Positives = 454/466 (97%) sp P95789 ATPB_STRMU ATP SYNTHASE BETA CHAIN gb AAD13383.1 (U31170) ATPase, beta subunit [Streptococcus mutans] Length = 468</p>

SeqID 2269	SA-914.1	Contig130 (27507-27920 p)	85	<p>Identities = 102/138 (73%), Positives = 121/138 (86%), Gaps = 1/138 (0%) dbj BA23756.1 (AB09314) proton-translocating ATPase, epsilon subunit [Streptococcus bovis] Length = 138</p> <p>Identities = 248/423 (58%), Positives = 323/423 (75%), Gaps = 5/423 (1%) sp P70965 NUA1_BACSU UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE 1 (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EFT) pir JAG9862 UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA - Bacillus subtilis emb CA03688.1 (Z91356) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis] emb CAB15693.1 (Z99122) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis] Length = 436</p>
SeqID 2270	SA-916.1	Contig130 (28276-29549 p)	73	
SeqID 2271	SA-917.1	Contig130 (29817-30674 p)	69	<p>Identities = 167/287 (58%), Positives = 200/287 (69%), Gaps = 15/287 (5%) sp Q03158 NUCE_STRPN DNA-ENTRY NUCLEASE (COMPETENCE-SPECIFIC NUCLEASE) pir J10641 endA protein - Streptococcus pneumoniae emb CAA38134.1 (X54225) membrane nuclease [Streptococcus pneumoniae] Length = 274</p>
SeqID 2272	SA-918.1	Contig130 (30965-32005 p)	77	<p>Identities = 211/341 (61%), Positives = 272/341 (78%), Gaps = 2/341 (0%) sp P17921 SYFA_BACSU PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (PHENYLALANINE-TRNA LIGASE ALPHA CHAIN) (PHERS) pir YFBSA phenylalanine-TRNA ligase (EC 6.1.1.20) alpha chain - Bacillus subtilis emb CAA9903.1 (Z75208) phenylalanyl-RNA synthetase beta subunit [Bacillus subtilis] emb CAB14824.1 (Z99118) phenylalanyl-RNA synthetase (alpha subunit) [Bacillus subtilis] Length = 344</p>

SeqID 2273	SA-919.1	Contig130 (32088-32605 p)	51	<p>Identities = 61/169 (36%), Positives = 100/169 (59%) sp P1340 PAIA_BACSU PROTEASE SYNTHASE AND SPORULATION NEGATIVE REGULATORY PROTEIN PAI 1 emb CAB15205.1 (Z99120) transcriptional regulator [Bacillus subtilis] Length = 172</p>
SeqID 2274	SA-920.1	Contig130 (32863-35065 p)	64	<p>Identities = 376/805 (46%), Positives = 523/805 (64%), Gaps = 6/805 (0%) sp P17922 SYFB_BACSU PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS) p P17FBSB phenylalanine--tRNA ligase (EC 6.1.1.2) beta chain - Bacillus subtilis emb CAA99564.1 (Z75208) phenylalanyl-tRNA synthetase beta subunit [Bacillus subtilis] emb CAB14823.1 (Z99118) phenylalanyl-tRNA synthetase (beta subunit) [Bacillus subtilis] Length = 804</p>
SeqID 2275	SA-921.1	Contig130 (35137-35805 m)	63	<p>Identities = 105/196 (53%), Positives = 141/196 (71%), Gaps = 1/196 (0%) p P1B65023 hypothetical protein b2475 - Escherichia coli (strain K-12) gb AAC75528.1 (AE000334)orf, hypothetical protein [Escherichia coli K12] Length = 287</p>
SeqID 2276	SA-923.1	Contig130 (35916-39149 p)	56	<p>Identities = 363/1093 (33%), Positives = 606/1093 (55%), Gaps = 67/1093 (6%) p P1T30307 rexB protein - Lactococcus lactis gb AAC12966.1 (U76424) exonuclease RexB [Lactococcus lactis] Length = 1099</p>
SeqID 2277	SA-925.1	Contig130 (39136-42762 p)	61	<p>Identities = 518/1212 (42%), Positives = 744/1212 (60%), Gaps = 73/1212 (6%) p P1T30308 rexA protein - Lactococcus lactis gb AAC12966.1 (U76424) exonuclease RexA [Lactococcus lactis] Length = 1173</p>
SeqID 2278	SA-926.1	Contig130 (42775-43701 p)	47	<p>Identities = 88/306 (28%), Positives = 149/306 (47%), Gaps = 17/306 (5%) ref NP_053049.1 hypothetical protein [Plasmid pNZ4000] gb AAD40365.1 (AF036485) hypothetical protein [Plasmid pNZ4000] Length = 302</p>

SeqID 2279	SA-928.2	Contig130 (43576-45052 m)	95	<p>Identities = 443/462 (95%), Positives = 447/462 (95%), Gaps = 4/462 (0%) emb CAAB61255.1 (A251564) thiophene degradation protein F [Streptococcus agalactiae] Length = 462</p>
SeqID 2280	SA-93.1	Contig131 (26252-26124 m)	75	<p>Identities = 176/289 (60%), Positives = 224/289 (76%), Gaps = 1/289 (0%) sp O34607 SDHA_BACSU PROBABLE L-SERINE DEHYDRATASE, ALPHA CHAIN (L-SERINE DEAMINASE) (SDH) (L-SD) pir G69879 L-serine dehydratase homolog yhpA - Bacillus subtilis emb CAA74259.1 (Y13937) putative YhpP protein [Bacillus subtilis] emb CAB13459.1 (Z99112) similar to L-serine dehydratase [Bacillus subtilis] Length = 300</p>
SeqID 2281	SA-930.2	Contig117 (7623-8582 m)	76	<p>Identities = 241/316 (76%), Positives = 265/316 (83%) gb AAK05072.1 AE006332.1 (AE006332) ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1) [Lactococcus lactis subsp. lactis] Length = 325</p>
SeqID 2282	SA-931.2	Contig117 (8785-10944 m)	67	<p>Identities = 367/701 (52%), Positives = 488/701 (69%), Gaps = 19/701 (2%) gb AAD41036.1 AF112535.3 (AF112535) ribonucleotide reductase alpha-chain [Corynebacterium glutamicum] Length = 707</p>
SeqID 2283	SA-932.2	Contig117 (11022-11246 m)	67	<p>Identities = 42/70 (60%), Positives = 53/70 (75%) sp Q48708 NRDH_LACLC GLUTAREDOXIN-LIKE PROTEIN NRDH emb CAA63372.1 (X92690) glutaredoxin-like protein [Lactococcus lactis] Length = 72</p>
SeqID 2284	SA-934.1	Contig117 (11628-11891 p)	92	<p>Identities = 86/87 (98%), Positives = 87/87 (99%) dbj BAA78048.1 (AB027569) histidine containing protein [Streptococcus bovis] Length = 87</p>
SeqID 2285	SA-936.1	Contig117 (11896-13629 p)	95	<p>Identities = 533/577 (92%), Positives = 559/577 (96%) dbj BAA78049.1 (AB027569) phosphoenolpyruvate-protein phosphotransferase [Streptococcus bovis] Length = 577</p>

SeqID 2286	SA-937.1	Contig117 (13779-15206 p)	80	<p>IDENTITIES = 0/117 (0%) Positives = 0/117 (0%)</p> <p>spIQ59931[GAPN_STRIMU NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (NADP+)] (TRIOSEPHOSPHATE DEHYDROGENASE) p[HA57151] glyceraldhyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - Streptococcus mutans p[db11EUH1A] Chain A, Apo Form Of A NADp Dependent Aldehyde Dehydrogenase From Streptococcus Mutans p[db11EUH1B] Chain B, Apo Form Of A NADp Dependent Aldehyde Dehydrogenase From Streptococcus Mutans p[db11EUH1C] Chain C, Apo Form Of A NADp Dependent Aldehyde Dehydrogenase From Streptococcus Mutans p[db11EUH1D] Chain D, Apo Form Of A NADp Dependent Aldehyde Dehydrogenase From Streptococcus Mutans p[db12EUH1A] Chain A, Holo Form Of A NADp Dependent Aldehyde Dehydrogenase Complex With NADP+ p[db12EUH1B] Chain B, Holo Form Of A NADp Dependent Aldehyde Dehydrogenase Complex With NADP+</p> <p>IDENTITIES = 133/439 (30%) Positives = 232/439 (52%) Gaps = 20/439 (4%) emb CAB86552.1 (AJ251472) peptidoglycan GicNAC deacetylase [Streptococcus pneumoniae] Length = 463</p>
SeqID 2287	SA-939.1	Contig117 (15346-16599 p)	54	<p>IDENTITIES = 70/115 (60%) Positives = 78/115 (66%) Gaps = 6/115 (5%) dbj BA035959.1 (AB042839) secretory protein SA1-B [Staphylococcus aureus] Length = 233</p>
SeqID 2288	SA-94.1	Contig131 (24440-25117 p)	32	<p>IDENTITIES = 138/343 (40%) Positives = 200/343 (58%) Gaps = 9/343 (2%) p[IC69813] RNA helicase homolog yfmL - Bacillus subtilis dbj BA022326.1 (D86417) yfmL [Bacillus subtilis] emb CAB12572.1 (Z39108) similar to RNA helicase [Bacillus subtilis] Length = 376</p>
SeqID 2289	SA-941.1	Contig117 (16630-17712 m)	54	

SeqID 2290	SA-942.1	Contig117 (178573-18486 p)	79	<p>Identities = 132/207 (63%), Positives = 167/207 (79%) sp Q32033 URK_BACSU URIDINE KINASE (URIDINE MONOPHOSPHOKINASE) prj 569728 uridine kinase udk - Bacillus subtilis emb CAB14675.1 (Z99117) uridine kinase [Bacillus subtilis] Length = 211</p>
SeqID 2291	SA-943.1	Contig117 (18573-19070 p)	54	<p>Identities = 66/146 (45%), Positives = 95/146 (64%) prj F82706 conserved hypothetical protein XF1230 [imported] - Xylella fastidiosa (strain 9a5c) gb AAAF9400.1 AE003957.1 (AE003957) conserved hypothetical protein [Xylella fastidiosa] Length = 162</p>
SeqID 2292	SA-944.1	Contig117 (19070-20734 p)	84	<p>Identities = 408/558 (73%), Positives = 473/558 (84%), Gaps = 6/558 (1%) gb AAAF98348.1 (AF280764) DNA polymerase III gamma/tau subunits [Streptococcus pyogenes] Length = 556</p>
SeqID 2293	SA-945.1	Contig117 (20847-21017 p)	No Hits found	
SeqID 2294	SA-946.1	Contig117 (20998-21933 m)	50	<p>Identities = 103/315 (32%), Positives = 169/315 (52%), Gaps = 18/315 (5%) dbj BAB0504.1 (AP001512) transcriptional repressor of the biotin operon [Bacillus halodurans] Length = 323</p>
SeqID 2295	SA-947.1	Contig117 (22118-23314 p)	78	<p>Identities = 265/390 (67%), Positives = 325/390 (82%), Gaps = 1/390 (0%) sp P54419 METK_BACSU S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLMTRANSFERASE) (ADOMET SYNTHETASE) prj D68657 methionine adenosyltransferase (EC 2.5.1.6) - Bacillus subtilis gb AAC0242.1 (AF008220) SAM synthase [Bacillus subtilis] emb CAB15083.1 (Z99119) S-adenosyl(methionine) synthetase [Bacillus subtilis] Length = 400</p>
SeqID 2296	SA-948.1	Contig117 (23609-25740 p)	40	<p>Identities = 135/648 (20%), Positives = 261/648 (39%), Gaps = 90/648 (13%) emb CAB39037.2 (AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] Length = 1946</p>
SeqID 2297	SA-949.1	Contig117 (25807-26352 p)	No Hits found	
SeqID 2298	SA-950.1	Contig117 (26503-26640 p)	No Hits found	

SeqID 2299	SA-951.1	Contig117 (26745-27314 p)	34	Identities = 50/177 (28%), Positives = 81/177 (45%), Gaps = 31/177 (17%) pir B7247.1 hypothetical protein APE2411 - Aeropyrum pernix (strain K1) db BAA81426.1 (AP000064) 197aa long hypothetical protein [Aeropyrum pernix] Length = 197
SeqID 2300	SA-952.1	Contig117 (27311-27865 p)	63	Identities = 71/182 (39%), Positives = 121/182 (66%), Gaps = 31/182 (1%) pir A69859 hypothetical protein ykoE - Bacillus subtilis emb CA05602.1 (AJ002571) YkoE [Bacillus subtilis] emb CAB13180.1 (Z298110) ykoE [Bacillus subtilis] Length = 199
SeqID 2301	SA-953.1	Contig117 (27869-29071 p)	55	Identities = 139/450 (30%), Positives = 224/450 (48%), Gaps = 68/450 (15%) pir H69858 cation ABC transporter (ATP-binding protein) homolog ykoD - Bacillus subtilis emb CA05601.1 (AJ002571) YkoD [Bacillus subtilis] emb CAB13179.1 (Z298110) similar to cation ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 490
SeqID 2302	SA-954.1	Contig107 (488-1790 m)	No Hits found	
SeqID 2303	SA-955.1	Contig107 (1924-2223 m)	No Hits found	
SeqID 2304	SA-956.1	Contig107 (2234-3481 m)	58	Identities = 167/436 (38%), Positives = 248/436 (56%), Gaps = 44/436 (10%) db BAB07254.1 (AP001519) unknown [Bacillus halodurans] Length = 449
SeqID 2305	SA-957.1	Contig107 (3478-5109 m)	56	Identities = 194/548 (35%), Positives = 316/549 (57%), Gaps = 39/549 (6%) gb AAB06502.1 (U59302) relaxase [Lactococcus lactis subsp. lactis] Length = 563
SeqID 2306	SA-958.1	Contig107 (5081-5455 m)	40	Identities = 31/102 (30%), Positives = 53/102 (51%), Gaps = 2/102 (1%) gb AAAF72356.1 (AF192329) unknown [Enterococcus faecalis] Length = 109
SeqID 2307	SA-959.1	Contig107 (5458-6021 m)	No Hits found	
SeqID 2308	SA-96.1	Contig131 (23828-24307 p)	36	Identities = 54/98 (55%), Positives = 68/98 (69%), Gaps = 4/98 (4%) emb CAAG6725.1 (Y08498) aggregation promoting protein [Lactobacillus gasseri] Length = 297

SeqID 2309	SA-960.1	Contig107 (6024-6353 m)	No Hits found	15	Identities = 106/344 (30%), Positives = 175/344 (50%), Gaps = 21/344 (6%) refNP_047307.1 Lac [Lactococcus lactis] pir T43094 hypothetical protein - Lactococcus lactis plasmid pMRC01 gb AAC56005.1 (AE001272) LTrC [Lactococcus lactis] Length = 355
SeqID 2310	SA-961.1	Contig107 (6364-6663 m)	No Hits found		
SeqID 2311	SA-964.1	Contig107 (6715-9951 m)			
SeqID 2312	SA-966.1	Contig107 (9953-10318 m)	No Hits found		
SeqID 2313	SA-967.1	Contig107 (10360-12360 m)	42		Identities = 177/530 (33%), Positives = 296/530 (55%), Gaps = 22/530 (4%) gb AAAF72343.1 AF192329_4 (AF192329) Trsk-like protein [Enterococcus faecalis] Length = 564
SeqID 2314	SA-968.1	Contig107 (12405-12895 m)	32		Identities = 37/114 (32%), Positives = 56/114 (48%), Gaps = 10/114 (8%) pir E72215 oligopeptide ABC transporter, periplasmic oligopeptide-binding protein - Thermoboga maritima (strain MSB8) gb AAD36811.1 AE001813.3 (AE001813) oligopeptide ABC transporter, periplasmic oligopeptide-binding protein [Thermoboga maritima] Length = 642
SeqID 2315	SA-969.1	Contig107 (12918-13700 m)	31		Identities = 47/187 (25%), Positives = 84/187 (44%), Gaps = 21/187 (11%) pir S45089 hypothetical protein eta - Streptococcus pyogenes plasmid pDB101 pir S68123 hypothetical protein eta - Streptococcus pyogenes plasmid pMD101 emb CA447095.1 (X66468) orf eta [Streptococcus pyogenes] Length = 231
SeqID 2316	SA-970.1	Contig107 (13700-13872 m)	No Hits found		
SeqID 2317	SA-971.1	Contig107 (13992-14597 m)	No Hits found		
SeqID 2318	SA-973.1	Contig107 (14618-17308 m)	7		Identities = 54/133 (40%), Positives = 66/133 (49%), Gaps = 9/133 (6%) gb AAC61959.1 (AF051917) putative membrane protein TraG [Staphylococcus aureus] pir 200426/H traG protein [Staphylococcus sp.] Length = 358
SeqID 2319	SA-974.1	Contig107 (17287-17871 p)	No Hits found		

SeqID 2320	SA-975.1	Contig107 (18065-20356 m)	50	Identities = 233/769 (30%), Positives = 387/769 (50%), Gaps = 29/769 (3%) gb AAFP72347.1 AF192329.8 (AF192329) TrsE-like protein [Enterococcus faecalis] Length = 799
SeqID 2321	SA-976.2	Contig114 (16174-17361 m)	33	Identities = 77/279 (27%), Positives = 136/279 (48%), Gaps = 14/279 (5%) sp Q54955 CIAH_STRPN SENSOR PROTEIN CIAH prj 549545 histidine kinase - Streptococcus pneumoniae emb CA54466.1 (X77249) histidine kinase [Streptococcus pneumoniae] emb CA54565.1 (AJ005926) histidine kinase [Streptococcus pneumoniae] Length = 444
SeqID 2322	SA-977.1	Contig114 (14493-16028 m)	90	Identities = 403/511 (78%), Positives = 466/511 (90%) gb AAC05774.1 (AF051386) D-alanine-D-alanyl carrier protein ligase [Streptococcus mutans] Length = 516
SeqID 2323	SA-978.1	Contig114 (13231-14496 m)	81	Identities = 296/418 (70%), Positives = 351/418 (83%), Gaps = 1/418 (0%) gb AAC05775.1 (AF051356) integral membrane protein [Streptococcus mutans] Length = 420
SeqID 2324	SA-98.1	Contig131 (22758-23552 p)	67	Identities = 133/263 (50%), Positives = 131/263 (72%) prj F69742 hypothetical protein yofA - Bacillus subtilis emb CAB11923.1 (Z39104) yofA [Bacillus subtilis] Length = 265
SeqID 2325	SA-980.1	Contig114 (12977-13216 m)	85	Identities = 65/79 (82%), Positives = 74/79 (93%) gb AAC05776.1 (AF051356) D-alanyl carrier protein [Streptococcus mutans] gb AAC29040.1 (AF050517) unknown [Streptococcus mutans] gb AAC06286.1 (AF049357) Gtg3 [Streptococcus mutans] Length = 79
SeqID 2326	SA-981.1	Contig114 (11722-12984 m)	72	Identities = 238/421 (56%), Positives = 308/421 (72%), Gaps = 1/421 (0%) gb AAC29041.1 (AF050517) unknown [Streptococcus mutans] Length = 421
SeqID 2327	SA-982.1	Contig114 (11155-11472 m)	No Hits found	
SeqID 2328	SA-983.1	Contig114 (9663-11155 m)	19	Identities = 49/185 (26%), Positives = 85/185 (45%), Gaps = 46/185 (24%) db BA01041.1 (AB022220) gene_ic MLN21.14-unknown protein [Arabidopsis thaliana] Length = 507

SeqID 2329 SeqID 2330	SA-984.1 SA-985.1	Contig114 (9480-9872 m) Contig114 (9189-9479 m)	No Hits found No Hits found	
SeqID 2331	SA-986.2	Contig114 (8225-9007 m)	55	<p>Identities = 115/254 (45%), Positives = 172/254 (67%)</p> <p>sp P37545 YABD_BACSU PUTATIVE DEOXYRIBONUCLEASE YABD - pir J36068 conserved hypothetical protein yabD - Bacillus subtilis dbj BA05274.1 (D26185) unknown [Bacillus subtilis] emb CAB11815.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 255</p>
SeqID 2332	SA-987.2	Contig114 (7672-8241 m)	60	<p>Identities = 82/179 (45%), Positives = 117/179 (64%), Gaps = 4/179 (2%) sp P37547 YABF_BACSU HYPOTHETICAL 20.7 KD PROTEIN IN METS-KSGA INTERGENIC REGION - pir J36070 conserved hypothetical protein yabF - Bacillus subtilis dbj BA05276.1 (D26185) unknown [Bacillus subtilis] emb CAB11817.1 (Z99104) similar to hypothetical proteins [Bacillus subtilis] Length = 186</p>
SeqID 2333	SA-988.2	Contig114 (7219-7668 m)	39	<p>Identities = 39/121 (32%), Positives = 60/121 (49%), Gaps = 12/121 (9%) pir JAB3524 hypothetical protein PA0959 [Imported] - Pseudomonas aeruginosa (strain PAO1) gb AA0348.1 AE004530.1 (AE004530) hypothetical protein [Pseudomonas aeruginosa] Length = 209</p>

SeqID 2334	SA-989.1	Contig114 (5320-7192 m)	72	<p>Identities = 156/284 (54%), Positives = 215/284 (74%), Gaps = 2/284 (0%) spIP37468KSGA_BACSU DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-5-N, N-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) [HIGH LEVEL KASUGAMYCIN RESISTANCE PROTEIN KSGA] (KASUGAMYCIN DIMETHYLTRANSFERASE) pif[S6071 probable (adenine-N6,N6-)-dimethyltransferase (EC 2.1.1.-) ksgA - subtilis dbj BA05277.1 (D26165) high level kasugamycin resistance [Bacillus subtilis] emb CAB11818.1 (Z99104) dimethyladenosine transferase [Bacillus subtilis] Length = 292</p>
SeqID 2335	SA-99.1	Contig131 (21923-22765 p)	63	<p>Identities = 141/242 (58%), Positives = 188/242 (77%), Gaps = 1/242 (0%) pif E69742 ABC transporter (ATP-binding protein) homolog yobA - Bacillus subtilis dbj BAA10984.1 (D64126) unknown [Bacillus subtilis] emb CAB11922.1 (Z99104) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis] Length = 276</p>
SeqID 2336	SA-990.1	Contig114 (5465-6316 m)	51	<p>Identities = 94/278 (33%), Positives = 147/278 (52%), Gaps = 16/278 (5%) spIP42313YXJB_BACSU HYPOTHETICAL 31.5 KD PROTEIN IN KATB 3 REGION pif H70078 conserved hypothetical protein vxiB - Bacillus subtilis dbj BAA11703.1 (D33026) homologous to SwissProt-YEBH_ECOLI hypothetical protein; hypothetical [Bacillus subtilis] emb CAB15927.1 (Z99123) similar to hypothetical proteins [Bacillus subtilis] emb CAB15937.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] Length = 282</p>

SeqID 2337	SA-991.1	Contig114 (4437-5309 m)	69	Identities = 149/296 (50%), Positives = 204/296 (68%), Gaps = 14/296 (4%) [Bacillus subtilis] emb CA74251.1 (Y13937) YqoQ protein [Bacillus subtilis] emb CA713451.1 (Z99112) similar to hypothetical proteins [Bacillus subtilis] Length = 298
SeqID 2338	SA-993.1	Contig114 (3768-4430 m)	68	Identities = 112/211 (53%), Positives = 152/211 (71%) db BAB0621.1 (AP001515) unknown conserved protein [Bacillus halodurans] Length = 216
SeqID 2339	SA-994.1	Contig114 (3143-3775 m)	52	Identities = 75/220 (34%), Positives = 112/220 (50%), Gaps = 18/220 (8%) [Bacillus subtilis] emb CA74253.1 (Y13937) YqoQ protein [Bacillus subtilis] emb CA713451.1 (Z99112) yqoQ [Bacillus subtilis] Length = 214
SeqID 2340	SA-995.1	Contig114 (1867-3099 m)	54	Identities = 157/393 (39%), Positives = 238/393 (59%), Gaps = 3/393 (0%) [Xyella fastidiosa] emb CA74253.1 (Y13937) YqoQ protein [Xyella fastidiosa] emb CA713451.1 (Z99112) yqoQ [Xyella fastidiosa] Length = 456
SeqID 2341	SA-996.1	Contig114 (938-1877 m)	61	Identities = 139/313 (44%), Positives = 196/313 (62%), Gaps = 6/313 (1%) [Staphylococcus aureus] emb CA74253.1 (Y13937) YqoQ protein [Staphylococcus aureus] emb CA713451.1 (Z99112) yqoQ [Staphylococcus aureus] Length = 313
SeqID 2342	SA-997.1	Contig114 (27-839 m)	71	Identities = 142/270 (52%), Positives = 196/270 (72%), Gaps = 1/270 (0%) [Lactococcus lactis] emb CA74253.1 (Y13937) YqoQ protein [Lactococcus lactis] emb CA713451.1 (Z99112) yqoQ [Lactococcus lactis] Length = 271
SeqID 2343	SA-998.2	Contig127 (15315-15944 m)	30	Identities = 47/120 (39%), Positives = 69/120 (57%), Gaps = 5/120 (4%) [Enterococcus faecalis] emb CA74253.1 (Y13937) YqoQ protein [Enterococcus faecalis] emb CA713451.1 (Z99112) yqoQ [Enterococcus faecalis] Length = 120

SeqID 2344	SA-998.1	Contig127 (14524-15294 p)	59	Identities = 98/265 (36%), Positives = 161/265 (59%), Gaps = 4/265 (1%) sp Q06553 PROC_AQUAE PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) pir F70315 pyrroline carboxylate reductase - Aquifex aeolicus gb AAC08504.1 (AE000676) pyrroline carboxylate reductase [Aquifex aeolicus] Length = 265
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TABLEAU 2. Protéines de surface de *Streptococcus agalactiae*

	SEQ ID	N° IPF	Motif LPXTG	% identité/ similitude
1	886	18	LPHTG	24/37 : Sec (Surface exclusion protéine) <i>E. faecalis</i>
2	386	1250	LPSTG	22/40 : Sec10 (Surface exclusion protéine) <i>Enterococcus faecalis</i> plasmid pCF10
3	1669	280	LPKTG	50/65 : pullulanase <i>S. pneumoniae</i>
4	1895	523	LPATG	90/91 : alpha like protéine <i>S. agalactiae</i>
5	806	1716	LPSTG	31/46 : M-like protéine <i>S. equi</i>
6	1183	2140	LPLTG	36/60 : cell-division protein homolog ywef <i>B. subtilis</i> 34/56 : stage V sporulation protein E <i>B. halodurans</i>
7	1346	2337	LPKTG	25/38 : Unknown <i>B. halodurans</i>
8	1942	571	LPSTG	50/60 : Hemagglutinine <i>S. gordonii</i>
9	2129	765	LPNTG	28/43 : sdrc <i>S. aureus</i>
10	2046	678	LPKTG	57/70 : putative cyclo-nucleotide phosphodiesterase <i>Strep. dysgalactiae</i> susp. <i>equismilis</i>
11	618	1503	LPKTG	49/65 : celle envelope proteinase <i>S. thermophilus</i>
12	1227	220	LPSTG	30/43 : SspB (adhesion) <i>S. gordonii</i>
13	1954	584	LPKTG	26/48 : hypothetical serine riche repeat prot <i>S. pombe</i>
14	1493	2495	LPKTG	23/47 : gene drosophile
15	1955	585	LPKTG	30/46 : 6-aminohexanoate-cyclic-dimer hydrolase <i>Deinococcus radiodurans</i>
16	943	1861	LPKTG	50/62 : hypothetical protein 2 <i>S. mutans</i>
17	1221	2192	LPKTG	35/48 : <i>C. elegans</i> UNC-89 (6642 aa)
18	613	15	LPSTG	37/52 : SpaA : Ag de surface de <i>S. sobrinus</i>
19	382	1247	LPSTG	38/52 : SpaA : Ag de surface de <i>S. sobrinus</i>
20	792	17	LPKTG	30 /47 : hypothetical protéine iota de <i>S. pyogenes</i> plasmid pDB101
21	383	1248	LPRTG	38/52 : hypothetical protéine iota de <i>S. pyogenes</i> plasmid pDB101
22	1418	2414	LPSTG	33/47 : oriC <i>E. faecalis</i> , plasmid pAM-beta -1
				Autres protéines possibles (IPXTG, FPXTG)
23	2171	807	IPQTG	31/43 : Inconnue <i>B. Halodurans</i> 29/41 : fimbrial SU <i>Actinomyces naeslundii</i> 24 :41 : putative cell-surface adhesin SdrF [<i>Staphylococcus epidermidis</i>]
24	1343	2334	IPQTG	27/38 : hypothetical protein 2 <i>L. leichmanii</i> 23/38 : fimbrial SU <i>Actinomyces naeslundii</i>
25	659	1551	FPKTG	37/50 : fibronectin binding protein I <i>S. pyogenes</i>

TABLEAU 3. Liste des phases codantes annotées identifiées par l'analyse de la séquence génomique complète SEQ ID N°2345					Fonctions Prédites	
SEQ ID (ADN)	SEQ ID (Protéine)	Anticodons	Protéine N°	Positions / Sens (p=plus, m=minius)		
SEQ ID n° 4482	2346	142	SA-1000.1	202338-203305 m	similar to glutaryl-aminopeptidase and/or to endo-1,4-beta-glucanase	
SEQ ID n° 4483	2347	143	SA-1001.1	203490-203729 m	Unknown	
SEQ ID n° 4484	2348	144	SA-1002.1	203890-204174 p	similar to unknown protein	
SEQ ID n° 4485	2349	145	SA-1003.1	204171-204494 p	similar to thioredoxin H1	
SEQ ID n° 4486	2350	146	SA-1004.1	204527-205153 p	weakly similar to phenylalanyl-RNA synthetase (beta subunit)	
SEQ ID n° 4487	2351	147	SA-1005.1	205207-205923 m	similar to unknown proteins	
SEQ ID n° 4488	2352	148	SA-1007.1	206004-206399 p	similar to single-strand binding protein	
SEQ ID n° 4489	2353	149	SA-101.1	2190539-2191378 m	Similar to ABC transporter (ATP-binding protein)	
SEQ ID n° 4490	2354	150	SA-1010.1	206522-207166 p	similar to unknown proteins	
SEQ ID n° 4491	2355	151	SA-1012.1	207193-208838 p	Similar to two-component sensor histidine kinase	
SEQ ID n° 4492	2356	152	SA-1013.1	208919-209659 p	Similar to two-component sensor response regulator	
SEQ ID n° 4493	2357	153	SA-1016.1	209829-210284 p	similar to unknown proteins	
SEQ ID n° 4494	2358	154	SA-1017.1	210286-211014 p	similar to unknown proteins	
SEQ ID n° 4495	2359	155	SA-1018.1	211257-212885 p	Similar to (oligopeptide) ABC transporter (binding protein)	
SEQ ID n° 4496	2360	157	SA-1019.1	212988-213975 p	Similar to oligopeptide ABC transporter (permease)	
SEQ ID n° 4497	2361	158	SA-102.1	2191378-2191917 m	similar to phosphatidylglycerophosphate synthase	
SEQ ID n° 4498	2362	159	SA-1020.1	213972-214793 p	Similar to ABC transporter (permease)	
SEQ ID n° 4499	2363	160	SA-1021.1	214805-215608 p	Similar to oligopeptide ABC transporter (ATP-binding protein)	
SEQ ID n° 4500	2364	161	SA-1022.2	215582-216218 p	Similar to oligopeptide ABC transporter (ATP-binding protein)	
SEQ ID n° 4501	2365	163	SA-1024.2	10743-10877 p	Hypothetical protein	
SEQ ID n° 4502	2366	164	SA-1025.2	10369-10740 p	similar to unknown protein	
SEQ ID n° 4503	2367	165	SA-1026.1	10110-10382 p	similar to unknown protein	
SEQ ID n° 4504	2368	166	SA-1028.1	6322-9819 p	similar to transcription-repair coupling factor	
SEQ ID n° 4505	2369	167	SA-1029.1	5750-6325 p	similar to peptidyl-HRNA hydrolase	
SEQ ID n° 4506	2370	168	SA-1030.1	2182043-2193326 m	similar to unknown proteins	
SEQ ID n° 4507	2371	169	SA-1031.1	4551-5666 p	similar to hypothetical GTP binding protein	
SEQ ID n° 4508	2372	170	SA-1031.1	4188-4391 p	Hypothetical protein	
SEQ ID n° 4509	2373	171	SA-1032.1	3789-3986 p	similar to unknown protein	
SEQ ID n° 4510	2374	172	SA-1033.1	2898-3776 p	similar to putative transcription regulator	
SEQ ID n° 4511	2375	173	SA-1034.1	1692-2828 p	beta subunit of DNA polymerase III	

SEQ ID n° 4512	2376	174	SA-1035.2	176-1537 p	replication initiation protein DnaA
SEQ ID n° 4513	2377	175	SA-1036.2	2217128-22171901 p	similar to chromosome partitioning protein ParB
SEQ ID n° 4514	2378	176	SA-1037.1	2215801-2217030 p	similar to serine protease
SEQ ID n° 4515	2379	177	SA-1038.1	2215801-2217030 p	similar to unknown protein
SEQ ID n° 4516	2380	178	SA-1039.1	2211963-2214542 p	similar to unknown transmembrane protein
SEQ ID n° 4517	2381	179	SA-1041	2211963-2214542 p	similar to unknown proteins
SEQ ID n° 4518	2382	180	SA-1041.1	2193328-2194572 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4519	2383	181	SA-1042.4	2210221-2211840 p	similar to unknown proteins
SEQ ID n° 4520	2384	182	SA-1044.2	2209283-2210155 p	similar to thiamine-phosphate pyrophosphorylase (ThiE)
SEQ ID n° 4521	2385	183	SA-1045.1	891360-892031 p	Similar to UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SEQ ID n° 4522	2386	184	SA-1046.1	892158-894073 p	Similar to acetyl transferase
SEQ ID n° 4523	2387	185	SA-1047.1	893519-896349 p	Similar to unknown proteins
SEQ ID n° 4524	2388	186	SA-1048.1	894066-896349 p	Similar to unknown proteins
SEQ ID n° 4525	2389	187	SA-1049.1	895372-896232 p	similar to methionine aminopeptidase
SEQ ID n° 4526	2390	188	SA-1051	896234-897154 p	similar to unknown proteins
SEQ ID n° 4527	2391	189	SA-1050.1	2194811-2195164 p	similar to unknown proteins
SEQ ID n° 4528	2392	190	SA-1051.1	897171-897626 m	similar to unknown proteins
SEQ ID n° 4529	2393	191	SA-1053.1	897808-898317 p	similar to unknown proteins
SEQ ID n° 4530	2394	192	SA-1054.1	898457-900415 p	similar to DNA ligase
SEQ ID n° 4531	2395	193	SA-1055.1	900427-901448 p	similar to unknown proteins
SEQ ID n° 4532	2396	194	SA-1056.1	901450-903750 p	Similar to pullulanase
SEQ ID n° 4533	2397	195	SA-1057.1	903956-905824 p	similar to 1,4-alpha-glucan branching enzyme
SEQ ID n° 4534	2398	196	SA-1058.1	905866-907005 p	similar to glucose-1-phosphate adenylyltransferase
SEQ ID n° 4535	2399	197	SA-1059.2	906995-908728 p	similar to glucose-1-phosphate adenylyltransferase
SEQ ID n° 4536	2400	198	SA-1062.1	908125-909555 p	similar to glycogen synthase
SEQ ID n° 4537	2401	201	SA-1062.2	2195167-2196276 p	Similar to recombination protein RecF
SEQ ID n° 4538	2402	202	SA-1063.1	1167875-1169149 m	similar to xanthine permease
SEQ ID n° 4539	2403	203	SA-1064.1	1166988-1167776 p	similar to nitrite or formate transporter
SEQ ID n° 4540	2404	204	SA-1065.1	1165664-1166889 p	similar to unknown protein (N-terminal part)
SEQ ID n° 4541	2405	205	SA-1066.1	1165028-1165630 p	Unknown, similar to unknown protein
SEQ ID n° 4542	2406	206	SA-1067.1	1164072-1165010 p	similar to other protein (putative thiamine biosynthesis lipoprotein)
SEQ ID n° 4543	2407	207	SA-1068.1	1163741-1163923 p	similar to 4-oxalocrotonate tautomerase
SEQ ID n° 4544	2408	208	SA-1069.1	1163034-1163603 m	thymidine kinase
SEQ ID n° 4545	2409	209	SA-107.1	1161920-1162989 m	peptide chain release factor 1
SEQ ID n° 4546	2410	210	SA-107.2	2162388-2167154 m	putative transmembrane protein similar to unknown protein

SEQ ID n° 4546	2410	210	SA-1071.1	1161090-1161920 m	similar to protoporphyrinogen oxidase
SEQ ID n° 4547	2411	211	SA-1072.1	1180501-1181097 m	similar to unknown protein
SEQ ID n° 4548	2412	212	SA-1073.1	1180563-1180409 m	serine hydroxymethyltransferase
SEQ ID n° 4549	2413	213	SA-1074.1	1188171-1189148 m	similar to unknown protein
SEQ ID n° 4550	2414	214	SA-1075.1	1188167-1188169 m	similar to unknown protein
SEQ ID n° 4551	2415	215	SA-1076.1	1158334-1158365 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4552	2416	216	SA-1077.1	1158400-1158633 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4553	2417	217	SA-1078.2	1153889-1154086 m	Unknown
SEQ ID n° 4554	2418	218	SA-1079.1	1152107-1153825 p	similar to phosphoglucosyltransferase
SEQ ID n° 4555	2419	219	SA-1080.1	2197210-2197872 m	similar to transcriptional regulator
SEQ ID n° 4556	2420	220	SA-1081.1	1151425-1151987 p	similar to unknown protein
SEQ ID n° 4557	2421	221	SA-1082.1	1150837-1151379 p	similar to pantothenate metabolism flavoprotein
SEQ ID n° 4558	2422	222	SA-1083.1	1150158-1150844 p	similar to flavoprotein
SEQ ID n° 4559	2423	223	SA-1084.1	1149168-1150004 m	similar to unknown protein
SEQ ID n° 4560	2424	224	SA-1085.1	1147976-1149175 m	similar to NADH-dependent oxidoreductase
SEQ ID n° 4561	2425	225	SA-1086.1	1146993-1147979 m	similar to unknown protein
SEQ ID n° 4562	2426	226	SA-1087.1	1146632-1146964 m	similar to glycine cleavage system H protein
SEQ ID n° 4563	2427	227	SA-1088.2	1145821-1146639 m	similar to unknown protein
SEQ ID n° 4564	2428	228	SA-1089.1	346400-347701 p	Similar to cellobiose-specific PTS enzyme IIC
SEQ ID n° 4565	2429	229	SA-1090.1	346078-346398 p	Similar to cellobiose-specific PTS enzyme IIB
SEQ ID n° 4566	2430	230	SA-1091.1	2197947-2199428 m	Similar to inosine monophosphate dehydrogenase
SEQ ID n° 4567	2431	231	SA-1092.1	345738-346061 p	Similar to cellobiose-specific PTS enzyme IIA
SEQ ID n° 4568	2432	232	SA-1093.1	344551-344534 p	similar to hypothetical transcriptional regulator
SEQ ID n° 4569	2433	233	SA-1094.1	343677-344432 p	similar to transcriptional regulator (DcoR family)
SEQ ID n° 4570	2434	234	SA-1095.1	342780-343566 m	similar to pyruvate formate-lyase activating enzyme
SEQ ID n° 4571	2435	235	SA-1096.1	342377-342733 p	similar to general stress protein GSP13
SEQ ID n° 4572	2436	236	SA-1097.1	340975-342375 p	C-terminal part similar to peptidyl-prolyl cis-trans isomerase
SEQ ID n° 4573	2437	237	SA-1098.1	340292-340933 p	Similar to two-component response regulator
SEQ ID n° 4574	2438	238	SA-1099.1	339280-340299 p	Similar to two-component sensor histidine kinase
SEQ ID n° 4575	2439	239	SA-1100.1	336568-339283 p	similar to unknown proteins
SEQ ID n° 4576	2440	240	SA-1101.1	1031773-1034922 m	similar to plasmid proteins
SEQ ID n° 4577	2441	241	SA-1102.1	2199585-2200070 m	similar to arginine repressor (ArgR)
SEQ ID n° 4578	2442	242	SA-1103.1	336474-336429 p	similar to hypothetical protein kinases
SEQ ID n° 4579	2443	243	SA-1104.1	335737-336474 p	similar to other proteins
SEQ ID n° 4580	2444	244	SA-1105.1	334377-335699 p	similar to RNA-binding protein Sun
SEQ ID n° 4581	2445	245	SA-1106.1	333452-334387 p	methionyl RNA formyltransferase

SEQ ID n° 4582	2446	247	SA-1104.1	331015-333405 p	primosomal replication factor Y (primosomal protein N)
SEQ ID n° 4583	2447	248	SA-1105.2	330630-330941 p	similar to unknown proteins
SEQ ID n° 4584	2448	249	SA-1107.2	141808-143196 p	similar to argininosuccinate lyase
SEQ ID n° 4585	2449	250	SA-1108.1	140599-141789 p	similar to argininosuccinate synthase
SEQ ID n° 4586	2450	251	SA-1109.1	139375-140445 p	similar to two-component sensor histidine kinase
SEQ ID n° 4587	2451	252	SA-111.1	2200080-2200760 m	similar to transcriptional regulator (Cp/Fnr family)
SEQ ID n° 4588	2452	253	SA-1110.1	138711-139382 p	similar to similar to two-component response regulator
SEQ ID n° 4589	2453	254	SA-1111.1	137994-138680 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4590	2454	255	SA-1112.1	136906-137994 p	similar to putative ABC transporter (permease)
SEQ ID n° 4591	2455	256	SA-1113.1	135738-136724 m	similar to transcription repressor of ribose operon
SEQ ID n° 4592	2456	257	SA-1114.1	134834-135745 m	similar to ribokinase
SEQ ID n° 4593	2457	258	SA-1115.1	134461-134859 m	similar to ribose ABC transporter (permease)
SEQ ID n° 4594	2458	259	SA-1116.1	132967-134445 m	similar to ribose ABC transporter (ATP-binding protein)
SEQ ID n° 4595	2459	260	SA-1118.1	132024-132965 m	similar to ribose ABC transporter (permease)
SEQ ID n° 4596	2460	261	SA-1119.1	131003-131971 m	similar to ribose ABC transporter (binding protein)
SEQ ID n° 4597	2461	262	SA-112.1	2200968-2201672 p	similar to unknown proteins
SEQ ID n° 4598	2462	263	SA-1120.1	129509-130853 p	glutamy-HRNA synthetase
SEQ ID n° 4599	2463	264	SA-1121.1	127681-128300 p	similar to mercuroyl (II) reductase
SEQ ID n° 4600	2464	265	SA-1122.1	127330-127627 p	similar to carbonic anhydrase
SEQ ID n° 4601	2465	266	SA-1123.2	125830-127194 p	similar to DNA repair protein RadA
SEQ ID n° 4602	2466	268	SA-1125.2	1963678-1964112 m	similar to N-acetylglucosamine-specific PTS system enzyme
SEQ ID n° 4603	2467	269	SA-1126.2	1962479-1963675 m	IIA
SEQ ID n° 4604	2468	270	SA-1127.1	1961930-1962424 m	similar to glucuronyl hydrolase
SEQ ID n° 4605	2469	271	SA-1129.1	1961028-1961894 m	similar to N-acetylglucosamine-specific PTS system enzyme
SEQ ID n° 4606	2470	272	SA-113.1	2201939-2203171 p	IIIC
SEQ ID n° 4607	2471	273	SA-1131.1	1960226-1961041 m	similar to arginine deiminase
SEQ ID n° 4608	2472	274	SA-1132.1	1958242-1960146 m	similar to N-acetylglucosamine-specific PTS system enzyme
SEQ ID n° 4609	2473	275	SA-1134.1	1957161-1958162 m	IIID
SEQ ID n° 4610	2474	276	SA-1135.1	1956476-1957090 p	similar to heparitin-sulfate lyase from Flavobacterium heparinum
SEQ ID n° 4611	2475	277	SA-1136.1	1955766-1956410 p	similar to transcriptional regulator (Lac family)
SEQ ID n° 4612	2476	278	SA-1137.1	1954491-1955654 m	similar to polypeptide deformylase
					similar to transcriptional regulator (Cp/Fnr family)
					similar to permease (major facilitator superfamily)

SEQ ID n° 4908	2772	598	SA-1483.1	110012-111048 p	Similar to transcription repressor of class I heat-shock (HrcA)
SEQ ID n° 4909	2773	599	SA-1484.1	111049-111621 p	Similar to heat shock protein GrpE
SEQ ID n° 4910	2774	600	SA-1486.3	111802-111831 p	Chaperone protein DnaK
SEQ ID n° 4911	2775	601	SA-1487.3	113920-115059 p	Chaperone protein DnaJ
SEQ ID n° 4912	2776	604	SA-1490.1	272173-272880 p	similar to unknown protein
SEQ ID n° 4913	2777	605	SA-1490.2	1650563-1650988 m	ribosomal protein L11
SEQ ID n° 4914	2778	606	SA-1491.1	1651199-1652581 m	similar to transmembrane efflux pump protein
SEQ ID n° 4915	2779	607	SA-1492.1	1652589-1653803 m	similar to hypothetical N-acetyl-L-lysine acid amidohydrolase
SEQ ID n° 4916	2780	608	SA-1493.1	1654062-1654987 p	similar to transcriptional regulator (LysR family)
SEQ ID n° 4917	2781	609	SA-1494.1	1655028-1655381 p	similar to unknown proteins
SEQ ID n° 4918	2782	610	SA-1495.1	1655410-1657125 m	similar to para-aminobenzoate synthase, component I
SEQ ID n° 4919	2783	611	SA-1498.1	1657207-1659648 m	similar to DNA translocase
SEQ ID n° 4920	2784	612	SA-1499.1	1659823-1660528 p	similar to peptidyl-prolyl cis-trans isomerase
SEQ ID n° 4921	2785	613	SA-15.3	745991-748792 p	similar to surface antigen proteins, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 4922	2786	614	SA-150.1	273140-274087 m	similar to unknown proteins
SEQ ID n° 4923	2787	615	SA-1500.1	1660678-1661511 m	similar to metal ABC transporter (permease)
SEQ ID n° 4924	2788	616	SA-1501.1	1661513-1662229 m	similar to metal ABC transporter (ATP-binding protein)
SEQ ID n° 4925	2789	617	SA-1502.2	1662400-1663328 m	similar to metal ABC transporter (binding protein)
SEQ ID n° 4926	2790	618	SA-1503.2	2080002-2084714 p	similar to CSA peptidase, putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 4927	2791	619	SA-1504.1	2084947-2085633 p	similar to two-component response regulator
SEQ ID n° 4928	2792	620	SA-1506.1	2085630-2087018 p	similar to two-component sensor histidine kinase
SEQ ID n° 4929	2793	621	SA-1507.1	2087111-2087719 p	Unknown
SEQ ID n° 4930	2794	622	SA-151.1	274084-274575 m	similar to RNA polymerase ECF sigma factor
SEQ ID n° 4931	2795	623	SA-1511.2	2087806-2090307 m	leucyl-HRNA synthetase
SEQ ID n° 4932	2796	624	SA-1512.2	356072-356626 p	similar to unknown proteins
SEQ ID n° 4933	2797	625	SA-1513.1	355330-355995 p	similar to competence protein ComFC
SEQ ID n° 4934	2798	627	SA-1515.1	354041-355330 p	competence protein ComFA
SEQ ID n° 4935	2799	628	SA-1516.1	353341-353985 m	similar to unknown proteins
SEQ ID n° 4936	2800	629	SA-1517.1	352324-353250 m	similar to cysteine synthetase A
SEQ ID n° 4937	2801	630	SA-1518.1	351094-352172 p	similar to glycerol dehydrogenase
SEQ ID n° 4938	2802	631	SA-1519.1	350348-351016 p	similar to hypothetical transaldolase
SEQ ID n° 4939	2803	632	SA-152.1	275157-275765 m	similar to transcriptional regulator (TetR/AcrR family)
SEQ ID n° 4940	2804	633	SA-1520.3	347882-350338 p	similar to formate acetyltransferase

SEQ ID n° 4941	2805	634	SA-1521.1	1269394-1269624 m	similar to unknown proteins
SEQ ID n° 4942	2806	635	SA-1522.1	1269707-1270729 m	similar to branched-chain-amino-acid aminotransferase
SEQ ID n° 4943	2807	636	SA-1523.1	1270842-1273301 m	similar to topoisomerase IV subunit A
SEQ ID n° 4944	2808	637	SA-1524.1	1273435-1275384 m	similar to DNA topoisomerase IV (subunit B)
SEQ ID n° 4945	2809	638	SA-1525.1	1275498-1276136 p	similar to unknown proteins
SEQ ID n° 4946	2810	639	SA-1526.1	1276202-1276855 m	Uracil DNA glycosylase
SEQ ID n° 4947	2811	640	SA-1527.1	1276984-1277439 m	similar to unknown proteins
SEQ ID n° 4948	2812	641	SA-1528.1	1277553-1278794 m	CMP-N-acetylneuraminic acid synthetase
SEQ ID n° 4949	2813	642	SA-153.1	275789-276886 m	similar to ABC transporter (permease)
SEQ ID n° 4950	2814	643	SA-1530.1	1278805-1279434 m	similar to glycosylation or acetyltransferase
SEQ ID n° 4951	2815	644	SA-1531.1	1279431-1280585 m	similar to UDP-N-acetylglucosamine-2-epimerase
SEQ ID n° 4952	2816	645	SA-1532.1	1280662-1281687 m	similar to N-acetylneuraminic acid synthetase
SEQ ID n° 4953	2817	646	SA-1533.1	1281687-1283087 m	capsular polysaccharide repeat unit transporter
SEQ ID n° 4954	2818	647	SA-1535.2	973749-974447 m	similar to ABC transporter (permease)
SEQ ID n° 4955	2819	648	SA-1536.1	972955-973737 m	putative ABC transporter (ATP-binding protein)
SEQ ID n° 4956	2820	649	SA-1537.1	972314-972819 p	similar to unknown transmembrane protein
SEQ ID n° 4957	2821	650	SA-1538.1	970960-971529 m	similar to acetyltransferase (chloramphenicol ?)
SEQ ID n° 4958	2822	651	SA-1539.1	969736-970839 p	Unknown
SEQ ID n° 4959	2823	652	SA-1543.1	968944-969738 p	similar to cation-transporting P-ATPase
SEQ ID n° 4960	2824	654	SA-1544.1	965894-966792 p	similar to peptide methionine sulfoxide reductase
SEQ ID n° 4961	2825	655	SA-1545.1	965894-966792 p	similar to unknown proteins
SEQ ID n° 4962	2826	656	SA-1546.1	965232-965885 p	similar to unknown proteins
SEQ ID n° 4963	2827	657	SA-1547.2	962493-965128 p	weakly similar to histidine triad protein, putative lipoprotein
SEQ ID n° 4964	2828	658	SA-155.1	2756889-277605 m	1,2 Transport/Binding proteins and lipoproteins
SEQ ID n° 4965	2829	659	SA-1551.2	656055-658727 p	Putative peptidoglycan bound protein (FPXG motif)
SEQ ID n° 4966	2830	660	SA-1552.1	658706-659008 p	similar to hypothetical sortase protein (N-terminal part)
SEQ ID n° 4967	2831	661	SA-1554.1	658966-659571 p	similar to putative surface protein (sortase)
SEQ ID n° 4968	2832	662	SA-1555.1	659787-660425 p	Unknown
SEQ ID n° 4969	2833	664	SA-1558.1	661523-661699 p	Unknown
SEQ ID n° 4970	2834	665	SA-156.2	277869-278552 m	similar to unknown proteins
SEQ ID n° 4971	2835	666	SA-1560.1	663083-663313 p	Unknown
SEQ ID n° 4972	2836	667	SA-1562.1	663374-664525 p	Putative cell wall protein, weakly similar to peptidase or esterase
SEQ ID n° 4973	2837	668	SA-1563.1	664725-665717 p	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4974	2838	669	SA-1564.1	665720-666538 p	similar to unknown proteins, putative transmembrane protein
SEQ ID n° 4975	2839	670	SA-1565.2	666540-667325 p	similar to unknown proteins, putative transmembrane protein

SEQ ID n° 4976	2840	671	SA-1567.3	1831820-1832131 m	Similar to unknown proteins
SEQ ID n° 4977	2841	672	SA-1568.3	1832242-1833135 p	Similar to Ribonuclease HII
SEQ ID n° 4978	2842	673	SA-157.2	278573-278694 m	Similar to unknown proteins
SEQ ID n° 4979	2843	674	SA-1570.1	1833151-1833744 p	Similar to signal peptidase 1
SEQ ID n° 4980	2844	675	SA-1571.2	1833873-1835293 p	Similar to putative exodeoxyribonuclease V
SEQ ID n° 4981	2845	676	SA-1573.3	1836407-1836869 p	Similar to unknown proteins
SEQ ID n° 4982	2846	677	SA-1574.1	1836960-1838054 p	Similar to DNA-damage-inducible protein P
SEQ ID n° 4983	2847	678	SA-1577.1	1838239-1840551 p	Similar to Pyruvate formate-lyase
SEQ ID n° 4984	2848	679	SA-1578.1	1840562-1841026 p	Similar to FMN-binding protein
SEQ ID n° 4985	2849	680	SA-1579.1	1841091-1841990 m	Similar to unknown proteins
SEQ ID n° 4986	2850	681	SA-1580.1	1841987-1842742 m	Similar to C3-degrading proteinase
SEQ ID n° 4987	2851	682	SA-1582.1	1842867-1843763 p	Similar to unknown protein
SEQ ID n° 4988	2852	683	SA-1584.3	1843842-1844690 m	Similar to glycerol uptake facilitator
SEQ ID n° 4989	2853	684	SA-1585.3	1844889-1845311 m	Similar to unknown protein
SEQ ID n° 4990	2854	685	SA-1586.2	1845329-1846531 m	Similar to efflux protein
SEQ ID n° 4991	2855	686	SA-1587.2	624205-625581 p	similar to ABC transporter (permease)
SEQ ID n° 4992	2856	687	SA-1588.1	623549-624203 p	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 4993	2857	688	SA-1589.1	622262-623539 p	similar to ABC transporter (permease)
SEQ ID n° 4994	2858	689	SA-159.2	279076-279783 p	similar to other proteins
SEQ ID n° 4995	2859	690	SA-1590.1	621359-621520 m	similar to unknown proteins
SEQ ID n° 4996	2860	691	SA-1591.1	620914-621186 p	similar to transposase
SEQ ID n° 4997	2861	692	SA-1593.1	620591-620851 p	similar to transposase
SEQ ID n° 4998	2862	693	SA-1594.1	620389-620569 p	similar to transposase
SEQ ID n° 4999	2863	694	SA-1595.1	619803-620207 p	similar to insertion element protein
SEQ ID n° 5000	2864	695	SA-1596.1	618920-619540 m	similar to integrase C-terminal part (truncated)
SEQ ID n° 5001	2865	696	SA-1597.1	619428-618775 p	ribosomal protein L19
SEQ ID n° 5002	2866	697	SA-1598.1	618652-617845 p	similar to unknown proteins
SEQ ID n° 5003	2867	698	SA-1599.1	616384-616659 p	similar to other proteins
SEQ ID n° 5004	2868	700	SA-160.2	280081-281209 p	similar to N-acetylglucosamine-6-phosphate deacetylase
SEQ ID n° 5005	2869	701	SA-1601.1	615654-616307 p	similar to flavodoxin
SEQ ID n° 5006	2870	702	SA-1602.1	614793-615805 p	similar to adenosine deaminase
SEQ ID n° 5007	2871	703	SA-1603.2	613582-614517 m	similar to unknown proteins
SEQ ID n° 5008	2872	704	SA-1604.2	1867026-1867295 p	30S ribosomal protein S14
SEQ ID n° 5009	2873	705	SA-1605.2	1867657-1868682 m	similar to low specificity L-threonine aldolase
SEQ ID n° 5010	2874	706	SA-1606.2	1868802-1869812 m	Similar to other proteins (includin putative glycoprotein endopeptidase)

SEQ ID n° 5011	2875	707	SA-1607.1	1869888-1870334 m	Similar to putative acyltransferase
SEQ ID n° 5012	2876	708	SA-1608.1	1870297-1870986 m	Similar to other proteins (includin putative glycoprotein endopeptidase)
SEQ ID n° 5013	2877	709	SA-1609.1	1871168-1871398 p	Similar to unknown proteins
SEQ ID n° 5014	2878	710	SA-161.2	1457718-1458158 m	Similar to hypothetical transcriptional regulator
SEQ ID n° 5015	2879	711	SA-1610.1	1871452-1873131 p	Similar to unknown proteins
SEQ ID n° 5016	2880	712	SA-1611.1	1873293-1873802 m	Similar to secreted unknown proteins -
SEQ ID n° 5017	2881	713	SA-1612.1	1873950-1875296 m	glutamine synthetase
SEQ ID n° 5018	2882	714	SA-1613.1	1875330-1875701 m	Similar to transcriptional regulator, MerR/GlnR family
SEQ ID n° 5019	2883	715	SA-1614.1	1875781-1876320 m	Similar to unknown protein
SEQ ID n° 5020	2884	717	SA-1616.1	1876583-1877779 m	Similar to phosphoglycerate kinase
SEQ ID n° 5021	2885	718	SA-1617.2	1877914-1878783 m	Similar to unknown lipoprotein
SEQ ID n° 5022	2886	719	SA-1619.2	2071134-2071673 p	Similar to other proteins
SEQ ID n° 5023	2887	720	SA-162.1	1455854-1457671 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5024	2888	721	SA-1620.1	2071874-2072969 p	similar to glycerol dehydrogenase
SEQ ID n° 5025	2889	722	SA-1621.1	2073124-2073831 m	similar to unknown protein
SEQ ID n° 5026	2890	723	SA-1622.1	2074178-2076022 m	similar to other proteins
SEQ ID n° 5027	2891	724	SA-1623.1	2076067-2078304 m	similar to cobalamin-independent methionine synthase MetC
SEQ ID n° 5028	2892	725	SA-1624.1	2078674-2078987 m	similar to unknown protein
SEQ ID n° 5029	2893	726	SA-1625.2	2078987-2079579 m	similar to putative transport protein
SEQ ID n° 5030	2894	727	SA-1626.3	517632-518201 p	Similar to unknown proteins
SEQ ID n° 5031	2895	728	SA-1627.1	518299-518883 p	Similar to unknown proteins
SEQ ID n° 5032	2896	729	SA-1628.1	518890-519446 p	Similar to unknown proteins
SEQ ID n° 5033	2897	730	SA-1629.1	519446-522100 p	valyl-RNA synthetase
SEQ ID n° 5034	2898	731	SA-163.1	1454110-1455864 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5035	2899	732	SA-1630.1	522336-523265 m	Similar to unknown proteins
SEQ ID n° 5036	2900	733	SA-1632.1	523682-524641 p	Similar to oxidoreductase
SEQ ID n° 5037	2901	734	SA-1634.1	524802-525704 p	Similar to putative divalent cation transport protein
SEQ ID n° 5038	2902	735	SA-1635.3	525864-526928 p	similar to unknown proteins
SEQ ID n° 5039	2903	736	SA-1636.2	1746531-1747739 m	Similar to transport proteins
SEQ ID n° 5040	2904	737	SA-1638.1	1745814-1746362 m	Similar to unknown proteins
SEQ ID n° 5041	2905	738	SA-164.1	1453376-1454002 m	similar to other proteins
SEQ ID n° 5042	2906	739	SA-1640.2	1744121-1745797 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5043	2907	740	SA-1641.2	1743298-1744128 m	Similar to hypothetical ABC transporter (permease)
SEQ ID n° 5044	2908	741	SA-1642.1	1742592-1743263 p	Similar to unknown proteins
SEQ ID n° 5045	2909	742	SA-1643.1	1741200-1742579 p	similar to Na ⁺ -transporting ATP synthase

SEQ ID n° 5046	2910	743	SA-1644.1	1740472-1741185 p	Similar to glucose-inhibited division protein GidB
SEQ ID n° 5047	2911	744	SA-1645.1	1739700-1740344 m	Similar to unknown proteins
SEQ ID n° 5048	2912	745	SA-1646.1	1738879-1739789 m	Similar to other proteins
SEQ ID n° 5049	2913	746	SA-1647.1	1738241-1739774 m	Similar to unknown proteins
SEQ ID n° 5050	2914	747	SA-1648.1	1737317-1738006 m	Similar to two-component response regulator
SEQ ID n° 5051	2915	748	SA-1649.2	1735622-1737327 m	Similar to two-component sensor histidine kinase
SEQ ID n° 5052	2916	749	SA-165.1	1452688-1453374 m	Similar to two-component response regulator
SEQ ID n° 5053	2917	750	SA-1660.2	1638729-1637205 m	similar to other proteins
SEQ ID n° 5054	2918	751	SA-1651.1	1635601-1636407 m	similar to unknown proteins
SEQ ID n° 5055	2919	752	SA-1653.1	1634709-1635206 m	similar to unknown proteins
SEQ ID n° 5056	2920	753	SA-1654.1	1634330-1634728 m	similar to diacylglycerol kinase
SEQ ID n° 5057	2921	754	SA-1655.1	1633389-1634288 m	similar to GTP binding proteins
SEQ ID n° 5058	2922	755	SA-1656.1	1632781-1633182 m	Unknown
SEQ ID n° 5059	2923	757	SA-1658.1	1631787-1632021 m	Unknown
SEQ ID n° 5060	2924	759	SA-166.1	1451489-1452688 m	Similar to two-component sensor histidine kinase
SEQ ID n° 5061	2925	760	SA-1660.1	1629232-1630824 p	Unknown
SEQ ID n° 5062	2926	761	SA-1662.1	1628167-1629015 m	similar to transcriptional regulator
SEQ ID n° 5063	2927	762	SA-1663.1	1627197-1628018 m	similar to formamidopyrimidine-DNA glycosylase
SEQ ID n° 5064	2928	763	SA-1665.1	1626613-1627200 m	similar to dephosphoerythrin A kinase
SEQ ID n° 5065	2929	764	SA-1667.1	1625788-1628489 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5066	2930	765	SA-1669.1	1624152-1625798 m	Unknown
SEQ ID n° 5067	2931	766	SA-167.1	1450485-1451343 m	similar to mevalonate kinase
SEQ ID n° 5068	2932	767	SA-1671.2	1622787-1623995 m	similar to efflux pump
SEQ ID n° 5069	2933	768	SA-1673.2	1988716-1990323 m	Similar to alpha-glucosidase
SEQ ID n° 5070	2934	769	SA-1674.1	1987633-1988628 m	Similar to UDP-galactose 4-epimerase
SEQ ID n° 5071	2935	770	SA-1675.1	1986932-1987612 p	similar to two-component response regulator
SEQ ID n° 5072	2936	771	SA-1676.1	1985404-1986930 p	similar to two-component sensor histidine kinase
SEQ ID n° 5073	2937	772	SA-1677.1	1983913-1985250 m	similar to organic acid transport protein
SEQ ID n° 5074	2938	774	SA-1679.4	1982725-1983888 m	similar to malic enzyme ((S)-malate:NAD+ oxidoreductase)
SEQ ID n° 5075	2939	775	SA-168.1	1449539-1450483 m	similar to mevalonate diphosphate decarboxylase
SEQ ID n° 5076	2940	776	SA-1680.2	1942117-1942581 m	Similar to transcriptional regulator CtsR
SEQ ID n° 5077	2941	777	SA-1681.2	1939673-1942120 m	Similar to endopeptidase Ctp ATP-binding chain C
SEQ ID n° 5078	2942	778	SA-1682.1	1938962-1939453 p	Similar to acyltransferase
SEQ ID n° 5079	2943	779	SA-1683.1	1938307-1938948 p	Similar to deoxypurine kinase subunit
SEQ ID n° 5080	2944	780	SA-1685.1	1937209-1938186 p	Similar to transcription regulator
SEQ ID n° 5081	2945	781	SA-1686.1	1936350-1937225 p	Similar to other proteins

SEQ ID n° 5082	2946	782	SA-1687.1	1934954-1936210 p	Similar to other proteins
SEQ ID n° 5083	2947	783	SA-1689.3	1934139-1934957 p	Similar to unknown proteins
SEQ ID n° 5084	2948	784	SA-1691.1	1448564-1449546 m	similar to phosphoenolpyruvate kinase
SEQ ID n° 5085	2949	786	SA-1694.1	28175-30318 p	cell wall separation
SEQ ID n° 5086	2950	788	SA-1696.1	31518-32693 p	similar to aminotransferase
SEQ ID n° 5087	2951	789	SA-1697.2	32693-33444 p	Similar to unknown protein
SEQ ID n° 5088	2952	790	SA-1698.2	1725796-1726299 m	Similar to unknown proteins
SEQ ID n° 5089	2953	791	SA-1699.1	1726385-1727716 m	Similar to UDP-N-acetylmuramate-alanine ligase
SEQ ID n° 5090	2954	792	SEQ ID n° 5091	1038856-1039578 m	similar to unknown protein, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5091	2955	793	SA-170.1	1447562-1448557 m	similar to Isopentenyl diphosphate isomerase
SEQ ID n° 5092	2956	794	SA-1700.1	1727726-1728343 m	Similar to unknown proteins
SEQ ID n° 5093	2957	795	SA-1702.1	1728508-1731606 m	Similar to SWI/SNF family helicase
SEQ ID n° 5094	2958	796	SA-1704.1	1731782-1733072 m	Similar to GTP binding protein
SEQ ID n° 5095	2959	797	SA-1705.1	1733120-1734022 m	Similar to primosome component (helicase loader) DnaI
SEQ ID n° 5096	2960	798	SA-1706.2	1734019-1735184 m	Similar to unknown proteins
SEQ ID n° 5097	2961	799	SA-1707.2	1735194-1735573 m	Similar to unknown protein
SEQ ID n° 5098	2962	800	SA-171.1	1447276-1447494 m	Unknown
SEQ ID n° 5099	2963	801	SA-1710.2	2102209-2103849 m	similar to unknown protein
SEQ ID n° 5100	2964	802	SA-1711.1	2101372-2102184 p	similar to other protein
SEQ ID n° 5101	2965	803	SA-1712.1	2098935-2101256 m	similar to penicillin-binding protein 2a
SEQ ID n° 5102	2966	804	SA-1714.1	2098525-2098698 m	similar to other protein
SEQ ID n° 5103	2967	806	SA-1716.2	2096282-2098213 m	putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 5104	2968	807	SA-1718.2	1809587-1810965 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5105	2969	808	SA-1719.1	1809587-1811672 m	Similar to unknown protein, putative ABC transporter (permease)
SEQ ID n° 5106	2970	809	SA-172.1	1448376-1447230 p	similar to unknown proteins
SEQ ID n° 5107	2971	810	SA-1720.1	1811672-1812268 m	Similar to unknown protein
SEQ ID n° 5108	2972	811	SA-1722.1	1812279-1812710 m	Similar to unknown protein
SEQ ID n° 5109	2973	812	SA-1723.1	1812725-1812880 m	Unknown
SEQ ID n° 5110	2974	813	SA-1724.1	1812894-1813433 m	Similar to 2,3-dihydroxybenzoate-AMP ligase (C-terminal domain)
SEQ ID n° 5111	2975	814	SA-1725.1	1813437-1814251 m	Similar to 2,3-dihydroxybenzoate-AMP ligase (enterobactin synthetase component E)
SEQ ID n° 5112	2976	815	SA-1726.1	1814489-1814843 m	Similar to transcription regulator

SEQ ID n° 5113	2977	816	SA-1728.1	1814891-1815343 m	Similar to late competence protein required for DNA binding and uptake comEB
SEQ ID n° 5114	2978	817	SA-1728.1	1815355-1816422 m	Similar to similar to Xaa-Pro dipeptidase
SEQ ID n° 5115	2979	818	SA-1730.1	1443361-1446275 p	similar to unknown proteins
SEQ ID n° 5116	2980	819	SA-1730.1	1816522-1817238 m	Similar to unknown proteins
SEQ ID n° 5117	2981	820	SA-1731.2	1817240-1818739 m	similar to multidrug resistance protein
SEQ ID n° 5118	2982	821	SA-1732.2	959883-960279 p	nucleoside-diphosphate kinase
SEQ ID n° 5119	2983	822	SA-1734.1	959293-959553 p	hypothetical
SEQ ID n° 5120	2984	824	SA-1737.1	957581-958246 p	similar to unknown proteins
SEQ ID n° 5121	2985	825	SA-1738.1	957263-957594 p	similar to unknown proteins
SEQ ID n° 5122	2986	826	SA-1739.1	956387-957256 p	similar to unknown proteins
SEQ ID n° 5123	2987	827	SA-174.1	1444818-1445274 p	similar to other proteins
SEQ ID n° 5124	2988	828	SA-1740.2	952282-956385 p	similar to unknown proteins
SEQ ID n° 5125	2989	829	SA-1742.1	2040862-2041353 p	Similar to putative acetyl transferase
SEQ ID n° 5126	2990	830	SA-1742.1	2041346-2042614 p	Similar to unknown proteins
SEQ ID n° 5127	2991	831	SA-1744.1	2043157-2043462 m	Unknown
SEQ ID n° 5128	2992	832	SA-1745.1	2043446-2043847 m	Unknown
SEQ ID n° 5129	2993	833	SA-1746.1	2043835-2045043 m	Similar to unknown proteins
SEQ ID n° 5130	2994	834	SA-1747.1	2045045-2045437 m	Unknown
SEQ ID n° 5131	2995	835	SA-1748.1	2045054-2045959 m	weakly similar to integrase
SEQ ID n° 5132	2996	837	SA-175.1	1444176-1444625 p	similar to unknown proteins
SEQ ID n° 5133	2997	838	SA-1750.1	2046386-2046522 m	hypothetical gene
SEQ ID n° 5134	2998	839	SA-1751.1	2046794-2047288 p	Similar to transcriptional regulator (phage related)
SEQ ID n° 5135	2999	840	SA-1753.2	774016-774840 p	Similar to unknown proteins
SEQ ID n° 5136	3000	841	SA-1754.1	773219-774016 p	Similar to unknown proteins
SEQ ID n° 5137	3001	842	SA-1755.1	769599-773128 p	Similar to chromosome segregation SMC protein
SEQ ID n° 5138	3002	843	SA-1756.1	768895-769681 p	Similar to ribonuclease III
SEQ ID n° 5139	3003	844	SA-1757.1	768351-768719 p	Similar to unknown proteins
SEQ ID n° 5140	3004	845	SA-1758.1	767539-768348 p	Similar to unknown proteins
SEQ ID n° 5141	3005	846	SA-1759.1	766186-767635 p	Similar to two-component sensor histidine kinase
SEQ ID n° 5142	3006	847	SA-176.1	1442801-1444064 p	similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
SEQ ID n° 5143	3007	848	SA-1760.1	765483-766193 p	similar to two-component response regulator
SEQ ID n° 5144	3008	850	SA-1762.2	1503364-1503699 m	Similar to unknown proteins
SEQ ID n° 5145	3009	851	SA-1763.1	1503763-1504949 m	Similar to chorismate synthase
SEQ ID n° 5146	3010	852	SA-1764.1	1504950-1506017 m	Similar to 3-dehydroquininate synthase
SEQ ID n° 5147	3011	853	SA-1765.1	1506111-1506788 m	similar to 3-dehydroquininate dehydratase

SEQ ID n° 5148	3012	854	SA-1766.1	1506788-1507845 m	Similar to unknown proteins
SEQ ID n° 5149	3013	855	SA-1767.1	1508080-1510224 p	Similar to unknown proteins
SEQ ID n° 5150	3014	856	SA-1768.2	1510465-1510824 m	50S ribosomal protein L20
SEQ ID n° 5151	3015	857	SA-1769.2	1513077-1513274 p	Similar to ferredoxin
SEQ ID n° 5152	3016	858			similar to 3-hydroxy-3-methylglutaryl-coenzyme A synthase (HMG-CoA synthase)
SEQ ID n° 5153	3017	859	SA-1770.1	1441627-1442799 p	Similar to unknown protein
SEQ ID n° 5154	3018	860	SA-1771.1	1513261-1513752 m	Similar to unknown protein
SEQ ID n° 5155	3019	861	SA-1772.1	1513781-1515001 m	Similar to tripeptidase
		862	SA-1773.1	1515137-1516771 m	Similar to unknown protein
SEQ ID n° 5156	3020	863	SA-1774.2	1516895-1518349 p	Similar to UDP-N-acetylmuramyl-D-glutamylyl-2, 6-diaminopimelate ligase
SEQ ID n° 5157	3021	864	SA-1775.2	1518504-1519298 p	similar to ferrichrome ABC transporter (ATP-binding protein)
SEQ ID n° 5158	3022	865	SA-1776.1	1519322-1520254 p	similar to ferrichrome ABC transporter (binding protein)
SEQ ID n° 5159	3023	866	SA-1777.1	1520270-1521295 p	similar to ferrichrome ABC transporter (permease)
SEQ ID n° 5160	3024	867	SA-1778.1	1521282-1522293 p	Similar to ferrichrome ABC transporter (permease)
SEQ ID n° 5161	3025	868	SA-1779.2	1522323-1522976 m	Similar to unknown protein
SEQ ID n° 5162	3026	869	SA-178.1	1440634-1441473 m	thymidylate synthase
SEQ ID n° 5163	3027	870	SA-1780.2	327377-328462 p	Similar to two-component sensor histidine kinase
SEQ ID n° 5164	3028	871	SA-1781.1	328640-327380 p	Similar to ABC transporter (permease)
SEQ ID n° 5165	3029	872	SA-1783.2	325757-326853 p	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5166	3030	873	SA-1784.2	324021-325828 p	similar to unknown proteins
SEQ ID n° 5167	3031	874	SA-1785.1	323350-323632 m	similar to autoinducer-2 production protein (LuxS)
SEQ ID n° 5168	3032	875	SA-1787.1	321682-323125 p	similar to unknown proteins
SEQ ID n° 5169	3033	876	SA-1788.1	320495-321849 p	similar to unknown proteins
SEQ ID n° 5170	3034	877	SA-179.1	1440060-1440554 m	similar to dihydrofolate reductase
SEQ ID n° 5171	3035	878	SA-1791.2	319693-320025 p	similar to unknown proteins
SEQ ID n° 5172	3036	879	SA-1792.2	1469012-1470220 m	similar to poly(A) polymerase
SEQ ID n° 5173	3037	880	SA-1793.1	1467133-1469001 p	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5174	3038	881	SA-1794.1	1466663-1467136 m	Similar to unknown proteins
SEQ ID n° 5175	3039	882	SA-1795.1	1464857-1466596 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5176	3040	883	SA-1796.1	1463083-1464852 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5177	3041	884	SA-1797.2	1462533-1463042 p	Similar to unknown proteins
SEQ ID n° 5178	3042	885	SA-1798.3	1568308-1569804 p	Similar to 4-alpha-glucanotransferase (amylomallase)
SEQ ID n° 5179	3043	886	SA-1799.3	1566032-1566296 m	Similar to glycogen phosphorylase
					similar to plasmid surface exclusion protein, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5180	3044		SA-18.1	1039655-1041916 m	

SEQ ID n° 5181	3045	887	SA-1801.2	572506-572721 p	similar to exodeoxyribonuclease VII small chain
SEQ ID n° 5182	3046	888	SA-1802.1	571188-572528 p	similar to exodeoxyribonuclease VII large chain
SEQ ID n° 5183	3047	889	SA-1803.1	570226-571052 p	similar to unknown proteins
SEQ ID n° 5184	3048	890	SA-1804.1	569375-570229 p	similar to bifunctional methylenelethylhydrofolate dehydrogenase / methylethylhydrofolate cyclohydrolase (FolD)
SEQ ID n° 5185	3049	891	SA-1806.1	567542-569236 p	similar to phosphomannomutase
SEQ ID n° 5186	3050	892	SA-1807.2	566521-567255 p	similar to amino acid ABC transporter (ATP-binding protein)
SEQ ID n° 5187	3051	893	SA-1808.3	565836-566528 p	Similar to amino acid ABC transporter (permease)
SEQ ID n° 5188	3052	894	SA-1809.2	513287-1133588 m	similar to ornithine 5-phosphate decarboxylase
SEQ ID n° 5189	3053	895	SA-1810.1	1438616-1439842 m	similar to ATP-dependent Clp protease subunit X
SEQ ID n° 5190	3054	896	SA-1810.1	1132245-1132874 m	similar to ornithine 5-phosphate decarboxylase
SEQ ID n° 5191	3055	897	SA-1812.1	1130941-1132233 m	similar to dihydroorotase
SEQ ID n° 5192	3056	898	SA-1813.1	1129853-1130776 m	similar to aspartate transcarbamoylase
SEQ ID n° 5193	3057	899	SA-1814.1	1128783-1129839 m	similar to glutaminase of carbamoyl-phosphate synthase (glutamine-hydrolyzing)
SEQ ID n° 5194	3058	900	SA-1815.1	1125580-1128732 m	similar to carbamoyl-phosphate synthase (glutamine-hydrolyzing)
SEQ ID n° 5195	3059	901	SA-1816.1	1125100-1125423 m	Unknown
SEQ ID n° 5196	3060	902	SA-1817.3	1124321-1125103 m	Unknown
SEQ ID n° 5197	3061	903	SA-1818.2	1714000-1714794 m	Similar to glutamate racemase
SEQ ID n° 5198	3062	904	SA-1819.1	1713029-1714003 m	Similar to unknown proteins
SEQ ID n° 5199	3063	905	SA-182.1	1438009-1438605 m	Similar to hypothetical GTP-binding protein
SEQ ID n° 5200	3064	906	SA-1820.1	1712526-1713047 m	Similar to unknown proteins
SEQ ID n° 5201	3065	907	SA-1821.1	1712056-1712529 m	Similar to unknown proteins
SEQ ID n° 5202	3066	908	SA-1822.1	1711326-1712066 m	Similar to integrase
SEQ ID n° 5203	3067	910	SA-1824.2	1710519-1711328 m	similar to unknown proteins
SEQ ID n° 5204	3068	911	SA-1825.2	1710038-1710522 m	similar to unknown proteins
SEQ ID n° 5205	3069	912	SA-1826.1	1709326-1710048 m	Similar to ribosomal large subunit pseudouridine synthase B (hypothetical)
SEQ ID n° 5206	3070	913	SA-1827.1	1709075-1709326 m	Similar to unknown protein
SEQ ID n° 5207	3071	915	SA-183.1	1437399-1438028 p	similar to transcriptional regulator
SEQ ID n° 5208	3072	916	SA-1830.1	1707612-1709051 p	Similar to TRK potassium uptake system protein TrkH
SEQ ID n° 5209	3073	917	SA-1832.2	1706258-1707607 p	Similar to TRK potassium uptake system protein TrkA
SEQ ID n° 5210	3074	918	SA-1834.1	2058938-2059792 m	similar to aminoglycoside 6-adenylyltransferase
SEQ ID n° 5211	3075	919	SA-1835.1	2059971-2060363 m	Unknown
SEQ ID n° 5212	3076	920	SA-1836.1	2060798-2061406 m	Unknown

SEQ ID n° 5213	3077	921	SA-1837.1	2061393-2061728 m	similar to unknown protein
SEQ ID n° 5214	3078	922	SA-1838.1	2062250-2062738 m	Unknown, similar to unknown protein
SEQ ID n° 5215	3079	923	SA-1839.1	2062907-2063668 m	similar to unknown protein (transmembrane)
SEQ ID n° 5216	3080	924	SA-1840.1	2063665-2064567 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5217	3081	925	SA-1841.1	2064772-2065848 m	similar to transcription regulator (N-terminal part)
SEQ ID n° 5218	3082	926	SA-1842.1	2066097-2066711 m	similar to unknown protein
SEQ ID n° 5219	3083	927	SA-1843.1	2066925-2067221 p	similar to unknown protein
SEQ ID n° 5220	3084	928	SA-1844.1	2067238-2067798 p	similar to unknown protein
SEQ ID n° 5221	3085	929	SA-1845.1	2068103-2068966 p	similar to unknown transmembrane protein
SEQ ID n° 5222	3086	930	SA-1846.1	2069123-2069425 m	similar to unknown protein
SEQ ID n° 5223	3087	931	SA-1847.2	2069598-2070365 m	CAMP factor
SEQ ID n° 5224	3088	932	SA-1849.1	1470405-1471253 m	similar to unknown proteins
SEQ ID n° 5225	3089	933	SA-185.1	1436804-1437127 m	Unknown
SEQ ID n° 5226	3090	934	SA-1850.1	1471253-1471633 m	similar to unknown proteins
SEQ ID n° 5227	3091	935	SA-1851.1	1471705-1472232 m	Unknown
SEQ ID n° 5228	3092	936	SA-1852.1	1472289-1472783 m	similar to unknown proteins
SEQ ID n° 5229	3093	938	SA-1855.1	1472972-1474936 m	Similar to fructose-specific PTS enzyme IIABC
SEQ ID n° 5230	3094	939	SA-1858.1	1474933-1475844 m	similar to Fructose-1-phosphate kinase
SEQ ID n° 5231	3095	940	SA-1859.1	1475841-1476650 m	similar to transcription repressor of fructose operon FruR
SEQ ID n° 5232	3096	941	SA-186.1	1435996-1436646 m	Unknown
SEQ ID n° 5233	3097	942	SA-1860.1	1475715-1477950 m	similar to Cell Wall Muropeptide Branching Enzyme
SEQ ID n° 5234	3098	943	SA-1861.1	1478094-1479725 m	similar to cell wall proteins, putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 5235	3099	944	SA-1862.1	1479940-1480663 m	similar to 2-dehydropanoate 2-reductase
SEQ ID n° 5236	3100	946	SA-1866.2	833223-834167 p	Similar to transcriptional regulator (Lac family)
SEQ ID n° 5237	3101	947	SA-1867.1	834226-835218 m	similar to esterase
SEQ ID n° 5238	3102	948	SA-1868.1	835394-836122 p	similar to unknown proteins
SEQ ID n° 5239	3103	949	SA-1869.1	836176-837213 p	similar to unknown proteins
SEQ ID n° 5240	3104	950	SA-1870.1	837293-837901 p	manganese-dependent superoxide dismutase
SEQ ID n° 5241	3105	951	SA-1871.1	838239-839090 p	Similar to transcription antiterminator
SEQ ID n° 5242	3106	952	SA-1872.2	839083-840951 p	Similar to beta-glucoside-specific PTS enzyme IIABC
SEQ ID n° 5243	3107	963	SA-1874.1	170247-171179 p	similar to oligopeptide ABC transporter (ATP-binding protein)
SEQ ID n° 5244	3108	954	SA-1875.1	169201-170247 p	similar to oligopeptide ABC transporter (ATP-binding protein)
SEQ ID n° 5245	3109	955	SA-1876.1	168157-169189 p	similar to oligopeptide ABC transporter (permease)
SEQ ID n° 5246	3110	956	SA-1878.1	167233-168147 p	similar to oligopeptide ABC transporter (permease)
SEQ ID n° 5247	3111	957	SA-1879.2	165459-167114 p	similar to oligopeptide ABC transporter (binding protein)

SEQ ID n° 5248	3112	958	SA-188.1	1434490-1435866 m	similar to amino acid transporter
SEQ ID n° 5249	3113	959	SA-188.2	82132-82437 p	ribosomal protein L24
SEQ ID n° 5250	3114	960	SA-188.2	82461-83003 p	ribosomal protein L5
SEQ ID n° 5251	3115	961	SA-188.1	83361-83759 p	ribosomal protein S8
SEQ ID n° 5252	3116	962	SA-188.1	83869-84405 p	ribosomal protein L6
SEQ ID n° 5253	3117	963	SA-188.5	84506-84862 p	ribosomal protein L18
SEQ ID n° 5254	3118	964	SA-188.6	84881-85375 p	ribosomal protein S5
SEQ ID n° 5255	3119	966	SA-188.8	85390-85569 p	ribosomal protein L30
SEQ ID n° 5256	3120	967	SA-189.1	85694-86134 p	ribosomal protein L15
SEQ ID n° 5257	3121	968	SA-189.2	86165-87459 p	similar to preprotein translocase SecY
SEQ ID n° 5258	3122	969	SA-189.2	87554-88192 p	adenylate kinase
SEQ ID n° 5259	3123	970	SA-189.4	61615-62718 p	Unknown
SEQ ID n° 5260	3124	971	SA-189.7	62804-64102 p	similar to adenylosuccinate lyase
SEQ ID n° 5261	3125	972	SA-188.8	64256-65156 p	similar to unknown proteins
SEQ ID n° 5262	3126	973	SA-189.9	65447-66445 p	similar to Holliday junction DNA helicase, subunit B
SEQ ID n° 5263	3127	974	SA-190.1	1433541-1434485 m	similar to homocysteine S-methyltransferase
SEQ ID n° 5264	3128	975	SA-190.3	66597-67034 p	similar to protein-tyrosine phosphatase
SEQ ID n° 5265	3129	976	SA-190.1	974448-974816 m	similar to transcriptional regulator (GntR family)
SEQ ID n° 5266	3130	977	SA-190.2	974981-978065 p	DNA polymerase III (alpha subunit)
SEQ ID n° 5267	3131	978	SA-190.4	978148-979168 p	similar to 6-phosphofructokinase
SEQ ID n° 5268	3132	979	SA-190.6	979217-980719 p	similar to pyruvate kinase
SEQ ID n° 5269	3133	980	SA-190.8	980890-981447 p	similar to type-1 signal peptidase
SEQ ID n° 5270	3134	981	SA-190.9	1996039-1996464 m	Similar to galactose 6-P isomerase (A subunit)
SEQ ID n° 5271	3135	982	SA-191.2	1431339-1433447 p	Similar to ATP-dependent Cip proteinase (ATP-binding subunit), Cld.
SEQ ID n° 5272	3136	983	SA-191.0	1995503-1996018 m	Similar to galactose 6-P isomerase (B subunit)
SEQ ID n° 5273	3137	984	SA-191.1	1994590-1995492 m	Similar to tagatase-6-phosphate kinase
SEQ ID n° 5274	3138	985	SA-191.2	1993581-1994568 m	Similar to tagatase 1,6-diph aldolase
SEQ ID n° 5275	3139	986	SA-191.3	1992631-1993527 m	Similar to unknown proteins
SEQ ID n° 5276	3140	987	SA-191.5	1991685-1992536 m	Similar to unknown proteins
SEQ ID n° 5277	3141	988	SA-191.6	1990451-1991584 m	Similar to sugar ABC transporter (ATP-binding protein)
SEQ ID n° 5278	3142	989	SA-191.3	2104079-2106230 m	similar to phosphopentomutase
SEQ ID n° 5279	3143	990	SA-191.9	2105297-2105968 m	similar to deoxyribose-phosphate aldolase
SEQ ID n° 5280	3144	991	SA-192.1	2105996-2107200 m	similar to transport system permease protein
SEQ ID n° 5281	3145	992	SA-192.1	2107221-2108000 m	similar to uridine phosphorylase
SEQ ID n° 5282	3146	993	SA-192.3	2108156-2108905 p	similar to transcriptional regulator (GntR family)

SEQ ID n° 5283	3147	994	SA-1924.1	2108908-2109204 p	Unknown
SEQ ID n° 5284	3148	995	SA-1926.2	2109304-2110926 p	chaperonin GroEL
SEQ ID n° 5285	3149	999	SA-1929.2	1348211-1348551 m	similar to multidrug resistance protein
SEQ ID n° 5286	3150	1000	SA-193.2	1430405-1430905 m	Ribosomal protein L10
SEQ ID n° 5287	3151	1001	SA-1930.1	1347385-1348152 p	Similar to unknown proteins
SEQ ID n° 5288	3152	1002	SA-1931.1	1345445-1347226 m	exonuclease ABC (subunit C)
SEQ ID n° 5289	3153	1003	SA-1932.2	1343622-1345403 p	Transmembrane N-terminal domain, C-terminal domain similar to hydrolases
SEQ ID n° 5290	3154	1004	SA-1933.2	1342850-1343452 m	similar to NADH dehydrogenase
SEQ ID n° 5291	3155	1005	SA-1934.2	1341397-1342803 m	similar to dipeptidase
SEQ ID n° 5292	3156	1006	SA-1935.1	1340716-1341300 m	similar to unknown proteins
SEQ ID n° 5293	3157	1007	SA-1937.1	1339667-1340701 m	similar to unknown proteins
SEQ ID n° 5294	3158	1009	SA-194.1	1429976-1430341 m	ribosomal protein L7/L12
SEQ ID n° 5295	3159	1010	SA-1940.3	782771-783706 p	Hpr (ser) kinase/phosphatase
SEQ ID n° 5296	3160	1012	SA-1942.1	782260-782943 p	Similar to unknown proteins
SEQ ID n° 5297	3161	1013	SA-1943.1	781741-782189 p	Similar to unknown proteins
SEQ ID n° 5298	3162	1014	SA-1944.1	779616-781778 p	Similar to unknown proteins
SEQ ID n° 5299	3163	1015	SA-1945.1	778468-779511 p	Similar to oxidoreductase
SEQ ID n° 5300	3164	1016	SA-1946.1	778207-778335 m	Similar to unknown proteins
SEQ ID n° 5301	3165	1017	SA-1949.1	777299-778201 m	Similar to unknown proteins
SEQ ID n° 5302	3166	1020	SA-1951.1	776487-777299 m	Similar to unknown proteins
SEQ ID n° 5303	3167	1021	SA-1952.2	774840-776450 p	Similar to signal recognition particle and to cell division protein FtsY
SEQ ID n° 5304	3168	1022	SA-1953.2	256648-257793 m	similar to glycine betaine/carnitine/choline ABC transporter (ATP-binding protein)
SEQ ID n° 5305	3169	1023	SA-1954.1	256013-256648 m	similar to choline ABC transporter (permease)
SEQ ID n° 5306	3170	1024	SA-1955.1	255084-256010 m	similar to glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein)
SEQ ID n° 5307	3171	1025	SA-1956.1	254433-255083 m	similar to glycine betaine/carnitine/choline ABC transporter (permease)
SEQ ID n° 5308	3172	1026	SA-1957.1	253190-254176 p	similar to efflux protein (truncated)
SEQ ID n° 5309	3173	1027	SA-1958.1	252257-253117 p	similar to transcriptional regulator (Rgg like)
SEQ ID n° 5310	3174	1028	SA-1959.1	251133-251414 p	Unknown
SEQ ID n° 5311	3175	1029	SA-196.1	1429562-1429735 m	Unknown
SEQ ID n° 5312	3176	1030	SA-1960.1	250713-251099 p	Unknown
SEQ ID n° 5313	3177	1031	SA-1961.1	250324-250728 p	pseudogene

SEQ ID n° 5314	3178	1032	SA-1962.2	249517-250104 p	Unknown
SEQ ID n° 5315	3179	1033	SA-1963.2	249110-249517 p	Unknown
SEQ ID n° 5316	3180	1034	SA-1966.1	1393216-1395234 m	similar to ATP-dependent helicase
SEQ ID n° 5317	3181	1035	SA-1967.1	1392522-1392881 m	similar to unknown proteins
SEQ ID n° 5318	3182	1036	SA-1968.1	1392147-1392512 m	similar to unknown proteins
SEQ ID n° 5319	3183	1037	SA-1969.1	1390283-1392160 m	similar to conjugative transposon relaxase
SEQ ID n° 5320	3184	1038	SA-1971.1	1428760-1429565 m	similar to plasmid protein (replication protein ?)
SEQ ID n° 5321	3185	1039	SA-1971.2	1389373-1390128 m	similar to lactose repressor
SEQ ID n° 5322	3186	1040	SA-1973.3	866024-866514 m	similar to unknown proteins
SEQ ID n° 5323	3187	1041	SA-1974.2	865181-865939 p	Similar to unknown proteins
SEQ ID n° 5324	3188	1042	SA-1976.2	864963-865178 p	similar to transcriptional regulator
SEQ ID n° 5325	3189	1043	SA-1976.2	864595-864918 p	Unknown
SEQ ID n° 5326	3190	1044	SA-1977.1	863331-864149 p	Similar to UDP-D-glucose:galactosyl glucosyltransferase
SEQ ID n° 5327	3191	1045	SA-1978.1	862527-863243 p	similar to unknown proteins
SEQ ID n° 5328	3192	1046	SA-198.1	1428091-1428513 m	similar to methyl transferase (from transposon)
SEQ ID n° 5329	3193	1047	SA-1982.1	859827-862445 p	Alanyl-RNA synthetase
SEQ ID n° 5330	3194	1048	SA-1983.2	859326-859811 p	similar to unknown proteins
SEQ ID n° 5331	3195	1049	SA-1985.2	1831275-1831817 m	Similar to unknown proteins
SEQ ID n° 5332	3196	1050	SA-1986.1	1828851-1831190 m	Similar to DNA mismatch repair protein MutS
SEQ ID n° 5333	3197	1051	SA-1987.1	1828347-1828847 m	Similar to unknown proteins
SEQ ID n° 5334	3198	1052	SA-1988.1	1827952-1828266 m	Similar to thioredoxin
SEQ ID n° 5335	3199	1053	SA-1989.1	1827313-1827906 p	Similar to transcriptional regulators
SEQ ID n° 5336	3200	1054	SA-199.1	1427312-1428664 m	3.2 DNA restriction/modification and repair
SEQ ID n° 5337	3201	1055	SA-1990.2	1826012-1827136 p	Similar to A/G-specific adenine glycosylase
SEQ ID n° 5338	3202	1056	SA-1992.2	1866095-1866887 m	Similar to unknown protein
SEQ ID n° 5339	3203	1057	SA-1993.1	1854859-1865041 p	Similar to unknown proteins
SEQ ID n° 5340	3204	1058	SA-1994.1	1864198-1864734 p	Similar to unknown proteins
SEQ ID n° 5341	3205	1059	SA-1995.1	1863567-1864154 m	Similar to other proteins
SEQ ID n° 5342	3206	1060	SA-1996.1	1862715-1863440 m	Similar to transcriptional regulator
SEQ ID n° 5343	3207	1061	SA-1997.1	1861455-1862645 p	Similar to Cyclopropane fatty acid synthase
SEQ ID n° 5344	3208	1062	SA-1998.1	1860995-1861294 p	Similar to unknown proteins
SEQ ID n° 5345	3209	1064	SA-2.1	1025155-1025412 m	Unknown
SEQ ID n° 5346	3210	1065	SA-20.1	1041931-1043013 m	similar to unknown proteins
SEQ ID n° 5347	3211	1066	SA-200.1	1426882-1427328 m	similar to unknown proteins
SEQ ID n° 5348	3212	1067	SA-2000.1	1859666-1860112 m	Similar to unknown proteins
SEQ ID n° 5349	3213	1068	SA-2004.2	1819075-1821903 m	exonuclease ABC (subunit A)

SEQ ID n° 5350	3214	1069	SA-2005.1	1822035-1822706 m	Similar to unknown proteins
SEQ ID n° 5351	3215	1070	SA-2006.1	1822731-1823675 m	Similar to transport protein
SEQ ID n° 5352	3216	1071	SA-2007.1	1823845-1824084 m	30S ribosomal protein S18
SEQ ID n° 5353	3217	1072	SA-2008.2	1824129-1824620 m	Similar to single strand binding protein
SEQ ID n° 5354	3218	1073	SA-2009.2	1824632-1824919 m	30S ribosomal protein S6
SEQ ID n° 5355	3219	1078	SA-2015.2	14009-15985 p	cell division protein Fish
SEQ ID n° 5356	3220	1079	SA-2017.2	13444-13986 p	similar to hypoxanthine guanine phosphoribosyltransferase
SEQ ID n° 5357	3221	1080	SA-2018.2	12165-13439 p	similar to other protein
SEQ ID n° 5358	3222	1081	SA-2019.3	10877-12163 p	weakly similar to beta-lactamase
SEQ ID n° 5359	3223	1082	SA-202.1	1428503-1428689 m	similar to unknown proteins
SEQ ID n° 5360	3224	1083	SA-2022.2	1569925-1570953 m	Similar to transcriptional regulator (Lac family)
SEQ ID n° 5361	3225	1084	SA-2024.1	1571209-1572456 p	similar to maltose ABC transporter (binding protein)
SEQ ID n° 5362	3226	1085	SA-2025.1	1572554-1573924 p	Similar to maltose/maliolodextrin ABC transport system (permease)
SEQ ID n° 5363	3227	1086	SA-2026.1	1573924-1574760 p	similar to maltolodextrin ABC transporter (permease)
SEQ ID n° 5364	3228	1087	SA-2028.1	1574991-1576463 p	similar to di-tripeptide ABC transporter (permease)
SEQ ID n° 5365	3229	1088	SA-2029.1	1576508-1576972 m	Similar to putative mutator MutT protein
SEQ ID n° 5366	3230	1089	SA-203.1	1426273-1426506 m	Unknown
SEQ ID n° 5367	3231	1090	SA-2030.2	1577056-1577244 m	Unknown
SEQ ID n° 5368	3232	1092	SA-2033.2	2150270-2150875 p	similar to plasmid replication protein
SEQ ID n° 5369	3233	1093	SA-2034.1	2149455-2150084 p	similar to unknown proteins
SEQ ID n° 5370	3234	1094	SA-2035.4	2148362-2149462 p	similar to other proteins
SEQ ID n° 5371	3235	1095	SA-2037.4	2148042-2148362 p	Unknown
SEQ ID n° 5372	3236	1096	SA-2038.1	2147391-2147840 p	Unknown
SEQ ID n° 5373	3237	1097	SA-2040.1	2145655-2147070 p	similar to unknown proteins
SEQ ID n° 5374	3238	1098	SA-2041.2	2145266-2145604 p	similar to cadmium-efflux system accessory protein
SEQ ID n° 5375	3239	1099	SA-2042.2	2144840-2148254 p	putative transport protein
SEQ ID n° 5376	3240	1100	SA-2045.2	75018-76298 p	hypothetical transport protein
SEQ ID n° 5377	3241	1101	SA-2047.1	73423-74913 p	similar to threonine synthase
SEQ ID n° 5378	3242	1102	SA-2048.1	72286-73302 p	similar to alcohol dehydrogenase
SEQ ID n° 5379	3243	1103	SA-205.1	1425689-1426270 m	Unknown
SEQ ID n° 5380	3244	1104	SA-2050.2	69465-72107 p	similar to alcohol-acetaldehyde dehydrogenase
SEQ ID n° 5381	3245	1105	SA-2051.2	849073-849753 p	similar to unknown proteins
SEQ ID n° 5382	3246	1106	SA-2052.1	847892-848920 m	Similar to S-adenosylmethionine RNA ribosyltransferase
SEQ ID n° 5383	3247	1107	SA-2053.1	847368-847805 m	Similar to transcriptional regulator, MarR family
SEQ ID n° 5384	3248	1108	SA-2054.1	846249-847313 p	Similar to unknown proteins

SEQ ID n° 5385	3249	1109	SA-2056.1	844892-846148 p	Similar to permease (gluconate ?)
SEQ ID n° 5386	3250	1110	SA-2059.2	843725-844867 p	Similar to putative glycerate kinase
SEQ ID n° 5387	3251	1111	SA-2060.1	1425120-1425608 m	similar to unknown proteins
SEQ ID n° 5388	3252	1112	SA-2060.1	842464-843558 m	Similar to unknown proteins
SEQ ID n° 5389	3253	1113	SA-2061.2	840968-842395 p	Similar to beta-glucosidase
SEQ ID n° 5390	3254	1114	SA-2062.2	81395-81659 p	ribosomal protein S17
SEQ ID n° 5391	3255	1115	SA-2063.2	81167-81373 p	ribosomal protein L29
SEQ ID n° 5392	3256	1116	SA-2065.1	80744-81157 p	ribosomal protein L16
SEQ ID n° 5393	3257	1117	SA-2066.1	80087-80740 p	ribosomal protein S3
SEQ ID n° 5394	3258	1118	SA-2067.1	79730-80074 p	ribosomal protein L22
SEQ ID n° 5395	3259	1119	SA-2069.1	79435-79714 p	ribosomal protein S19
SEQ ID n° 5396	3260	1120	SA-2071.1	1423303-1425120 m	similar to plasmid transfer complex protein TrkK
SEQ ID n° 5397	3261	1121	SA-2071.1	78504-79337 p	ribosomal protein L2
SEQ ID n° 5398	3262	1122	SA-2072.1	78190-78486 p	ribosomal protein L23
SEQ ID n° 5399	3263	1123	SA-2073.1	77567-78190 p	ribosomal protein L4
SEQ ID n° 5400	3264	1124	SA-2074.2	76917-77543 p	ribosomal protein L3
SEQ ID n° 5401	3265	1125	SA-2075.2	76504-76812 p	ribosomal protein S10
SEQ ID n° 5402	3266	1127	SA-2077.3	1351826-1352680 p	similar to transposase (truncated)
SEQ ID n° 5403	3267	1128	SA-2078.2	1363404-1363694 p	similar to transposase, N-terminal part
SEQ ID n° 5404	3268	1129	SA-2079.2	1362139-1363350 m	Unknown
SEQ ID n° 5405	3269	1130	SA-208.1	1423041-1423283 m	Unknown
SEQ ID n° 5406	3270	1131	SA-2082.3	1358151-1361603 m	streptococcal C5a peptidase
SEQ ID n° 5407	3271	1132	SA-2083.4	1800964-1802403 p	Similar to sucrose-6-phosphate hydrolase
SEQ ID n° 5408	3272	1133	SA-2084.1	1802405-1803367 p	Similar to transcriptional regulator (LacI family)
SEQ ID n° 5409	3273	1134	SA-2085.1	1803454-1803888 m	Similar to transcription termination protein NusB
SEQ ID n° 5410	3274	1135	SA-2086.1	1803881-1804270 m	Similar to unknown proteins
SEQ ID n° 5411	3275	1136	SA-2087.1	1804356-1804919 m	Similar to unknown proteins
SEQ ID n° 5412	3276	1137	SA-2090.1	1806098-1807619 m	similar to translation elongation factor EF-P
SEQ ID n° 5413	3277	1139	SA-2092.2	1807809-1809566 p	similar to ABC transporter (binding protein)
SEQ ID n° 5414	3278	1140	SA-2095.2	464590-466939 p	glucose-6-phosphate isomerase
SEQ ID n° 5415	3279	1141	SA-2096.1	466261-466788 p	similar to unknown protein
SEQ ID n° 5416	3280	1142	SA-2097.1	466786-467456 p	similar to unknown protein
SEQ ID n° 5417	3281	1143	SA-2099.1	467588-468631 p	similar to putative ABC transporter (binding protein)
SEQ ID n° 5418	3282	1144	SA-21.1	1043024-1043371 m	Unknown
SEQ ID n° 5419	3283	1145	SA-210.1	1422170-1423024 m	similar to unknown protein from conjugative transposon
SEQ ID n° 5420	3284	1146	SA-2100.1	468722-469621 m	similar to UDP-glucose pyrophosphorylase

SEQ ID n° 5421	3285	1147	SA-2101.1	469658-470674 m	similar to glycerol-3-phosphate dehydrogenase
SEQ ID n° 5422	3286	1148	SA-2102.1	470844-471173 p	similar to ribonuclease P protein component
SEQ ID n° 5423	3287	1149	SA-2103.2	471186-472001 p	similar to unknown protein and to B. subtilis SpoIIJ protein
SEQ ID n° 5424	3288	1150	SA-2104.2	2047351-2048703 m	Unknown
SEQ ID n° 5425	3289	1151	SA-2105.1	2048713-2049804 m	Unknown
SEQ ID n° 5426	3290	1152	SA-2106.1	2050044-2050988 m	similar to hypothetical transcriptional regulator
SEQ ID n° 5427	3291	1153	SA-2107.1	2051052-2051441 m	Unknown
SEQ ID n° 5428	3292	1154	SA-2108.1	2052439-2052756 p	Unknown
SEQ ID n° 5429	3293	1155	SA-2111.1	1421755-1422108 m	similar to unknown protein from conjugative transposons
SEQ ID n° 5430	3294	1156	SA-2110.1	2052805-2052933 p	Unknown
SEQ ID n° 5431	3295	1157	SA-2112.1	2053374-2053664 p	Similar to unknown proteins
SEQ ID n° 5432	3296	1158	SA-2113.1	2053763-2054137 p	Unknown
SEQ ID n° 5433	3297	1159	SA-2115.1	2054427-2055155 p	Unknown
SEQ ID n° 5434	3298	1160	SA-2116.1	2055450-2055644 p	Unknown
SEQ ID n° 5435	3299	1161	SA-2117.1	2055763-2056128 m	Unknown
SEQ ID n° 5436	3300	1162	SA-2118.2	2056356-2056754 m	Unknown
SEQ ID n° 5437	3301	1163	SA-2119.2	1523036-1523971 m	Similar to manganese-dependent inorganic pyrophosphatase
SEQ ID n° 5438	3302	1164	SA-212.1	1419453-1421798 m	similar to plasmid transfer complex protein TraE
SEQ ID n° 5439	3303	1165	SA-2120.1	1524088-1524876 m	Similar to pyruvate-formate lyase activating enzyme
SEQ ID n° 5440	3304	1166	SA-2122.1	1524944-1526278 m	Similar to unknown protein
SEQ ID n° 5441	3305	1167	SA-2123.1	1526468-1527024 m	Similar to unknown proteins
SEQ ID n° 5442	3306	1168	SA-2124.1	1527017-1527952 m	Similar to unknown protein
SEQ ID n° 5443	3307	1169	SA-2125.3	1528045-1528686 m	Similar to unknown protein
SEQ ID n° 5444	3308	1170	SA-2126.3	1528667-1529251 m	similar to unknown protein
SEQ ID n° 5445	3309	1171	SA-2128.2	1352904-1353194 p	similar to transposase
SEQ ID n° 5446	3310	1172	SA-2128.1	1353352-1353732 p	degenerate transposase
SEQ ID n° 5447	3311	1173	SA-2130.1	1353776-1354036 p	degenerate transposase
SEQ ID n° 5448	3312	1174	SA-2131.1	1354082-1354315 p	Degenerate transposase
SEQ ID n° 5449	3313	1175	SA-2132.1	1354514-1356982 m	Similar to histidine triad protein
SEQ ID n° 5450	3314	1176	SA-2133.2	1356995-1357915 m	laminin-binding surface protein
SEQ ID n° 5451	3315	1177	SA-2134.2	625678-626331 p	similar to two-component response regulator VncR
SEQ ID n° 5452	3316	1178	SA-2136.1	626328-627647 p	similar to two-component sensor histidine kinase VncS
SEQ ID n° 5453	3317	1179	SA-2137.1	627699-628358 m	Similar to transposase C-terminal end (truncated)
SEQ ID n° 5454	3318	1180	SA-2138.1	628524-628724 p	Similar to unknown proteins
SEQ ID n° 5455	3319	1182	SA-214.1	1416656-1419451 m	similar to plasmid and conjugative transposon protein
SEQ ID n° 5456	3320	1183	SA-2140.1	629379-630584 p	similar to FisW and RodA proteins

SEQ ID n° 5457	3321	1184	SA-2141.1	630703-631263 p	similar to unknown protein
SEQ ID n° 5458	3322	1185	SA-2143.2	631264-633216 p	DNA gyrase, subunit B
SEQ ID n° 5459	3323	1186	SA-2145.1	1900897-1901571 m	similar to two-component response regulator
SEQ ID n° 5460	3324	1187	SA-2146.1	1901927-1902061 m	ribosomal protein L34
SEQ ID n° 5461	3325	1188	SA-2147.1	1902245-1903600 m	Similar to unknown proteins
SEQ ID n° 5462	3326	1189	SA-2148.1	1903847-1905574 m	similar to betaine ABC transporter permease and substrate binding protein
SEQ ID n° 5463	3327	1190	SA-2149.2	1905593-1906816 m	similar to glycine betaine ABC transporter (ATP-binding protein)
SEQ ID n° 5464	3328	1191	SA-2156.2	2095537-2096076 m	similar to transcription antitermination factor nusG
SEQ ID n° 5465	3329	1192	SA-2157.1	2094285-2095490 p	similar to glycosyl transferase
SEQ ID n° 5466	3330	1193	SA-2158.1	2093024-2094220 p	similar to glycosyl transferase
SEQ ID n° 5467	3331	1194	SA-2159.1	2091974-2092819 m	similar to unknown protein
SEQ ID n° 5468	3332	1195	SA-2161.1	1415704-1415562 p	similar to unknown proteins
SEQ ID n° 5469	3333	1196	SA-2160.2	2090694-2091931 p	similar to transporter
SEQ ID n° 5470	3334	1197	SA-2161.2	1244116-1245459 p	similar to staphylokinase and streptokinase
SEQ ID n° 5471	3335	1198	SA-2162.1	1243011-1243697 m	similar to unknown protein
SEQ ID n° 5472	3336	1199	SA-2163.1	1241896-1242903 m	similar to unknown protein
SEQ ID n° 5473	3337	1200	SA-2165.1	1240446-1241822 m	similar to succinic semialdehyde dehydrogenase
SEQ ID n° 5474	3338	1201	SA-2166.1	1239758-1240303 m	similar to glycine betaine transporter (N-terminal end)
SEQ ID n° 5475	3339	1202	SA-2167.1	1238756-1239757 m	similar to glycine betaine transporter (C-terminal end)
SEQ ID n° 5476	3340	1203	SA-2168.1	1238248-1238733 p	similar to unknown protein C-terminal part
SEQ ID n° 5477	3341	1204	SA-2169.3	1237847-1238407 p	similar to unknown protein (N-terminal part)
SEQ ID n° 5478	3342	1205	SA-217.1	1415117-1415707 p	similar to unknown proteins
SEQ ID n° 5479	3343	1207	SA-2172.2	1100661-1102145 m	similar to carbon starvation protein A
SEQ ID n° 5480	3344	1208	SA-2173.1	1102301-1103035 m	similar to two-component response regulator lytR
SEQ ID n° 5481	3345	1209	SA-2174.1	1103047-1104786 m	similar to two-component sensor histidine kinase LytS
SEQ ID n° 5482	3346	1212	SA-2178.1	1106331-1106708 m	Unknown
SEQ ID n° 5483	3347	1213	SA-2180.3	1107097-1107420 m	Unknown
SEQ ID n° 5484	3348	1214	SA-2182.3	1107768-1108301 m	Unknown
SEQ ID n° 5485	3349	1215	SA-2184.1	825634-827220 p	Similar to ATP-dependent RNA helicase, DEAD-box family
SEQ ID n° 5486	3350	1216	SA-2185.1	824569-825399 p	putative ABC transporter (binding protein)
SEQ ID n° 5487	3351	1217	SA-2186.1	823891-824553 p	similar to ABC transporter (permease)
SEQ ID n° 5488	3352	1218	SA-2187.1	823164-823998 p	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5489	3353	1219	SA-2188.1	822663-823043 p	Similar to unknown proteins
SEQ ID n° 5490	3354	1220	SA-2190.1	821033-822577 p	Similar to peptide-chain-release factor 3

SEQ ID n° 5491	3355	1221	SA-2192.2	819318-820856 p	Similar to surface proteins, putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 5492	3356	1222	SA-2195.3	1140455-1142050 m	similar to cardiolipin synthetase
SEQ ID n° 5493	3357	1223	SA-2196.2	1142169-1143639 m	similar to formate-tetrahydrofolate ligase
SEQ ID n° 5494	3358	1224	SA-2197.2	1143928-1144947 m	similar to lipotein-protein ligase
SEQ ID n° 5495	3359	1225	SA-2198.2	1144974-1145852 m	similar to unknown protein
SEQ ID n° 5496	3360	1226	SA-220.1	1043463-1045295 m	similar to ATP-dependent Clp protease ATP-binding subunit CtpA
SEQ ID n° 5497	3361	1227	SA-220.1	1410000-1414904 m	Putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 5498	3362	1228	SA-2200.2	120068-121351 p	similar to trigger factor (prolyl isomerase)
SEQ ID n° 5499	3363	1229	SA-2201.1	119069-119911 m	similar to unknown protein
SEQ ID n° 5500	3364	1230	SA-2202.1	118463-1186032 p	similar to unknown protein
SEQ ID n° 5501	3365	1231	SA-2203.1	118002-118466 p	similar to unknown protein
SEQ ID n° 5502	3366	1232	SA-2204.1	117234-117992 p	similar to phosphomethylpyrimidine kinase
SEQ ID n° 5503	3367	1233	SA-2205.1	116495-117271 p	similar to rRNA pseudouridine synthase A
SEQ ID n° 5504	3368	1234	SA-2206.2	115177-116424 p	Similar to other proteins
SEQ ID n° 5505	3369	1235	SA-2207.2	573586-574413 p	similar to unknown proteins
SEQ ID n° 5506	3370	1236	SA-2208.2	574400-574873 p	similar to transcriptional regulator
SEQ ID n° 5507	3371	1237	SA-2210.1	574885-576543 p	similar to DNA repair and recombination protein RecN
SEQ ID n° 5508	3372	1238	SA-2212.1	576656-577492 p	similar to unknown proteins
SEQ ID n° 5509	3373	1239	SA-2213.1	577467-578324 p	similar to unknown proteins
SEQ ID n° 5510	3374	1240	SA-2214.2	578299-578901 p	Similar to unknown proteins
SEQ ID n° 5511	3375	1242	SA-2216.2	1250993-1251574 m	similar to unknown proteins
SEQ ID n° 5512	3376	1243	SA-2217.1	1250789-1250883 m	similar to unknown protein
SEQ ID n° 5513	3377	1244	SA-2219.1	1250191-1250733 m	similar to unknown protein
SEQ ID n° 5514	3378	1245	SA-222.1	1409808-1409989 m	Unknown
SEQ ID n° 5515	3379	1246	SA-2220.1	1249935-1250132 m	similar to unknown protein
SEQ ID n° 5516	3380	1247	SA-2221.1	1249362-1249913 m	similar to unknown protein
SEQ ID n° 5517	3381	1248	SA-2222.1	1248557-1249198 m	similar to transcriptional regulator, GntR family
SEQ ID n° 5518	3382	1249	SA-2223.1	1247788-1248552 m	similar to unknown protein
SEQ ID n° 5519	3383	1250	SA-2224.1	1247129-1247788 m	similar to other protein
SEQ ID n° 5520	3384	1251	SA-2225.1	1245662-1247056 m	similar to thiol peroxidase
SEQ ID n° 5521	3385	1252	SA-2226.2	1245953-1246466 p	similar to unknown proteins
SEQ ID n° 5522	3386	1253	SA-2227.2	2001195-2001659 m	Similar to PTS enzyme IIA
SEQ ID n° 5523	3387	1254	SA-2228.1	2000888-2001193 m	Similar to PTS enzyme IIB
SEQ ID n° 5524	3388	1255	SA-2231.1	1999400-2000848 m	Similar to galactitol-specific PTS enzyme IIC

SEQ ID n° 5525	3389	1256	SA-2232.2	Similar to neuraminidase
SEQ ID n° 5526	3390	1257	SA-2233.2	Similar to putative rhamnosyltransferase
SEQ ID n° 5527	3391	1258	SA-2235.1	Similar to nucleotide-sugar dehydratase
SEQ ID n° 5528	3392	1259	SA-2236.1	Similar to 4-diphosphocytidyl-2C-methyl-D-erythritol synthase
SEQ ID n° 5529	3393	1260	SA-2237.1	Similar to Pneumococcal LicD2 protein involved in phosphorylcholine metabolism
SEQ ID n° 5530	3394	1261	SA-2238.1	possible surface protein
SEQ ID n° 5531	3395	1262	SA-2239.1	Similar to unknown protein
SEQ ID n° 5532	3396	1263	SA-224.1	Unknown
SEQ ID n° 5533	3397	1264	SA-2240.1	Similar to putative glycosyl transferase
SEQ ID n° 5534	3398	1265	SA-2241.4	similar to rhamnosyltransferase
SEQ ID n° 5535	3399	1266	SA-2242.3	similar to unknown protein
SEQ ID n° 5536	3400	1267	SA-2244.3	similar to unknown protein
SEQ ID n° 5537	3401	1268	SA-2245.1	similar to amino acid ABC transporter
SEQ ID n° 5538	3402	1270	SA-2247.1	similar to amino acid (glutamine) ABC transporter (binding protein)
SEQ ID n° 5539	3403	1271	SA-2248.3	Unknown
SEQ ID n° 5540	3404	1272	SA-225.1	similar to phosphate ABC transporter (permease)
SEQ ID n° 5541	3405	1275	SA-2253.4	similar to phosphate ABC transporter (permease)
SEQ ID n° 5542	3406	1276	SA-2254.2	similar to phosphate ABC transporter (permease)
SEQ ID n° 5543	3407	1277	SA-2255.1	similar to phosphate ABC transporter (permease)
SEQ ID n° 5544	3408	1278	SA-2256.1	similar to phosphate ABC transporter (permease)
SEQ ID n° 5545	3409	1279	SA-2258.2	similar to phosphate uptake regulatory protein
SEQ ID n° 5546	3410	1280	SA-2259.2	similar to hypochelical ABC transporter (permease)
SEQ ID n° 5547	3411	1281	SA-2260.1	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5548	3412	1282	SA-2261.3	similar to DNA topoisomerase I
SEQ ID n° 5549	3413	1284	SA-2264.3	similar to 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
SEQ ID n° 5550	3414	1285	SA-2265.2	similar to transcriptional regulator
SEQ ID n° 5551	3415	1286	SA-2266.2	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5552	3416	1287	SA-2267.1	Similar to (metal) ABC transporter (permease)
SEQ ID n° 5553	3417	1288	SA-2268.2	similar to DNase (competence related)
SEQ ID n° 5554	3418	1289	SA-2269.2	similar to amino acid permease
SEQ ID n° 5555	3419	1290	SA-2271.1	Similar to small protein SmpB
SEQ ID n° 5556	3420	1291	SA-2272.2	similar to exoribonuclease R
SEQ ID n° 5557	3421	1292	SA-2274.2	Similar to ABC transporter (ATP-binding protein)

SEQ ID n° 5558	3422	1293	SA-2276.1	2112289-2113185 m	Similar to ABC transporter (permease)
SEQ ID n° 5559	3423	1294	SA-2278.1	2113201-2114183 m	putative ABC transporter (binding protein)
SEQ ID n° 5560	3424	1295	SA-2279.1	2114628-2115425 m	similar to unknown proteins
SEQ ID n° 5561	3425	1296	SA-2280.1	2115611-2116471 p	similar to unknown proteins
SEQ ID n° 5562	3426	1297	SA-2281.2	2116514-2117245 p	similar to unknown proteins
SEQ ID n° 5563	3427	1298	SA-2282.2	1065700-1066194 m	Unknown
SEQ ID n° 5564	3428	1299	SA-2283.1	1066231-1066419 m	Unknown
SEQ ID n° 5565	3429	1300	SA-2285.1	1068541-1068106 m	similar to signal recognition particle chain Fth
SEQ ID n° 5566	3430	1301	SA-2287.1	1068174-1068456 m	similar to unknown protein
SEQ ID n° 5567	3431	1302	SA-2288.2	1068545-1068858 m	similar to two-component sensor histidine kinase
SEQ ID n° 5568	3432	1303	SA-2289.2	8276654-828428 m	Similar to unknown proteins
SEQ ID n° 5569	3433	1304	SA-2291.1	828563-829303 p	Similar to other proteins
SEQ ID n° 5570	3434	1305	SA-2292.1	829403-830056 p	Similar to competence protein ComEA
SEQ ID n° 5571	3435	1307	SA-2294.2	830049-832277 p	Similar to competence protein CelB (ComEC)
SEQ ID n° 5572	3436	1308	SA-2295.2	832403-833212 p	Similar to unknown proteins
SEQ ID n° 5573	3437	1309	SA-2296.2	1540196-1541044 m	Similar to rhamnosyl transferase I
SEQ ID n° 5574	3438	1310	SA-2297.1	1539087-1540206 m	Similar to putative hexosyltransferase
SEQ ID n° 5575	3439	1311	SA-2298.1	1537486-1539015 p	Similar to transcription regulator
SEQ ID n° 5576	3440	1312	SA-23.1	1045297-1047045 m	similar to plasmid DNA topoisomerase
SEQ ID n° 5577	3441	1313	SA-230.1	1402425-1408625 m	similar to putative helicase and methylase
SEQ ID n° 5578	3442	1314	SA-2300.3	1534487-1537202 m	Similar to fibronectin binding protein, peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5579	3443	1315	SA-2302.2	1095272-1096246 m	similar to ferrichrome ABC transporter (permease)
SEQ ID n° 5580	3444	1316	SA-2303.1	1096243-1097205 m	similar to (iron?) ABC transporter (permease)
SEQ ID n° 5581	3445	1317	SA-2304.1	1097444-1097992 m	similar to sugar O-acetyltransferase
SEQ ID n° 5582	3446	1318	SA-2305.1	1098013-1098712 m	similar to ribonuclease HI
SEQ ID n° 5583	3447	1319	SA-2306.1	1098761-1098812 m	similar to unknown protein, hypothetical GTP binding protein
SEQ ID n° 5584	3448	1320	SA-2307.2	1099888-1100460 m	similar to unknown proteins
SEQ ID n° 5585	3449	1321	SA-2308.2	852521-853672 p	similar to multidrug resistance protein
SEQ ID n° 5586	3450	1322	SA-2309.1	853724-854671 p	similar to hypothetical transcription factor
SEQ ID n° 5587	3451	1323	SA-231.1	1402054-1402353 m	Unknown
SEQ ID n° 5588	3452	1324	SA-2311.1	854687-856492 p	group B oligopeptidase PepB
SEQ ID n° 5589	3453	1325	SA-2312.1	856687-857313 p	similar to hypothetical phosphoglycolate phosphatase
SEQ ID n° 5590	3454	1326	SA-2313.1	857387-858094 p	similar to methyltransferase
SEQ ID n° 5591	3455	1327	SA-2314.2	858155-859084 p	similar to protease maturation protein

SEQ ID n° 5592	3456	1328	SA-2315.2	2119955-2122153 m	similar to anaerobic (class III) ribonucleotide reductase large subunit chain
SEQ ID n° 5593	3457	1329	SA-2316.1	2119737-2119980 m	Unknown
SEQ ID n° 5594	3458	1330	SA-2317.1	2118792-2119724 m	similar to oxidoreductase
SEQ ID n° 5595	3459	1331	SA-2318.1	2118292-2118783 m	similar to unknown proteins
SEQ ID n° 5596	3460	1332	SA-2319.2	2117602-2118219 m	similar to anaerobic ribonucleotide reductase activator
SEQ ID n° 5597	3461	1333	SA-232.1	2107744-1402043 m	Unknown
SEQ ID n° 5598	3462	1334	SA-2322.2	1501840-1503189 m	Similar to glutathione reductase
SEQ ID n° 5599	3463	1335	SA-2324.1	1901345-1501797 p	Similar to unknown protein (secreted protein)
SEQ ID n° 5600	3464	1336	SA-2326.1	1499953-1501098 m	Similar to iron-sulfur cofactor synthesis protein (NIFS like)
SEQ ID n° 5601	3465	1337	SA-2327.2	1498737-1498951 m	Similar to hypothetical thiamine biosynthesis protein Thi
SEQ ID n° 5602	3466	1338	SA-2329.3	1497457-1498635 m	similar to capsular polyglutamate biosynthesis
SEQ ID n° 5603	3467	1339	SA-233.1	1400941-1401578 m	Unknown
SEQ ID n° 5604	3468	1340	SA-2330.2	143337-144218 p	similar to fructose-bisphosphate aldolase class-II
SEQ ID n° 5605	3469	1341	SA-2331.2	144303-145220 m	similar to L-2-hydroxyisocaproate dehydrogenase
SEQ ID n° 5606	3470	1342	SA-2332.2	145469-145647 p	50S ribosomal protein L28
SEQ ID n° 5607	3471	1343	SA-2334.1	1532350-1534374 m	putative pepidoglycan linked protein (LPXTG motif)
SEQ ID n° 5608	3472	1344	SA-2335.2	1531360-1532238 m	Similar to sortase protein
SEQ ID n° 5609	3473	1345	SA-2336.1	1530476-1531360 m	Similar to sortase protein
SEQ ID n° 5610	3474	1346	SA-2337.2	1529553-1530479 m	Putative pepidoglycan linked protein (LPXTG motif)
SEQ ID n° 5611	3475	1347	SA-2339.2	1289559-1290257 m	capsular polysaccharide chain length regulator/exporter
SEQ ID n° 5612	3476	1348	SA-234.1	1399815-1400900 m	similar to unknown proteins
SEQ ID n° 5613	3477	1349	SA-2340.2	1288158-1289546 m	similar to glucose-1-phosphate transferase
SEQ ID n° 5614	3478	1350	SA-2341.1	1287685-1288134 m	beta-1,4-galactosyltransferase enhancer
SEQ ID n° 5615	3479	1351	SA-2342.1	1287212-1287685 m	beta-1,4-galactosyltransferase
SEQ ID n° 5616	3480	1352	SA-2343.1	1286070-1287215 m	capsular polysaccharide repeating-unit polymerase
SEQ ID n° 5617	3481	1353	SA-2344.1	1285105-1286073 m	similar to glycosyl transferase
SEQ ID n° 5618	3482	1354	SA-2345.1	1284124-1285071 m	similar to glycosyl transferase
SEQ ID n° 5619	3483	1355	SA-2346.2	1283084-1284040 m	capsular polysaccharide biosynthesis protein
SEQ ID n° 5620	3484	1356	SA-2348.1	1217890-1218570 m	similar to DNA repair protein RadC
SEQ ID n° 5621	3485	1357	SA-2349.1	1217239-1217877 p	similar to unknown protein
SEQ ID n° 5622	3486	1359	SA-235.1	1399530-1399760 m	Unknown
SEQ ID n° 5623	3487	1360	SA-2350.1	1216137-1217094 p	similar to unknown protein
SEQ ID n° 5624	3488	1361	SA-2351.2	1215620-1216735 p	similar to iron-sulfur cofactor synthesis protein or cysteine desulfurase
SEQ ID n° 5625	3489	1364	SA-2354.1	1552093-1552347 m	similar to putative thiamine transferase

SEQ ID n° 5626	3490	1365	SA-2355.1	1553364-1554218 m	dTDP-L-thiamine synthase
SEQ ID n° 5627	3491	1366	SA-2356.1	1554308-1554649 m	similar to unknown protein
SEQ ID n° 5628	3492	1367	SA-2357.1	1554758-1555867 m	RNA polymerase major sigma factor RpoD
SEQ ID n° 5629	3493	1368	SA-2358.2	1555875-1557683 m	DNA primase
SEQ ID n° 5630	3494	1369	SA-2359.3	121540-122115 p	similar to DNA-directed RNA polymerase (delta subunit)
SEQ ID n° 5631	3495	1370	SA-236.1	1399144-1399533 m	Unknown
SEQ ID n° 5632	3496	1371	SA-2360.1	122388-123992 p	similar to GTP synthetase
SEQ ID n° 5633	3497	1372	SA-2361.3	124101-125027 p	similar to unknown protein
SEQ ID n° 5634	3498	1373	SA-2362.2	108765-1088643 m	similar to unknown proteins
SEQ ID n° 5635	3499	1375	SA-2365.1	1085068-1085668 m	Unknown
SEQ ID n° 5636	3500	1376	SA-2366.1	1083763-1085034 m	similar to unknown protein
SEQ ID n° 5637	3501	1377	SA-2367.1	1083319-1083750 m	similar to unknown protein
SEQ ID n° 5638	3502	1378	SA-2368.1	1082343-1083227 m	similar to RNA pseudouridine 55 synthase
SEQ ID n° 5639	3503	1379	SA-2369.2	1081398-1082330 m	macrolide-efflux protein
SEQ ID n° 5640	3504	1380	SA-237.1	1398807-1399097 m	Unknown
SEQ ID n° 5641	3505	1381	SA-2370.3	1723907-1725709 m	Similar to other proteins
SEQ ID n° 5642	3506	1382	SA-2371.1	1723352-1723834 m	Similar to transcription elongation factor GreA
SEQ ID n° 5643	3507	1383	SA-2372.2	1721788-1723248 m	Similar to putative amidase
SEQ ID n° 5644	3508	1384	SA-2373.2	1560344-1561387 m	Similar to ammonium transporter
SEQ ID n° 5645	3509	1385	SA-2374.1	1561467-1562564 p	Similar to unknown protein
SEQ ID n° 5646	3510	1386	SA-2376.1	1562631-1563617 m	Similar to unknown protein
SEQ ID n° 5647	3511	1387	SA-2377.1	1563780-1564085 p	Similar to unknown protein
SEQ ID n° 5648	3512	1388	SA-2378.2	1564243-1565616 m	Similar to glycerol (sugar)-3-phosphate transporter
SEQ ID n° 5649	3513	1389	SA-238.1	1398261-1398737 m	Similar to phage repressor-like protein
SEQ ID n° 5650	3514	1390	SA-2380.2	890576-891346 p	similar to hydroxyethyl thiazole kinase (ThiM)
SEQ ID n° 5651	3515	1391	SA-2381.1	889777-890574 p	similar to phosphomethylpyrimidine kinase (ThiD)
SEQ ID n° 5652	3516	1392	SA-2382.1	889066-889752 p	Similar to putative thiamin biosynthesis protein
SEQ ID n° 5653	3517	1394	SA-2384.2	888320-889012 p	Similar to unknown proteins
SEQ ID n° 5654	3518	1395	SA-2385.1	1541041-1542465 m	Similar to capsular polysaccharide synthesis protein
SEQ ID n° 5655	3519	1396	SA-2387.1	1542465-1543829 m	Similar to unknown proteins
SEQ ID n° 5656	3520	1397	SA-2388.2	1543831-1544778 m	Similar to putative thiamosyltransferase
SEQ ID n° 5657	3521	1398	SA-239.1	1397491-1398261 m	similar to unknown proteins
SEQ ID n° 5658	3522	1399	SA-2390.2	1458427-1460499 p	similar to 5'-nucleotidase, putative peptidoglycan bound protein (LPXTN motif)
SEQ ID n° 5659	3523	1400	SA-2391.1	1460536-1460946 m	similar to polypeptide deformylase
SEQ ID n° 5660	3524	1401	SA-2392.2	1461016-1462365 m	similar to NADP-specific glutamate dehydrogenase

SEQ ID n° 5661	3525	1402	SA-2394.2	1133801-1135033 m	similar to unknown protein
SEQ ID n° 5662	3526	1403	SA-2395.2	1135073-1136614 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5663	3527	1404	SA-2396.2	1480878-1481946 m	similar to ABC protein, putative transmembrane protein
SEQ ID n° 5664	3528	1405	SA-2397.1	1482083-1483075 m	similar to thioredoxin reductase
SEQ ID n° 5665	3529	1406	SA-2398.1	1483056-1483808 m	similar to RNA (guanine-N1)-methyltransferase
SEQ ID n° 5666	3530	1407	SA-2399.3	1483798-1484316 m	similar to 16S rRNA processing protein RimM
SEQ ID n° 5667	3531	1408	SA-2400.2	1395238-1397478 m	similar to unknown proteins
SEQ ID n° 5668	3532	1409	SA-2404.2	1798860-1800779 m	Similar to sucrose-specific PTS enzyme IABC
SEQ ID n° 5669	3533	1410	SA-2405.2	515623-156378 m	Similar to methyltransferase
SEQ ID n° 5670	3534	1411	SA-2406.1	515284-515602 m	similar to unknown proteins
SEQ ID n° 5671	3535	1412	SA-2407.1	514957-515262 m	similar to unknown proteins
SEQ ID n° 5672	3536	1413	SA-2409.2	514161-514739 p	similar to integrase (C-terminal part)
SEQ ID n° 5673	3537	1414	SA-2412	319054-319872 p	similar to unknown proteins
SEQ ID n° 5674	3538	1415	SA-2410.1	513604-514035 p	similar to integrase (N-terminal part)
SEQ ID n° 5675	3539	1416	SA-2411.1	513228-513554 p	Similar to unknown phage proteins
SEQ ID n° 5676	3540	1417	SA-2412.1	512516-513055 p	Unknown
SEQ ID n° 5677	3541	1418	SA-2414.1	511516-512277 p	Similar to plasmid related proteins, Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5678	3542	1419	SA-2415.2	510934-511491 p	Unknown
SEQ ID n° 5679	3543	1420	SA-2416.2	510521-510934 p	Unknown
SEQ ID n° 5680	3544	1421	SA-2418.2	1069842-1070522 m	similar to two-component response regulator
SEQ ID n° 5681	3545	1422	SA-2419.2	1070684-1073233 m	similar to lysyl-aminopeptidase
SEQ ID n° 5682	3546	1423	SA-242.2	318380-318679 m	similar to recombination protein U (RecU)
SEQ ID n° 5683	3547	1424	SA-2420.2	1495953-1497267 m	50S ribosomal protein L21
SEQ ID n° 5684	3548	1426	SA-2422.2	1495608-1495946 m	Similar to unknown proteins
SEQ ID n° 5685	3549	1427	SA-2423.1	1495293-1495586 m	50S ribosomal protein L27
SEQ ID n° 5686	3550	1428	SA-2424.1	1495172-1496077 m	Similar to transcriptional regulator (LysR/MarR family)
SEQ ID n° 5687	3551	1429	SA-2425.1	1494699-1495163 m	Similar to prolipoprotein signal peptidase
SEQ ID n° 5688	3552	1430	SA-2426.3	1493825-1494715 m	Similar to ribosomal large subunit pseudouridine synthase B (hypothetical)
SEQ ID n° 5689	3553	1431	SA-2428.3	1880206-1882284 m	translation elongation factor G
SEQ ID n° 5690	3554	1432	SA-2429.2	1265526-1266473 p	similar to unknown proteins
SEQ ID n° 5691	3555	1433	SA-2430.1	1266592-1267668 p	similar to bacteriophage integrase
SEQ ID n° 5692	3556	1434	SA-2431.3	1267848-1268050 m	similar to ribosomal protein S1-like DNA-binding protein
SEQ ID n° 5693	3557	1436	SA-2433.2	1942754-1943215 p	Similar to other proteins
SEQ ID n° 5694	3558	1437	SA-2434.4	1943374-1944414 m	translation elongation factor EF-Ts

SEQ ID n° 5695	1438	SA-2435.4	1944508-1945278 m	ribosomal protein S2
SEQ ID n° 5696	3560	SA-2437.2	1290286-1290960 m	putative chain length regulator CpsC
SEQ ID n° 5697	3561	SA-2438.1	1290969-1291700 m	Unknown
SEQ ID n° 5698	3562	SA-244.2	316147-318384 m	similar to penicillin-binding protein 1A
SEQ ID n° 5699	3563	SA-2440.3	1291706-1293163 m	Unknown
SEQ ID n° 5700	3564	SA-2443.1	2153854-2153899 p	similar to other proteins (C-terminal end)
SEQ ID n° 5701	3565	SA-2443.1	2152902-2153897 p	Unknown
SEQ ID n° 5702	3566	SA-2445.2	2151206-2152471 p	similar to integrase
SEQ ID n° 5703	3567	SA-2446.2	1369720-1370286 m	similar to plasmid replication protein
SEQ ID n° 5704	3568	SA-2447.1	1369483-1369686 m	Unknown
SEQ ID n° 5705	3569	SA-2448.1	1368284-1369465 m	Similar to integrase (phage-related protein)
SEQ ID n° 5706	3570	SA-2450.2	1206681-1207373 p	Similar to unknown protein
SEQ ID n° 5707	3571	SA-2453.2	849904-850805 p	similar to N-acetylglucosamine-6-phosphate isomerase
SEQ ID n° 5708	3572	SA-2454.1	850677-851633 m	similar to unknown protein
SEQ ID n° 5709	3573	SA-2455.2	851729-852448 p	similar to 16S pseudouridylate synthase
SEQ ID n° 5710	3574	SA-2457.3	67418-69196 p	similar to unknown proteins
SEQ ID n° 5711	3575	SA-2458.3	67041-67421 p	similar to unknown proteins
SEQ ID n° 5712	3576	SA-2459.3	1715970-1716491 p	Similar to unknown proteins
SEQ ID n° 5713	3577	SA-246.1	314767-316101 p	similar to cysteine aminopeptidase C
SEQ ID n° 5714	3578	SA-2460.1	1718559-1717246 m	Similar to unknown proteins
SEQ ID n° 5715	3579	SA-2461.1	1717271-1717774 m	Similar to unknown proteins
SEQ ID n° 5716	3580	SA-2462.1	1717812-1718555 m	Similar to hypothetical rRNA methylase
SEQ ID n° 5717	3581	SA-2463.1	1718587-1718885 p	similar to acylphosphatase
SEQ ID n° 5718	3582	SA-2464.2	1718950-1719382 p	Similar to unknown proteins
SEQ ID n° 5719	3583	SA-2466.2	1715787-1716482 m	Similar to amino acid ABC transporter (permease)
SEQ ID n° 5720	3584	SA-2467.1	1715125-1715775 m	similar to ABC transporter (permease)
SEQ ID n° 5721	3585	SA-2468.2	1714510-1715076 p	similar to unknown proteins
SEQ ID n° 5722	3586	SA-2469.2	1713324-1714343 p	similar to unknown proteins
SEQ ID n° 5723	3587	SA-247.1	313833-314854 p	similar to NH3-dependent NAD+ synthetase
SEQ ID n° 5724	3588	SA-2470.2	785354-785629 m	Similar to unknown proteins
SEQ ID n° 5725	3589	SA-2471.1	784882-785313 p	Similar to unknown proteins
SEQ ID n° 5726	3590	SA-2472.1	784487-784885 p	Similar to unknown proteins
SEQ ID n° 5727	3591	SA-2473.3	783699-784472 p	similar to prolipoprotein diacylglycerol transferase
SEQ ID n° 5728	3592	SA-2477.2	1492009-1493079 m	Similar to carbamoyl-phosphate synthase, small subunit
SEQ ID n° 5729	3593	SA-2479.2	1490355-1491953 m	similar to carbamoyl-phosphate synthase
SEQ ID n° 5730	3594	SA-248.1	312376-313936 p	similar to unknown proteins

SEQ ID n° 5731	3595	1482	SA-2480.2	1094514-1095275 m	similar to ferrichrome ABC transporter (ATP-binding protein)
SEQ ID n° 5732	3596	1483	SA-2482.2	1093424-1094452 m	similar to ferrichrome ABC transporter (binding protein)
SEQ ID n° 5733	3597	1484	SA-2483.2	1092444-1093286 m	similar to DNA processing Smf protein
SEQ ID n° 5734	3598	1485	SA-2486.2	1614454-1615286 m	similar to oxidoreductase
SEQ ID n° 5735	3599	1486	SA-2498.3	1488909-1490153 m	similar to unknown protein
SEQ ID n° 5736	3600	1487	SA-249.1	311304-312218 p	similar to thioredoxin reductase
SEQ ID n° 5737	3601	1488	SA-2430.2	1488196-1488906 m	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5738	3602	1489	SA-2491.2	1486934-1488181 m	similar to unknown protein
SEQ ID n° 5739	3603	1490	SA-2492.2	981705-983519 p	similar to glucosamine-fructose-6-phosphate aminotransferase
SEQ ID n° 5740	3604	1491	SA-2493.2	1137253-1138329 m	similar to aspartate-semialdehyde dehydrogenase
SEQ ID n° 5741	3605	1493	SA-2495.1	1138538-1139770 m	highly repetitive peptidoglycan bound protein (LPX TG motif)
SEQ ID n° 5742	3606	1494	SA-2497.2	1080942-1081355 m	similar to unknown protein
SEQ ID n° 5743	3607	1495	SA-2498.2	1080688-1080949 m	similar to unknown protein
SEQ ID n° 5744	3608	1496	SA-2499.3	1079914-1080878 m	similar to myo-inositol monophosphatase
SEQ ID n° 5745	3609	1497	SA-25.1	1047228-1051968 m	similar to plasmid proteins
SEQ ID n° 5746	3610	1498	SA-250.1	311011-311235 p	similar to unknown proteins
SEQ ID n° 5747	3611	1499	SA-2500.3	1078536-1079846 p	conserved protein
SEQ ID n° 5748	3612	1500	SA-2501.3	1704700-1706052 m	similar to amino acid permease
SEQ ID n° 5749	3613	1501	SA-2502.2	1703979-1704527 m	Similar to rRNA methylase
SEQ ID n° 5750	3614	1502	SA-2503.2	1702874-1703843 m	similar to aminotransferase
SEQ ID n° 5751	3615	1503	SA-2504.2	1701935-1702564 p	uracil phosphoribosyltransferase
SEQ ID n° 5752	3616	1505	SA-2507.2	34466-35705 p	similar to acyl carrier protein
SEQ ID n° 5753	3617	1506	SA-2508.1	34463-35455 p	similar to fatty acid phospholipid synthesis protein
SEQ ID n° 5754	3618	1507	SA-2509.2	33507-34385 p	similar to unknown transmembrane protein
SEQ ID n° 5755	3619	1508	SA-251.1	310146-310889 p	Similar to amino acid ABC transporter (ATP-binding protein)
SEQ ID n° 5756	3620	1509	SA-2510.2	1207444-1208444 m	similar to cation (K ⁺) transport protein
SEQ ID n° 5757	3621	1510	SA-2511.1	1209579-1210340 m	Similar to oxidoreductase
SEQ ID n° 5758	3622	1511	SA-2512.2	1210402-1211394 m	phosphotransacetylase
SEQ ID n° 5759	3623	1512	SA-2513.2	329975-330604 p	similar to guanylate kinase
SEQ ID n° 5760	3624	1513	SA-2514.1	329104-329808 p	similar to unknown proteins
SEQ ID n° 5761	3625	1514	SA-2515.2	328464-329054 p	Similar to two-component response regulator
SEQ ID n° 5762	3626	1515	SA-2516.2	1615535-1616237 p	similar to putative NAD(P)H-flavin oxidoreductase
SEQ ID n° 5763	3627	1516	SA-2517.1	1616325-1616717 p	similar to S-D-lactoylglutathione methylglyoxal lyase
SEQ ID n° 5764	3628	1517	SA-2518.1	1616846-1617772 p	similar to putative sugar transferase
SEQ ID n° 5765	3629	1519	SA-252.1	309343-310146 p	Similar to amino acid ABC transporter (permease)

SEQ ID n° 5766	3630	1520	SA-2520.3	152358-154232 p	similar to unknown proteins
SEQ ID n° 5767	3631	1521	SA-2522.2	1486533-1486805 m	30S ribosomal protein S16
SEQ ID n° 5768	3632	1522	SA-2523.2	1486281-1486523 m	similar to unknown protein
SEQ ID n° 5769	3633	1523	SA-2524.2	1484638-1486149 m	similar to transcription regulator RofA related
SEQ ID n° 5770	3634	1524	SA-2525.2	960415-962247 p	similar to GTP binding proteins
SEQ ID n° 5771	3635	1525	SA-2526.2	1364617-1366431 m	Exonuclease motif predicted by PFAM
SEQ ID n° 5772	3636	1527	SA-253.1	308436-309248 p	Similar to amino acids ABC transporter (binding protein)
SEQ ID n° 5773	3637	1528	SA-2531.3	1368847-1369082 p	similar to a DNA polymerase like protein from <i>Plasmodium falciparum</i>
SEQ ID n° 5774	3638	1529	SA-2532.1	1062952-1063155 m	Unknown
SEQ ID n° 5775	3639	1530	SA-2533.1	649127-649315 p	Unknown
SEQ ID n° 5776	3640	1531	SA-2534.1	649051-649233 p	pseudogene
SEQ ID n° 5777	3641	1532	SA-2535.1	579004-579279 p	HU like DNA-binding protein
SEQ ID n° 5778	3642	1533	SA-2536.1	572721-573593 p	similar to geranyltransferase (farnesyl diphosphate synthase)
SEQ ID n° 5779	3643	1534	SA-2537.2	565465-565695 p	similar to unknown proteins
SEQ ID n° 5780	3644	1535	SA-2541.2	2046191-2046337 m	Unknown
SEQ ID n° 5781	3645	1541	SA-2548.1	1263082-1263228 m	similar to unknown proteins
SEQ ID n° 5782	3646	1542	SA-2549.1	1264885-1265175 p	Unknown
SEQ ID n° 5783	3647	1543	SA-255.1	305985-308298 p	similar to ATP-dependent RNA helicase
SEQ ID n° 5784	3648	1546	SA-2555.2	507784-508122 p	Unknown
SEQ ID n° 5785	3649	1547	SA-2556.1	1622361-1622597 m	Similar to protein-export protein SecG
SEQ ID n° 5786	3650	1549	SA-2558.1	1631019-1631248 m	Unknown
SEQ ID n° 5787	3651	1550	SA-2559.1	659421-659609 m	similar to transposase
SEQ ID n° 5788	3652	1551	SA-256.1	305847-306857 p	similar to phospho-N-acetylmuranoyl-pentapeptide transferase
SEQ ID n° 5789	3653	1552	SA-2560.1	660639-660797 p	similar to unknown proteins
SEQ ID n° 5790	3654	1559	SA-257.1	303587-305845 p	similar to penicillin-binding protein 2X
SEQ ID n° 5791	3655	1560	SA-2571.3	984145-984786 p	Similar to ABC transporter (permease)
SEQ ID n° 5792	3656	1561	SA-2572.1	983681-984010 p	similar to unknown proteins
SEQ ID n° 5793	3657	1564	SA-2576.2	164970-1650459 m	ribosomal protein L1
SEQ ID n° 5794	3658	1566	SA-258.1	303257-303583 p	similar to cell division protein FtsL
SEQ ID n° 5795	3659	1567	SA-2582.2	1123914-1124204 m	similar to unknown protein
SEQ ID n° 5796	3660	1568	SA-2583.3	2056908-2057630 m	similar to unknown proteins
SEQ ID n° 5797	3661	1572	SA-259.1	302295-303242 p	similar to unknown proteins
SEQ ID n° 5798	3662	1575	SA-2596.1	1720081-1720746 m	similar to amino acid ABC transporter (permease)

SEQ ID n° 5799	3663	1576	SA-2597.2	Unknown, similar to amino acid ABC transporter (binding protein)
SEQ ID n° 5800	3664	1577	SA-2598.3	1077491-1078357 m
SEQ ID n° 5801	3665	1578	SA-2599.1	similar to phosphate ABC transporter (binding protein)
SEQ ID n° 5802	3666	1579	SA-260.1	Similar to drug-export protein
SEQ ID n° 5803	3667	1580	SA-261.1	Unknown
SEQ ID n° 5804	3668	1589	SA-261.1	similar to Gamma-glutamyl phosphate reductase
				similar to gamma-glutamyl kinase
				similar to Similar to beta-glucoside specific PTS system enzyme
SEQ ID n° 5805	3669	1595	SA-263.1	IIBC
SEQ ID n° 5806	3670	1596	SA-263.1	Unknown
SEQ ID n° 5807	3671	1598	SA-264.1	Transmembrane protein similar to unknown proteins
SEQ ID n° 5808	3672	1602	SA-265.1	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 5809	3673	1604	SA-265.1	Hypothetical gene
SEQ ID n° 5810	3674	1606	SA-265.1	ribosomal protein L14
SEQ ID n° 5811	3675	1608	SA-266.1	similar to unknown proteins
SEQ ID n° 5812	3676	1613	SA-267.1	similar to transketolase
SEQ ID n° 5813	3677	1616	SA-267.1	Similar to unknown proteins
SEQ ID n° 5814	3678	1617	SA-268.1	similar to transcriptional regulatory protein (N-terminal part)
SEQ ID n° 5815	3679	1622	SA-269.1	similar to NADH oxidase
SEQ ID n° 5816	3680	1624	SA-269.1	similar to phage protein
SEQ ID n° 5817	3681	1626	SA-270.1	similar to glycerol uptake facilitator
SEQ ID n° 5818	3682	1627	SA-270.1	similar to unknown protein
SEQ ID n° 5819	3683	1629	SA-270.1	50S ribosomal protein L35
SEQ ID n° 5820	3684	1630	SA-2709.1	translation initiation factor IF-3
SEQ ID n° 5821	3685	1631	SA-271.1	glycerol-3-phosphate dehydrogenase
SEQ ID n° 5822	3686	1632	SA-2710.1	Similar to cytidine monophosphate kinase
SEQ ID n° 5823	3687	1634	SA-2712.1	Similar to unknown proteins (serine rich)
SEQ ID n° 5824	3688	1636	SA-272.1	glycerol kinase
SEQ ID n° 5825	3689	1641	SA-273.1	similar to unknown proteins
SEQ ID n° 5826	3690	1643	SA-274.1	similar to unknown proteins
SEQ ID n° 5827	3691	1646	SA-275.1	glycyl-tRNA synthetase (beta subunit)
SEQ ID n° 5828	3692	1648	SA-276.1	Similar to unknown proteins
SEQ ID n° 5829	3693	1651	SA-276.1	Similar to unknown proteins
SEQ ID n° 5830	3694	1652	SA-276.1	Similar to acyl carrier protein phosphodiesterase
SEQ ID n° 5831	3695	1655	SA-2768.2	glyceraldehyde 3-phosphate dehydrogenase
SEQ ID n° 5832	3696	1658	SA-2768.2	similar to unknown proteins

SEQ ID n° 5833	3697	1660	SA-277.1	282183-283097 p	glycyl-HRNA synthetase (alpha subunit)
SEQ ID n° 5834	3698	1663	SA-2772.1	1106781-1107011 m	Unknown
SEQ ID n° 5835	3699	1666	SA-278.2	281328-281870 p	similar to unknown proteins
SEQ ID n° 5836	3700		SA-2787.3	1919967-1920950 m	similar to transcriptional regulator (Lac family)
SEQ ID n° 5837	3701		SA-2789.1	508125-508481 p	Unknown
SEQ ID n° 5838	3702		SA-2790.2	508546-508968 m	Unknown
SEQ ID n° 5839	3703		SA-2791.2	508975-509313 m	similar to transcriptional regulator (phage related)
SEQ ID n° 5840	3704		SA-2798.2	517062-517363 p	Similar to unknown proteins
SEQ ID n° 5841	3705	1668	SA-28.1	730066-732432 p	Similar to unknown proteins
SEQ ID n° 5842	3706		SA-280.2	1336040-1339788 m	Similar to pullulanase, Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5843	3707	1669	SA-2801.2	516696-516943 p	Similar to unknown proteins
SEQ ID n° 5844	3708		SA-2803.2	503314-510102 p	hypothetical protein
SEQ ID n° 5845	3709		SA-2804.2	1613541-1614263 p	similar to pseudouridylate synthase
SEQ ID n° 5846	3710		SA-2813.1	236431-236653 p	similar to transcriptional regulator
SEQ ID n° 5847	3711		SA-2815.2	30442-31410 p	similar to ribose-phosphate pyrophosphokinase
SEQ ID n° 5848	3712	1670	SA-282.1	1334988-1335905 m	similar to putative permease
SEQ ID n° 5849	3713		SA-2822.1	2154545-2155606 m	Unknown
SEQ ID n° 5850	3714		SA-2823.2	437597-438925 p	similar to unknown plasmid protein
SEQ ID n° 5851	3715		SA-2829.1	763687-764895 p	Unknown
SEQ ID n° 5852	3716	1671	SA-283.1	1334770-1334946 p	Similar to unknown proteins
SEQ ID n° 5853	3717		SA-2831.1	763222-763533 p	Unknown
SEQ ID n° 5854	3718		SA-2832.1	759654-760991 p	similar to plasmid proteins
SEQ ID n° 5855	3719		SA-2833.1	756757-757404 p	similar to unknown proteins
SEQ ID n° 5856	3720		SA-2834.1	756452-756757 p	Unknown
SEQ ID n° 5857	3721		SA-2837.2	2208347-2209039 m	similar to unknown proteins
SEQ ID n° 5858	3722		SA-2839.1	2111022-2111308 m	chaperonin GroES
SEQ ID n° 5859	3723		SA-2840.1	2057634-2058251 m	Similar to ABC transporter (A TP-binding protein)
SEQ ID n° 5860	3724		SA-2842.2	717307-718062 m	Similar to ABC transporter (A TP-binding protein)
SEQ ID n° 5861	3725		SA-2843.1	716495-717295 m	Similar to amino acid ABC transporter (binding protein)
SEQ ID n° 5862	3726		SA-2849.1	125222-125668 p	similar to deoxyuridine 5 -triphosphate nucleotidylhydrolase (dUTPase)
SEQ ID n° 5863	3727	1672	SA-285.1	1333769-1334659 m	similar to tRNA isopentenylpyrophosphate transferase
SEQ ID n° 5864	3728		SA-2853.1	883008-88526 p	translation initiation factor IF-1
SEQ ID n° 5865	3729		SA-2854.2	1351575-1351865 p	similar to transposase
SEQ ID n° 5866	3730		SA-2855.1	1363655-1364491 p	similar to transposase, C-terminal part

SEQ ID n° 5867	3731		SA-2856.1	1493128-1493649 m	similar to pyrimidine biosynthetic operon repressor
SEQ ID n° 5868	3732		SA-2857.2	1557873-1559250 p	large conductance mechanosensitive channel protein MscL
SEQ ID n° 5869	3733	1673	SA-286.1	1332440-1333678 m	similar to GTP-binding protein
SEQ ID n° 5870	3734		SA-2860.1	1169149-1169370 m	similar to xanthine phosphoribosyltransferase
SEQ ID n° 5871	3735		SA-2861.1	1245656-1245863 p	similar to hypothetical transcriptional regulator
SEQ ID n° 5872	3736		SA-2862.1	1251589-1251837 m	similar to unknown proteins
SEQ ID n° 5873	3737		SA-2863.1	1251885-1252130 m	similar to unknown proteins
SEQ ID n° 5874	3738		SA-2866.1	762834-763217 p	similar to putative plasmid replication protein
SEQ ID n° 5875	3739		SA-2867.1	762543-762921 p	Unknown
SEQ ID n° 5876	3740		SA-2868.1	761728-762546 p	similar to plasmid partition protein ParA
SEQ ID n° 5877	3741		SA-2869.1	761005-761589 p	Unknown
SEQ ID n° 5878	3742	1674	SA-287.1	1331800-1332447 m	similar to unknown proteins
SEQ ID n° 5879	3743		SA-2870.1	759383-759640 p	Unknown
SEQ ID n° 5880	3744		SA-2871.1	757414-759363 p	similar to plasmid protein
SEQ ID n° 5881	3745		SA-2872.1	755988-756221 p	Unknown
SEQ ID n° 5882	3746		SA-2874.1	753724-755931 p	similar to unknown protein
SEQ ID n° 5883	3747		SA-2875.1	753122-753804 p	Unknown
SEQ ID n° 5884	3748		SA-2877.1	749873-753022 p	similar to plasmid protein
SEQ ID n° 5885	3749		SA-2878.1	749623-749880 p	Unknown
SEQ ID n° 5886	3750		SA-2879.1	748964-749395 p	similar to single-strand binding protein
SEQ ID n° 5887	3751	1675	SA-288.1	1330829-1331758 m	Similar to unknown proteins
SEQ ID n° 5888	3752		SA-2880.1	1036003-1038804 m	similar to surface antigen proteins, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5889	3753		SA-2882.1	745217-745939 p	similar to unknown protein, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5890	3754		SA-2883.1	742789-745140 p	Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5891	3755		SA-2885.1	741782-742864 p	Unknown
SEQ ID n° 5892	3756		SA-2896.1	741424-741771 p	No similarity
SEQ ID n° 5893	3757		SA-2897.1	739413-741332 p	similar to ATP-dependent Clp protease ATP-binding subunit CtpA
SEQ ID n° 5894	3758		SA-2898.1	737750-739498 p	similar to DNA topoisomerase III
SEQ ID n° 5895	3759		SA-2899.1	406767-411497 p	similar to plasmid proteins
SEQ ID n° 5896	3760		SA-2891.1	732558-732815 p	Unknown
SEQ ID n° 5897	3761		SA-2893.1	1052360-1054726 m	similar to unknown proteins
SEQ ID n° 5898	3762		SA-2894.1	729554-730012 p	Unknown
SEQ ID n° 5899	3763		SA-2895.1	1055255-1056055 m	similar to unknown proteins

SEQ ID n° 5900	3764	SA-2896.1	728390-728737 p	Unknown
SEQ ID n° 5901	3765	SA-2897.1	728080-728397 p	Unknown
SEQ ID n° 5902	3766	SA-29.1	1054780-1052338 m	Unknown
SEQ ID n° 5903	3767	SA-290.1	1330066-1330827 m	similar to oxidoreductase
SEQ ID n° 5904	3768	SA-2900.1	727411-727686 p	Unknown
SEQ ID n° 5905	3769	SA-2902.1	726446-727288 p	hypothetical start codon
SEQ ID n° 5906	3770	SA-2903.1	725380-726384 p	Unknown
SEQ ID n° 5907	3771	SA-2905.1	724346-725301 m	Unknown
SEQ ID n° 5908	3772	SA-2906.1	724104-724352 p	Unknown
SEQ ID n° 5909	3773	SA-2907.1	723919-724089 p	Unknown
SEQ ID n° 5910	3774	SA-2908.1	723358-723768 p	Unknown
SEQ ID n° 5911	3775	SA-291.1	1327871-1330069 m	similar to single-strand DNA-specific exonuclease
SEQ ID n° 5912	3776	SA-2910.1	722916-723365 p	RecJ
SEQ ID n° 5913	3777	SA-2911.1	1052066-1052512 m	Unknown
SEQ ID n° 5914	3778	SA-2912.1	721852-722280 p	similar to unknown proteins
SEQ ID n° 5915	3779	SA-2913.1	721637-721840 p	Unknown
SEQ ID n° 5916	3780	SA-2914.1	1063411-1064904 m	similar to plasmid replication protein
SEQ ID n° 5917	3781	SA-2916.1	719648-719875 p	Unknown
SEQ ID n° 5918	3782	SA-2917.1	719536-719855 p	Unknown
SEQ ID n° 5919	3783	SA-2918.1	719436-719530 p	hypothetical gene
SEQ ID n° 5920	3784	SA-2918.1	719103-719432 p	Unknown
SEQ ID n° 5921	3785	SA-292.1	1325155-1327719 m	similar to putative hydrolytic protein
SEQ ID n° 5922	3786	SA-2921.3	1558627-1559130 m	similar to unknown proteins
SEQ ID n° 5923	3787	SA-2922.1	1559213-1560019 m	Similar to amino acid ABC transporter (binding protein)
SEQ ID n° 5924	3788	SA-2926.1	1882439-1882909 m	ribosomal protein S7
SEQ ID n° 5925	3789	SA-2928.1	1882931-1883344 m	ribosomal protein S12
SEQ ID n° 5926	3790	SA-293.1	1324514-1325032 m	similar to adenine phosphoribosyltransferase
SEQ ID n° 5927	3791	SA-2939.1	1982190-1982534 m	similar to hypothetical thioredoxin
SEQ ID n° 5928	3792	SA-294.1	1323716-1324396 m	similar to unknown proteins
SEQ ID n° 5929	3793	SA-2940.1	1981772-1982113 m	similar to unknown proteins
SEQ ID n° 5930	3794	SA-2945.1	1755545-1755901 m	similar to unknown proteins
SEQ ID n° 5931	3795	SA-2946.1	1701220-1701810 m	ATP-dependent CLP protease proteolytic subunit
SEQ ID n° 5932	3796	SA-2947.1	1700875-1701120 m	similar to unknown proteins
SEQ ID n° 5933	3797	SA-295.1	1322929-1323612 m	similar to unknown proteins
SEQ ID n° 5934	3798	SA-2951.2	1558347-1558523 m	ribosomal protein S21

SEQ ID n° 5935	3799	SA-2954.1	1350730-1351386 p	similar to unknown proteins
SEQ ID n° 5936	3800	SA-2955.1	1350071-1350568 m	similar to unknown proteins
SEQ ID n° 5937	3801	SA-296.1	1322151-1322939 m	similar to unknown proteins
SEQ ID n° 5938	3802	SA-2961.1	1138745-1137083 m	similar to N-terminal first 100 amino acids of anaerobic ribonucleotide reductase
SEQ ID n° 5939	3803	SA-297.1	1321039-1322142 m	similar to probable D-amino acid oxidase
SEQ ID n° 5940	3804	SA-2973.2	433313-433570 p	Unknown
SEQ ID n° 5941	3805	SA-2974.2	431344-433293 p	similar to plasmid transfer complex protein
SEQ ID n° 5942	3806	SA-2975.2	427052-427534 p	Unknown
SEQ ID n° 5943	3807	SA-2976.2	423803-428952 p	similar to plasmid proteins
SEQ ID n° 5944	3808	SA-2977.2	419921-422722 p	similar to surface antigen proteins, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5945	3809	SA-2978.1	718598-719052 p	Unknown
SEQ ID n° 5946	3810	SA-2979.1	718373-718551 p	Unknown
SEQ ID n° 5947	3811	SA-298.5	1320126-1320980 m	glucose-1-phosphate thymidyltransferase
SEQ ID n° 5948	3812	SA-2985.2	437152-437463 p	Unknown
SEQ ID n° 5949	3813	SA-2985.2	436764-437147 p	similar to replication initiation protein from <i>Staphylococcus</i> plasmid
SEQ ID n° 5950	3814	SA-2987.2	436473-436751 p	Unknown
SEQ ID n° 5951	3815	SA-2988.2	435568-436476 p	similar to plasmid partition protein ParA
SEQ ID n° 5952	3816	SA-2989.1	434935-435519 p	Unknown
SEQ ID n° 5953	3817	1686	1319519-1320112 m	Unknown
SEQ ID n° 5954	3818	SA-299.5	433584-434821 p	dTDP-4-keto-5-deoxyglucose-3,5-epimerase
SEQ ID n° 5955	3819	SA-2990.1	430587-431334 p	similar to plasmid proteins
SEQ ID n° 5956	3820	SA-2992.1	430382-430687 p	similar to unknown protein
SEQ ID n° 5957	3821	SA-2993.1	429918-430151 p	Unknown
SEQ ID n° 5958	3822	SA-2995.1	427654-429861 p	Unknown
SEQ ID n° 5959	3823	SA-2997.1	423553-423810 p	similar to unknown proteins
SEQ ID n° 5960	3824	SA-2998.1	422894-423325 p	Unknown
SEQ ID n° 5961	3825	1687	1025432-1027381 m	similar to single-strand binding protein
SEQ ID n° 5962	3826	1688	728737-729537 p	similar to plasmid transfer complex protein
SEQ ID n° 5963	3827	SA-300.1	419147-419869 p	similar to membrane nuclease
SEQ ID n° 5964	3828	SA-3000.1	416809-419070 p	Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5965	3829	SA-3001.1	416809-419070 p	similar to plasmid surface exclusion protein, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 5966	3830	SA-3002.1	415712-416794 p	similar to unknown proteins
		SA-3003.1	415354-415701 p	Unknown

SEQ ID n° 5967	3831		similar to ATP-dependent Ctp protease ATP-binding subunit
SEQ ID n° 5968	3832	SA-3004.1	413430-415262 p
SEQ ID n° 5969	3833	SA-3005.1	411660-413429 p
SEQ ID n° 5970	3834	SA-3007.2	736332-737567 p
SEQ ID n° 5971	3835	SA-3008.1	405491-406748 p
SEQ ID n° 5972	3836	SA-301.1	1318266-1319312 m
SEQ ID n° 5973	3837	SA-3010.1	403999-406365 p
SEQ ID n° 5974	3838	SA-3011.1	403487-403945 p
SEQ ID n° 5975	3839	SA-3012.1	402670-403470 p
SEQ ID n° 5976	3840	SA-3013.1	402323-402670 p
SEQ ID n° 5977	3841	SA-3014.1	402013-402330 p
SEQ ID n° 5978	3842	SA-3016.1	401344-401619 p
SEQ ID n° 5979	3843	SA-3018.1	400373-401221 p
SEQ ID n° 5980	3844	SA-3019.1	399313-400317 p
SEQ ID n° 5981	3845	SA-3021.1	396278-399234 m
SEQ ID n° 5982	3846	SA-3022.1	398037-398285 p
SEQ ID n° 5983	3847	SA-3023.1	397879-398022 p
SEQ ID n° 5984	3848	SA-3025.1	397291-397701 p
SEQ ID n° 5985	3849	SA-3027.1	396849-397298 p
SEQ ID n° 5986	3850	SA-3028.1	396213-396659 p
SEQ ID n° 5987	3851	SA-3029.1	395765-396213 p
SEQ ID n° 5988	3852	SA-3030.1	395570-395773 p
SEQ ID n° 5989	3853	SA-3031.1	393821-395314 p
SEQ ID n° 5990	3854	SA-3033.1	393581-393808 p
SEQ ID n° 5991	3855	SA-3034.1	393469-393588 p
SEQ ID n° 5992	3856	SA-3035.1	393284-393463 p
SEQ ID n° 5993	3857	SA-3036.1	393036-393365 p
SEQ ID n° 5994	3858	SA-306.1	1314996-1318214 p
SEQ ID n° 5995	3859	SA-307.1	1314297-1314779 m
SEQ ID n° 5996	3860	SA-3071.1	1313846-1314307 m
SEQ ID n° 5997	3861	SA-3072.1	917642-918033 p
SEQ ID n° 5998	3862	SA-3073.1	733435-733630 p
SEQ ID n° 5999	3863	SA-308.1	732894-733436 p
SEQ ID n° 6000	3864	SA-309.1	1312564-1313754 m
SEQ ID n° 6001	3865	SA-311.1	1311348-1312574 m
			1056055-1056402 m

SEQ ID n° 6002	3866	1697	SA-311.1	1309556-1311238 m	similar to alpha-acetolactate synthase
SEQ ID n° 6003	3867	1698	SA-312.1	1308823-1309542 m	similar to alpha-acetolactate decarboxylase
SEQ ID n° 6004	3868		SA-3125.1	83021-83206 p	ribosomal protein S14
SEQ ID n° 6005	3869		SA-3126.1	88592-88668 p	ribosomal protein L36
SEQ ID n° 6006	3870	1699	SA-313.2	1307114-1308769 p	similar to hypothetical fibronectin-binding protein
SEQ ID n° 6007	3871	1700	SA-314.2	1305752-1306756 m	similar to unknown proteins
SEQ ID n° 6008	3872	1701	SA-315.1	1304876-1305739 m	Similar to ABC transporter (permease)
SEQ ID n° 6009	3873	1702	SA-316.1	1304115-1304876 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 6010	3874	1703	SA-318.1	1302157-1303818 m	similar to unknown proteins
SEQ ID n° 6011	3875	1704	SA-319.1	1301312-1302100 m	similar to tubulin esterase
SEQ ID n° 6012	3876	1705	SA-32.1	1058395-1058712 m	Unknown
SEQ ID n° 6013	3877	1706	SA-320.1	1300512-1301222 m	similar to unknown proteins
SEQ ID n° 6014	3878	1708	SA-322.1	1299603-1300274 m	similar to ribose 5-phosphate isomerase
SEQ ID n° 6015	3879	1709	SA-323.1	1298335-1299546 m	similar to phosphopentomutase
SEQ ID n° 6016	3880	1710	SA-324.1	1297877-1298284 m	similar to arsenate reductase (hypothetical)
SEQ ID n° 6017	3881	1711	SA-325.1	1297029-1297838 m	similar to purine nucleoside phosphorylase
SEQ ID n° 6018	3882	1712	SA-327.1	1295771-1297027 m	putative transport protein
SEQ ID n° 6019	3883	1713	SA-327.1	1295077-1295787 m	similar to purine-nucleoside phosphorylase
SEQ ID n° 6020	3884	1714	SA-328.1	1294301-1295068 m	similar to unknown proteins
SEQ ID n° 6021	3885	1715	SA-329.2	1293353-1294276 p	similar to transcriptional regulator (LysR family)
SEQ ID n° 6022	3886	1716	SA-330.2	60992-61249 p	similar to unknown proteins
SEQ ID n° 6023	3887	1717	SA-331.2	59909-60962 p	similar to phosphoribosylaminimidazole carboxylase II
SEQ ID n° 6024	3888	1718	SA-333.1	59431-59922 p	similar to phosphoribosylaminimidazole carboxylase
SEQ ID n° 6025	3889	1719	SA-334.1	57888-59150 p	similar to phosphoribosylamine-glycine ligase
SEQ ID n° 6026	3890	1720	SA-335.1	56801-57604 m	similar to unknown proteins
SEQ ID n° 6027	3891	1721	SA-336.1	55801-56776 p	similar to acetyl xylan esterase (hypothetical)
SEQ ID n° 6028	3892	1722	SA-337.1	54912-55793 p	similar to glucose kinase and to XylR transcriptional regulator
SEQ ID n° 6029	3893	1723	SA-338.1	53978-54895 p	similar to N-acetylserine aminidase
SEQ ID n° 6030	3894	1724	SA-339.1	53319-53981 p	similar to unknown proteins
SEQ ID n° 6031	3895	1725	SA-34.1	1057106-1057381 m	Unknown
SEQ ID n° 6032	3896	1726	SA-340.1	52865-53299 p	similar to unknown proteins
SEQ ID n° 6033	3897	1727	SA-342.1	52013-52843 p	Similar to ABC transporter (permease)
SEQ ID n° 6034	3898	1728	SA-343.1	51116-52003 p	Similar to sugar ABC transporter (permease)
SEQ ID n° 6035	3899	1729	SA-344.1	49712-51028 p	Similar to ABC transporter (binding protein)
SEQ ID n° 6036	3900	1730	SA-345.1	48967-49665 p	similar to unknown proteins

SEQ ID n° 6037	3901	1731	SA-347.1	47416-46720 p	group B streptococcal surface immunogenic protein
SEQ ID n° 6038	3902	1732	SA-348.1	46370-47289 p	similar to Streptococcus equi zocin A endopeptidase
SEQ ID n° 6039	3903	1733	SA-351.1	44630-46177 p	similar to bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
SEQ ID n° 6040	3904	1734	SA-352.1	43858-44610 p	similar to unknown proteins
SEQ ID n° 6041	3905	1735	SA-353.1	43287-43835 p	similar to Phosphoribosylglycinamide formyltransferase
SEQ ID n° 6042	3906	1736	SA-356.1	42097-43119 p	similar to phosphoribosylglycinamide cyclo-ligase
SEQ ID n° 6043	3907	1737	SA-357.1	40615-42089 p	similar to phosphoribosylpyrophosphate amidotransferase
SEQ ID n° 6044	3908	1738	SA-36.1	1057504-1068352 m	Unknown
SEQ ID n° 6045	3909	1740	SA-363.1	36656-40381 p	similar to Phosphoribosylformylglycinamide synthase
SEQ ID n° 6046	3910	1741	SA-364.2	35929-36533 p	similar to phosphoribosylaminoimidazole succinocarboxamide synthase
SEQ ID n° 6047	3911	1742	SA-366.2	562906-565167 m	similar to ATP-dependent protease ClpE
SEQ ID n° 6048	3912	1743	SA-367.1	562285-562720 m	Similar to unknown proteins
SEQ ID n° 6049	3913	1744	SA-368.1	561899-562201 m	similar to unknown proteins
SEQ ID n° 6050	3914	1745	SA-37.1	1058408-1059412 m	similar to unknown proteins
SEQ ID n° 6051	3915	1746	SA-370.1	558990-561782 p	isoleucyl-RNA synthetase
SEQ ID n° 6052	3916	1747	SA-371.1	557935-558706 p	similar to cell division protein DivIVA
SEQ ID n° 6053	3917	1748	SA-372.1	557137-557925 p	similar to unknown proteins
SEQ ID n° 6054	3918	1749	SA-373.1	556881-557135 p	Similar to unknown proteins
SEQ ID n° 6055	3919	1750	SA-374.1	556273-556378 p	Similar to unknown proteins
SEQ ID n° 6056	3920	1751	SA-375.1	555590-556261 p	Similar to unknown proteins
SEQ ID n° 6057	3921	1752	SA-376.1	554301-555581 p	cell division protein FlzZ
SEQ ID n° 6058	3922	1753	SA-377.1	552906-554279 p	Similar to cell division protein DivB
SEQ ID n° 6059	3923	1754	SA-379.1	551497-552833 p	Similar to undecaprenyl-PP-MurNAc-pentapeptide-UDP-GlcNAc
SEQ ID n° 6060	3924	1755	SA-380.1	550417-551493 p	GlcNAc transferase
SEQ ID n° 6061	3925	1756	SA-381.1	548059-550414 p	Similar to UDP-N-acetylmuramoylalanine-D-glutamate ligase
SEQ ID n° 6062	3926	1757	SA-382.1	548684-548929 p	Similar to unknown proteins
SEQ ID n° 6063	3927	1758	SA-384.1	546798-548639 p	similar to putative GTP-binding elongation factor
SEQ ID n° 6064	3928	1759	SA-385.1	546196-546566 p	similar to unknown proteins
SEQ ID n° 6065	3929	1760	SA-387.1	545206-546174 p	similar to glucose kinase
SEQ ID n° 6066	3930	1761	SA-388.1	545000-545209 p	similar to unknown proteins

SEQ ID n° 6067	3931	1762	SA-389.1	544450-544845 m	similar to unknown proteins
SEQ ID n° 6068	3932	1763	SA-39.1	1059491-1060447 p	Unknown
SEQ ID n° 6069	3933	1764	SA-390.1	543617-544449 p	similar to endonuclease III
SEQ ID n° 6070	3934	1765	SA-391.1	542475-543704 p	similar to other proteins
SEQ ID n° 6071	3935	1766	SA-392.1	541439-542482 p	Similar to Acetyl-CoA acetyltransferase (truncated)
SEQ ID n° 6072	3936	1767	SA-393.1	540863-541378 p	Unknown
SEQ ID n° 6073	3937	1768	SA-394.1	539746-540738 m	similar to biotin synthetase
SEQ ID n° 6074	3938	1769	SA-395.1	539206-539745 m	similar to other proteins
SEQ ID n° 6075	3939	1770	SA-396.1	538572-539138 p	similar to Antitranslate synthase component II (Glutamine amidotransferase)
SEQ ID n° 6076	3940	1771	SA-397.1	538705-538444 p	similar to ABC transporter (exporter) (ATP-binding protein)
SEQ ID n° 6077	3941	1772	SA-398.1	534970-536715 p	similar to ABC transporter (exporter) (ATP-binding protein)
SEQ ID n° 6078	3942	1773	SA-399.1	534259-534774 p	Similar to unknown proteins
SEQ ID n° 6079	3943	1774	SA-4.2	1027391-1028038 m	similar to unknown protein
SEQ ID n° 6080	3944	1775	SA-40.1	1060440-1060688 m	Unknown
SEQ ID n° 6081	3945	1776	SA-400.1	533163-534259 p	similar to unknown proteins
SEQ ID n° 6082	3946	1777	SA-401.2	532524-533102 p	similar to unknown proteins
SEQ ID n° 6083	3947	1778	SA-402.2	531121-532455 p	Similar to unknown proteins
SEQ ID n° 6084	3948	1779	SA-403.1	529973-531046 p	Similar to unknown proteins
SEQ ID n° 6085	3949	1780	SA-405.1	529498-529863 p	similar to phosphopantetheine adenylyltransferase
SEQ ID n° 6086	3950	1781	SA-407.1	529211-529501 p	Unknown
SEQ ID n° 6087	3951	1782	SA-409.1	528447-529199 p	similar to unknown proteins
SEQ ID n° 6088	3952	1783	SA-411.1	1060703-1060846 m	Unknown
SEQ ID n° 6089	3953	1784	SA-410.1	528080-528529 m	Similar to unknown proteins
SEQ ID n° 6090	3954	1785	SA-411.2	527043-528035 p	Similar to asparagine synthetase
SEQ ID n° 6091	3955	1786	SA-412.2	1653493-1664140 p	Similar to metal-dependent transcriptional regulator
SEQ ID n° 6092	3956	1787	SA-413.1	1664180-1664869 m	Similar to 5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase
SEQ ID n° 6093	3957	1788	SA-414.1	1664879-1665148 m	Similar to unknown proteins
SEQ ID n° 6094	3958	1789	SA-415.1	1665148-1665702 m	Similar to ADP-ribose pyrophosphatase
SEQ ID n° 6095	3959	1790	SA-416.1	1665723-1667102 m	Similar to UDP-N-acetylglucosamine pyrophosphorylase
SEQ ID n° 6096	3960	1791	SA-417.1	1667346-1667789 m	Similar to unknown proteins
SEQ ID n° 6097	3961	1792	SA-418.1	1667772-1668149 m	Similar to unknown proteins
SEQ ID n° 6098	3962	1793	SA-419.1	1668238-1669194 m	Similar to oxidoreductase
SEQ ID n° 6099	3963	1794	SA-42.1	1061024-1061434 m	Unknown
SEQ ID n° 6100	3964	1795	SA-420.1	1669191-1669445 m	similar to unknown proteins C-terminal end

SEQ ID n° 6101	3965	1797	SA-422.1	1669406-1669648 m	Unknown
SEQ ID n° 6102	3966	1799	SA-424.1	1669887-1670585 m	similar to oxidoreductases
SEQ ID n° 6103	3967	1800	SA-425.1	1670578-1670814 m	Similar to unknown proteins
SEQ ID n° 6104	3968	1801	SA-426.1	1670904-1671152 m	Similar to unknown proteins
SEQ ID n° 6105	3969	1802	SA-427.1	1671350-1671850 m	similar to other proteins
SEQ ID n° 6106	3970	1803	SA-428.1	1672090-1672545 m	Similar to unknown proteins (C-terminal end)
SEQ ID n° 6107	3971	1804	SA-429.1	1672546-1673502 m	Similar to other proteins (N-terminal part)
SEQ ID n° 6108	3972	1805	SA-430.1	1673642-1675801 m	Similar to unknown proteins
SEQ ID n° 6109	3973	1806	SA-431.1	1675808-1677253 m	Similar to other proteins
SEQ ID n° 6110	3974	1807	SA-432.1	1677248-1677923 m	Unknown
SEQ ID n° 6111	3975	1808	SA-433.1	1677975-1678586 m	Unknown
SEQ ID n° 6112	3976	1809	SA-434.2	1679034-1680371 m	Similar to branched-chain amino acid transporter
SEQ ID n° 6113	3977	1810	SA-435.1	1680567-1682564 m	methionyl-RNA synthetase
SEQ ID n° 6114	3978	1811	SA-436.1	1682707-1683582 p	Similar to other proteins
SEQ ID n° 6115	3979	1812	SA-437.1	1683740-1684435 m	Similar to unknown proteins
SEQ ID n° 6116	3980	1813	SA-438.1	1684771-1685988 p	Similar to PTS enzyme IIC
SEQ ID n° 6117	3981	1814	SA-439.1	1685972-1686814 p	Similar to unknown proteins
SEQ ID n° 6118	3982	1815	SA-44.1	1061427-1061876 m	Unknown
SEQ ID n° 6119	3983	1816	SA-441.1	1686891-1687718 p	Similar to 3'-exo-deoxyribonuclease
SEQ ID n° 6120	3984	1817	SA-442.1	1687789-1688115 m	Similar to other proteins
SEQ ID n° 6121	3985	1818	SA-443.1	1688117-1688930 m	similar to OB-alkylguanine-DNA-alkyltransferase
SEQ ID n° 6122	3986	1819	SA-445.1	1688648-1688930 m	similar to phosphoglycerate dehydrogenase
SEQ ID n° 6123	3987	1820	SA-446.1	1688982-1690440 m	similar to unknown proteins
SEQ ID n° 6124	3988	1821	SA-447.1	1690509-1691600 m	similar to phosphoserine aminotransferase
SEQ ID n° 6125	3989	1822	SA-448.1	1691733-1692368 p	Similar to other proteins
SEQ ID n° 6126	3990	1823	SA-45.1	722280-722725 p	Unknown
SEQ ID n° 6127	3991	1824	SA-450.1	1692538-1693501 m	Similar to unknown proteins
SEQ ID n° 6128	3992	1825	SA-451.1	1693507-1693833 m	Similar to unknown proteins
SEQ ID n° 6129	3993	1826	SA-452.1	1693864-1694727 m	similar to DNA polymerase III (delta subunit)
SEQ ID n° 6130	3994	1827	SA-453.1	1694747-1695382 m	similar to thymidylate kinase
SEQ ID n° 6131	3995	1828	SA-454.1	1695471-1696130 m	Similar to acetyl dehydrogenase
SEQ ID n° 6132	3996	1829	SA-455.1	1696149-1696889 m	similar to amino acid ABC transporter (ATP-binding protein)
SEQ ID n° 6133	3997	1830	SA-456.1	1696869-1697623 m	similar to amino acid ABC transporter (ATP-binding protein)
SEQ ID n° 6134	3998	1831	SA-457.1	1697624-1698577 m	similar to ABC transporter (permease)
SEQ ID n° 6135	3999	1832	SEQ ID n° 6135	1698580-1699449 m	similar to amino acid ABC transporter (permease)
SEQ ID n° 6136	4000	1833	SA-46.1	1062512-1062940 m	Unknown

SEQ ID n° 6137	4001	1834	SA-460.3	1699565-1700721 m	similar to branched-chain amino acid ABC transporter, amino acid-binding protein
SEQ ID n° 6138	4002	1835	SA-462.1	365287-365721 p	similar to transcriptional regulator (MarR family)
SEQ ID n° 6139	4003	1836	SA-463.1	365721-366692 p	similar to beta-ketolactoyl-ACP synthase III
SEQ ID n° 6140	4004	1837	SA-464.1	366750-366974 p	similar to acyl carrier protein
SEQ ID n° 6141	4005	1838	SA-465.1	367129-368088 p	similar to putative trans-2-enoyl-ACP reductase II
SEQ ID n° 6142	4006	1839	SA-466.1	368108-369034 p	similar to malonyl CoA-acyl carrier protein transacylase
SEQ ID n° 6143	4007	1840	SA-467.1	369043-369777 p	similar to beta-ketolactoyl-ACP reductase
SEQ ID n° 6144	4008	1841	SA-468.1	369793-371028 p	similar to 3-oxoacyl-acyl-carrier protein synthase
SEQ ID n° 6145	4009	1842	SA-469.1	371027-371827 p	similar to biotin carboxyl carrier protein
SEQ ID n° 6146	4010	1843	SA-47.1	719888-721381 p	similar to plasmid replication protein E
SEQ ID n° 6147	4011	1844	SA-470.1	371524-371948 p	similar to beta-hydroxyacyl-ACP dehydratase
SEQ ID n° 6148	4012	1845	SA-471.1	371984-373354 p	similar to acetyl-CoA carboxylase biotin carboxylase subunit
SEQ ID n° 6149	4013	1846	SA-472.1	373363-374238 p	similar to acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
SEQ ID n° 6150	4014	1847	SA-473.1	374231-375004 p	similar to acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
SEQ ID n° 6151	4015	1848	SA-474.1	375474-376106 p	similar to sakacin A production response regulator
SEQ ID n° 6152	4016	1849	SA-475.1	376152-377429 m	[Streptococcus mutans] hypothetical
SEQ ID n° 6153	4017	1850	SA-477.1	377720-378787 p	seryl-tRNA synthetase
SEQ ID n° 6154	4018	1851	SA-478.1	378825-379187 m	similar to unknown protein
SEQ ID n° 6155	4019	1853	SA-480.1	379306-380217 m	similar to mannose-specific PTS enzyme IID
SEQ ID n° 6156	4020	1854	SA-481.1	380232-381044 m	similar to mannose-specific PTS enzyme IIC
SEQ ID n° 6157	4021	1855	SA-483.1	381077-382087 m	similar to mannose-specific PTS enzyme IID
SEQ ID n° 6158	4022	1856	SA-484.1	382390-383202 m	similar to unknown protein
SEQ ID n° 6159	4023	1857	SA-485.1	383291-383876 p	putative transmembrane protein
SEQ ID n° 6160	4024	1858	SA-486.1	383965-384576 p	similar to unknown transmembrane protein
SEQ ID n° 6161	4025	1860	SA-488.1	384679-386100 p	similar to unknown transmembrane protein
SEQ ID n° 6162	4026	1861	SA-489.1	386249-386692 p	similar to unknown protein
SEQ ID n° 6163	4027	1862	SA-49.2	1065262-1065354 m	Unknown
SEQ ID n° 6164	4028	1863	SA-490.1	386665-387206 p	similar to unknown protein
SEQ ID n° 6165	4029	1864	SA-491.1	387215-388522 p	similar to transcription regulator, hypothetical
SEQ ID n° 6166	4030	1865	SA-493.1	388586-388882 m	similar to unknown protein
SEQ ID n° 6167	4031	1866	SA-494.1	388879-389298 m	similar to cell-cycle regulation histidine triad (HIT) protein
SEQ ID n° 6168	4032	1867	SA-495.1	389634-390137 p	Unknown

SEQ ID n° 6169	4033	1868	SA-487.2	1252542-1254821 m	similar to ATP-dependent DNA helicase
SEQ ID n° 6170	4034	1869	SA-498.1	1254927-1255313 m	similar to unknown proteins
SEQ ID n° 6171	4035	1870	SA-499.1	1255446-1255771 m	similar to uracil permease
SEQ ID n° 6172	4036	1871	SA-50.2	1028038-1028343 m	Unknown
SEQ ID n° 6173	4037	1872	SA-50.1	1065137-1065256 m	Unknown
SEQ ID n° 6174	4038	1873	SA-500.1	1257368-1258714 p	similar to probable amino-acid transporter
SEQ ID n° 6175	4039	1874	SA-501.1	1258778-1260013 p	similar to putative cation efflux system protein
SEQ ID n° 6176	4040	1875	SA-502.1	1260172-1260564 p	similar to unknown proteins
SEQ ID n° 6177	4041	1876	SA-503.2	1260545-1261240 p	similar to unknown proteins
SEQ ID n° 6178	4042	1877	SA-504.2	1261309-1261932 p	similar to unknown proteins
SEQ ID n° 6179	4043	1878	SA-505.1	1262334-1262480 m	Unknown
SEQ ID n° 6180	4044	1879	SA-506.1	1262533-1262964 p	Unknown
SEQ ID n° 6181	4045	1880	SA-507.1	1263261-1263695 p	Unknown
SEQ ID n° 6182	4046	1881	SA-508.2	1264088-1264876 p	similar to repressor protein - phage associated
SEQ ID n° 6183	4047	1882	SA-509.2	1211420-1212304 m	Similar to putative pseudouridine synthase
SEQ ID n° 6184	4048	1883	SA-511.1	1065360-1065689 m	Unknown
SEQ ID n° 6185	4049	1884	SA-510.1	1212301-1213137 m	Similar to unknown protein
SEQ ID n° 6186	4050	1885	SA-511.1	1213112-1213783 m	Similar to unknown protein
SEQ ID n° 6187	4051	1886	SA-512.1	1213893-1214465 p	Similar to unknown protein
SEQ ID n° 6188	4052	1887	SA-513.1	1214642-1215616 p	Similar to Phosphoribosylpyrophosphate synthetase
SEQ ID n° 6189	4053	1890	SA-517.1	362167-363519 m	similar to aspartokinase
SEQ ID n° 6190	4054	1891	SA-518.1	363613-364263 p	similar to unknown protein
SEQ ID n° 6191	4055	1892	SA-519.3	364400-365191 p	similar to enoyl-CoA isomerase
SEQ ID n° 6192	4056	1893	SA-52.1	392531-393025 p	Unknown
SEQ ID n° 6193	4057	1894	SA-520.2	507494-507787 p	Similar to unknown proteins
SEQ ID n° 6194	4058	1895	SA-523.4	503448-506828 p	similar to alpha protein, putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 6195	4059	1896	SA-524.1	502012-503205 m	similar to transcriptional regulator (AraC/XylS family)
SEQ ID n° 6196	4060	1897	SA-526.1	501293-501817 p	similar to transcriptional regulator tetR-family
SEQ ID n° 6197	4061	1898	SA-527.3	500298-501161 m	similar to cation efflux system protein
SEQ ID n° 6198	4062	1899	SA-528.3	499630-500213 m	similar to similar to oxydoreductases, N-terminal part
SEQ ID n° 6199	4063	1900	SA-529.1	499359-499829 m	similar to oxydoreductase (C-terminal part)
SEQ ID n° 6200	4064	1901	SA-53.1	392306-392494 p	Unknown
SEQ ID n° 6201	4065	1902	SA-530.1	498794-499249 m	similar to alcohol dehydrogenase (N-terminal part)
SEQ ID n° 6202	4066	1903	SA-531.1	498213-498908 m	similar to alcohol dehydrogenase (C-terminal part)
SEQ ID n° 6203	4067	1904	SA-532.1	497808-498197 m	similar to transcriptional regulator (MerR family)

SEQ ID n° 6204	4068	1905	SA-533.1	497403-497798 m	Similar to other proteins
SEQ ID n° 6205	4069	1906	SA-534.1	497052-497378 m	Similar to decarboxylase
SEQ ID n° 6206	4070	1907	SA-535.1	496691-496975 m	Similar to unknown proteins
SEQ ID n° 6207	4071	1908	SA-536.1	495961-496452 m	Similar to hypothetical transcriptional regulators
SEQ ID n° 6208	4072	1909	SA-537.1	495528-495917 p	Similar to unknown proteins
SEQ ID n° 6209	4073	1910	SA-538.1	492348-495515 p	Similar to surface proteins, putative peptidoglycan bound protein (LPXTS motif)
SEQ ID n° 6210	4074	1911	SA-542	391173-392213 p	similar to ABC transporter (permease)
SEQ ID n° 6211	4075	1912	SA-540.1	490117-492285 p	Similar to ribonucleoside-diphosphate reductase 2 alpha subunit
SEQ ID n° 6212	4076	1913	SA-541.1	489702-490115 p	Similar to unknown proteins
SEQ ID n° 6213	4077	1914	SA-542.2	488691-489701 p	similar to ribonucleoside-diphosphate reductase beta chain
SEQ ID n° 6214	4078	1915	SA-544.1	487230-488138 p	similar to rhamnosyltransferase
SEQ ID n° 6215	4079	1918	SA-547.2	483319-487020 p	Putative peptidoglycan bound protein (LPXTS motif) similar to CSA peptidase
SEQ ID n° 6216	4080	1919	SA-548.2	482703-483131 p	similar to unknown proteins
SEQ ID n° 6217	4081	1920	SA-549.1	481905-482669 p	Similar to purine nucleoside phosphorylase
SEQ ID n° 6218	4082	1921	SA-552	390466-391171 p	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 6219	4083	1922	SA-550.1	480283-481638 p	Similar to other proteins including hypothetical methyltransferases
SEQ ID n° 6220	4084	1923	SA-551.1	479408-480184 m	Similar to unknown proteins
SEQ ID n° 6221	4085	1924	SA-552.1	478791-479324 m	Similar to unknown proteins
SEQ ID n° 6222	4086	1925	SA-554.2	1577255-1578580 m	Similar to unknown proteins
SEQ ID n° 6223	4087	1926	SA-555.1	1578573-1580081 m	Similar to putative glucosyl transferase
SEQ ID n° 6224	4088	1927	SA-557.1	1580095-1582482 m	Similar to preprotein translocase secA
SEQ ID n° 6225	4089	1928	SA-558.1	1582489-1583461 m	Similar to unknown proteins
SEQ ID n° 6226	4090	1929	SA-559.1	1583468-1585017 m	Similar to unknown protein
SEQ ID n° 6227	4091	1931	SA-560.1	1585024-1586568 m	Similar to unknown protein
SEQ ID n° 6228	4092	1932	SA-561.1	1586568-1587797 m	Similar to preprotein translocase secY
SEQ ID n° 6229	4093	1933	SA-562.1	1587921-1589117 m	Similar to hypothetical glucosyl transferase
SEQ ID n° 6230	4094	1934	SA-563.1	1589178-1590053 m	Similar to putative glycosyltransferase
SEQ ID n° 6231	4095	1935	SA-565.1	1590046-1591230 m	Similar to putative glycosyl transferase
SEQ ID n° 6232	4096	1936	SA-566.1	1591220-1592461 m	Similar to putative glycosyl transferase
SEQ ID n° 6233	4097	1937	SA-567.1	1592458-1593663 m	Similar to putative glycosyl transferase
SEQ ID n° 6234	4098	1938	SA-568.1	1593672-1594679 m	Similar to unknown proteins
SEQ ID n° 6235	4099	1940	SA-57.1	2155624-2155007 m	Unknown

SEQ ID n° 6236	4100	1942	SA-571.1	1595010-1599942 m	Similar to streptococcal hemagglutinin from <i>Streptococcus</i>
SEQ ID n° 6237	4101	1943	SA-572.1	1593925-1600821 p	gordonii, Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 6238	4102	1944	SA-573.1	1600918-1602909 m	Similar to transcription regulator RofA related
SEQ ID n° 6239	4103	1945	SA-574.1	1602970-1603890 m	exonuclease ABC chain B
SEQ ID n° 6240	4104	1946	SA-575.1	1604073-1606256 p	Similar to unknown proteins
SEQ ID n° 6241	4105	1947	SA-576.1	1603265-1605986 p	glutamine ABC transporter permease and substrate binding protein
SEQ ID n° 6242	4106	1948	SA-577.1	1607145-1607495 p	glutamine ABC transporter ATP-binding protein
SEQ ID n° 6243	4107	1949	SA-578.1	1607597-1607745 m	Unknown
SEQ ID n° 6244	4108	1950	SA-579.1	1607771-1609084 m	Similar to unknown proteins
SEQ ID n° 6245	4109	1952	SA-582.1	1609451-1610592 p	Similar to GTP-binding protein
SEQ ID n° 6246	4110	1954	SA-584.1	1610726-1611304 m	Similar to aminopeptidase
SEQ ID n° 6247	4111	1955	SA-585.4	1611414-1613456 m	Putative peptidoglycan bound serine rich protein (LPXTG motif)
SEQ ID n° 6248	4112	1957	SA-589.2	1797911-1798792 m	similar to amidase or hydrolase, putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 6249	4113	1959	SA-590.1	1796846-1797793 m	Similar to fructokinase
SEQ ID n° 6250	4114	1960	SA-591.1	1794209-1795737 m	Similar to mannose-6-phosphate isomerase
SEQ ID n° 6251	4115	1961	SA-592.2	1793076-1794083 m	Similar to preprotein translocase SecA subunit
SEQ ID n° 6252	4116	1962	SA-593.2	1792597-1793051 m	similar to 2-dehydro-3-deoxyphosphonate aldolase
SEQ ID n° 6253	4117	1963	SA-594.2	1791595-1792695 m	similar to holo-acyl-carrier protein synthase
SEQ ID n° 6254	4118	1964	SA-597.1	1789964-1791502 m	similar to alanine racemase
SEQ ID n° 6255	4119	1965	SA-598.1	1787869-1789884 m	Similar to immunogenic secreted protein
SEQ ID n° 6256	4120	1966	SA-599.1	1786684-1787578 m	Similar to ATP-dependent DNA helicase RecG
SEQ ID n° 6257	4121	1967	SA-601	1628574-1628807 m	Similar to oxidoreductase
SEQ ID n° 6258	4122	1968	SA-601	1715917-17159709 m	Unknown
SEQ ID n° 6259	4123	1969	SA-601.1	1785688-1785656 p	hypothetical gene
SEQ ID n° 6260	4124	1970	SA-601.1	1784691-1785653 p	Similar to shikimate 5-dehydrogenase
SEQ ID n° 6261	4125	1971	SA-602.1	1783240-1784622 m	Similar to L-asparaginase
SEQ ID n° 6262	4126	1972	SA-603.2	1782732-1783184 p	Similar to unknown proteins
SEQ ID n° 6263	4127	1973	SA-604.2	1781253-1782464 p	Similar to unknown proteins
SEQ ID n° 6264	4128	1974	SA-605.1	1780342-1781127 m	Similar to putative aminotransferase
SEQ ID n° 6265	4129	1975	SA-606.1	1779727-1780275 m	Similar to transcriptional regulator (Cody family)
SEQ ID n° 6266	4130	1976	SA-607.1	1778715-1779680 p	Similar to other proteins
SEQ ID n° 6267	4131	1977	SA-608.1	1777897-1778626 m	Similar to 3-hydroxyacyl-CoA dehydrogenase
					Similar to unknown proteins

SEQ ID n° 6268	4132	1978	SA-609.1	1777056-1777866 m	Similar to unknown proteins
SEQ ID n° 6269	4133	1979	SA-611.1	1774398-1777043 m	Similar to Pyruvate Phosphate Dikinase
SEQ ID n° 6270	4134	1980	SA-612.1	1773958-1774260 m	Similar to Glu-RNA Gln amidotransferase subunit C
SEQ ID n° 6271	4135	1981	SA-613.1	1772492-1773958 m	Similar to Glutaryl-RNA Gln amidotransferase subunit A
SEQ ID n° 6272	4136	1982	SA-614.1	1771050-1772492 m	Similar to Glu-RNA amidotransferase subunit B
SEQ ID n° 6273	4137	1983	SA-615.1	1770006-1770920 m	Similar to unknown proteins
SEQ ID n° 6274	4138	1984	SA-616.1	1769362-1769922 m	Similar to unknown proteins
SEQ ID n° 6275	4139	1985	SA-617.1	1768244-1769362 m	Similar to unknown proteins
SEQ ID n° 6276	4140	1986	SA-618.1	1767834-1768151 m	Similar to unknown proteins
SEQ ID n° 6277	4141	1987	SA-62.1	2156569-2157413 p	Similar to integrase, C-terminal part
SEQ ID n° 6278	4142	1988	SA-620.1	1767072-1767704 m	Similar to probable nicotinate-nucleotide adenyltransferase
SEQ ID n° 6279	4143	1989	SA-621.1	1765488-1767075 m	Similar to unknown proteins
SEQ ID n° 6280	4144	1990	SA-622.2	1765903-1766424 m	Similar to unknown proteins
SEQ ID n° 6281	4145	1991	SA-623.2	818453-819139 p	Similar to unknown proteins
SEQ ID n° 6282	4146	1992	SA-624.1	817104-818324 p	Similar to transporter (antiporter)
SEQ ID n° 6283	4147	1993	SA-625.1	815550-816917 p	Similar to UDP-N-acetylmutamoylalanine-D-glutamate, 2,6-diaminopimelate-D-alanine-D-alanine ligase
SEQ ID n° 6284	4148	1994	SA-626.1	814357-815403 p	Similar to D-alanine-D-alanine ligase
SEQ ID n° 6285	4149	1995	SA-627.1	813620-814216 p	Similar to recombination protein RecR
SEQ ID n° 6286	4150	1996	SA-628.1	811583-813605 p	Similar to penicillin binding protein 2B
SEQ ID n° 6287	4151	1997	SA-629.1	810739-811431 p	Similar to phosphoglycerate mutase
SEQ ID n° 6288	4152	1998	SA-63.1	2157770-2158441 p	Unknown
SEQ ID n° 6289	4153	1999	SA-630.1	809804-810562 p	Similar to triosephosphate isomerase
SEQ ID n° 6290	4154	2001	SA-633.1	808427-808623 p	elongation factor Tu
SEQ ID n° 6291	4155	2002	SA-635.1	806807-806075 p	Similar to cell division protein FisW and to RodA protein
SEQ ID n° 6292	4156	2003	SA-636.1	803906-806701 p	Similar to phosphoenolpyruvate carboxylase
SEQ ID n° 6293	4157	2004	SA-637.1	801698-803697 m	Similar to oligopeptidase
SEQ ID n° 6294	4158	2005	SA-638.1	801480-801939 p	Similar to unknown proteins
SEQ ID n° 6295	4159	2006	SA-639.1	800942-801466 p	Similar to unknown proteins
SEQ ID n° 6296	4160	2007	SA-64.1	2158526-2159197 p	Similar to two-component response regulator
SEQ ID n° 6297	4161	2008	SA-640.1	799937-800785 m	Similar to bacteriophage endolysin
SEQ ID n° 6298	4162	2009	SA-641.1	799287-799904 p	Similar to other proteins
SEQ ID n° 6299	4163	2010	SA-642.1	798519-798992 m	Similar to transcriptional regulator
SEQ ID n° 6300	4164	2011	SA-643.1	797856-798497 m	Similar to putative phosphoglycerate mutase
SEQ ID n° 6301	4165	2012	SA-644.1	796918-797820 p	Similar to unknown proteins
SEQ ID n° 6302	4166	2013	SA-646.1	795253-796743 m	Isyl-RNA synthetase

SEQ ID n° 6303	4167	2014	SA-647.1	794708-795178 p	Similar to riboflavin synthase complex beta chain
SEQ ID n° 6304	4168	2015	SA-648.1	793500-794693 p	Similar to GTP cyclohydrolase II/ 3,4-dihydroxy-2-butanone-4-phosphate synthase
SEQ ID n° 6305	4169	2016	SA-649.1	792832-793482 p	Similar to riboflavin synthase alpha chain
SEQ ID n° 6306	4170	2017	SA-65.1	2159181-2160545 p	Similar to two-component sensor histidine kinase
SEQ ID n° 6307	4171	2018	SA-651.1	791742-792851 p	Similar to riboflavin specific deaminase (diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase)
SEQ ID n° 6308	4172	2019	SA-653.1	789673-791013 p	Similar to manganese transporter
SEQ ID n° 6309	4173	2020	SA-654.2	788774-789571 p	Similar to unknown proteins
SEQ ID n° 6310	4174	2021	SA-655.2	789438-788650 p	Similar to unknown proteins
SEQ ID n° 6311	4175	2022	SA-656.2	787025-788311 p	Similar to putative peptidases
SEQ ID n° 6312	4176	2023	SA-657.2	786969-786985 p	Similar to putative peptidases
SEQ ID n° 6313	4177	2024	SA-658.2	2025535-2028718 m	Similar to glucose-specific PTS enzyme IIBC
SEQ ID n° 6314	4178	2027	SA-660.1	2025666-2028431 m	Similar to unknown protein
SEQ ID n° 6315	4179	2028	SA-661.1	2024637-2028389 m	Similar to two-component response regulator
SEQ ID n° 6316	4180	2029	SA-662.1	2024286-2024538 m	Similar to two-component sensor histidine kinase (C-terminal part)
SEQ ID n° 6317	4181	2030	SA-663.1	2023286-2024146 m	Similar to ABC transporter (ATP-binding protein)
SEQ ID n° 6318	4182	2031	SA-664.1	2022136-2023292 m	Putative transmembrane protein
SEQ ID n° 6319	4183	2033	SA-666.1	2020875-2021927 m	Similar to other proteins, putative transmembrane protein
SEQ ID n° 6320	4184	2034	SA-667.1	2020203-2020628 m	Similar to mannose-specific PTS enzyme IIA
SEQ ID n° 6321	4185	2036	SA-669.1	2019684-2020185 m	Similar to mannose-specific PTS enzyme IIB
SEQ ID n° 6322	4186	2037	SA-67.1	2160655-2162208 m	Similar to putative membrane arginine transporter
SEQ ID n° 6323	4187	2038	SA-670.1	2018869-2018878 m	Similar to mannose-specific PTS enzyme IIC
SEQ ID n° 6324	4188	2039	SA-671.1	2018045-2018872 m	Similar to mannose-specific PTS enzyme IID
SEQ ID n° 6325	4189	2040	SA-672.1	2016256-2017507 m	Similar to two-component sensor histidine kinase
SEQ ID n° 6326	4190	2041	SA-673.1	2015481-2016254 m	Similar to two-component response regulator
SEQ ID n° 6327	4191	2042	SA-674.1	2014432-2015469 m	Similar to iron ABC transporter (binding protein)
SEQ ID n° 6328	4192	2043	SA-675.1	2013713-2014210 p	Similar to unknown proteins
SEQ ID n° 6329	4193	2044	SA-676.1	2012676-2013713 p	Similar to glutamyl-aminopeptidase (hypothetical)
SEQ ID n° 6330	4194	2045	SA-677.1	2012210-2012665 p	Similar to unknown proteins (NrdI)
SEQ ID n° 6331	4195	2046	SA-678.1	2009651-2012053 p	Similar to nucleic acid (esterase), putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 6332	4196	2047	SA-68.1	2162302-2163228 m	Similar to carbamate kinase

SEQ ID n° 6333	4197	2048	SA-680.1	2007175-2009391 m	Similar to GTP pyrophosphokinase (stringent response protein RaA)
SEQ ID n° 6334	4198	2049	SA-681.1	2006772-2007165 m	Similar to unknown proteins
SEQ ID n° 6335	4199	2050	SA-682.1	2005544-2006467 m	Similar to adhesion proteins
					Similar to pneumococcal histidine triad protein B precursor (N-terminal part)
SEQ ID n° 6336	4200	2051	SA-686.1	2004072-2005517 m	Similar to pneumococcal histidine triad protein B precursor (C-terminal part)
					Similar to transcriptional regulator, DeoR family
SEQ ID n° 6337	4201	2052	SA-687.1	2002936-2004174 m	Similar to two-component response regulator
SEQ ID n° 6338	4202	2053	SA-688.2	2001878-2002654 p	Similar to ornithine carbamoyltransferase
SEQ ID n° 6339	4203	2054	SA-689.2	712522-713228 p	Similar to hexosyl transferase
SEQ ID n° 6340	4204	2055	SA-69.1	2163240-2164238 m	Similar to glucosyl transferase
SEQ ID n° 6341	4205	2056	SEQ ID n° 6341	710357-712300 p	Similar to hexosyl transferase
SEQ ID n° 6342	4206	2057	SA-691.1	708566-709900 p	Similar to hexosyl transferase
SEQ ID n° 6343	4207	2058	SA-692.1	707566-708564 p	Similar to alpha-amylase
SEQ ID n° 6344	4208	2059	SA-693.1	706055-707521 p	Catabolite control protein A
SEQ ID n° 6345	4209	2060	SA-694.2	704919-705923 p	Similar to X-Pro dipeptidase
SEQ ID n° 6346	4210	2061	SA-696.2	703624-704709 m	Similar to beta-N-acetylglucosaminidase
SEQ ID n° 6347	4211	2062	SA-697.1	701776-703566 p	Unknown
SEQ ID n° 6348	4212	2063	SA-698.1	700948-701760 p	Similar to oxidoreductase
SEQ ID n° 6349	4213	2064	SA-699.1	699956-700795 p	
SEQ ID n° 6350	4214	2066	SA-70.1	2164341-2165636 p	Similar to hypothetical two-component sensor histidine kinase
SEQ ID n° 6351	4215	2067	SA-700.1	698786-699832 p	Similar to D-mannosate hydrolase
SEQ ID n° 6352	4216	2068	SA-701.1	697368-698768 p	Similar to gluconate isomerase
SEQ ID n° 6353	4217	2069	SA-702.1	696734-697351 p	Similar to 2-dehydro-3-deoxyphosphogluconate aldolase
SEQ ID n° 6354	4218	2070	SA-704.1	695946-696817 p	Similar to transcriptional regulator (GntR family)
SEQ ID n° 6355	4219	2071	SA-705.1	694118-695917 p	Similar to beta-gluconidase
SEQ ID n° 6356	4220	2072	SA-706.1	693076-694101 p	Similar to 2-keto-3-deoxygluconate kinase
SEQ ID n° 6357	4221	2073	SA-707.1	691459-693009 p	Similar to transporter
SEQ ID n° 6358	4222	2074	SA-708.2	690261-691253 p	Similar to D-lactate dehydrogenase
SEQ ID n° 6359	4223	2075	SA-71.1	2165633-2166466 p	Similar to hypothetical two-component response regulator
SEQ ID n° 6360	4224	2076	SA-710.2	689189-690247 p	Similar to PTS enzyme IIC
SEQ ID n° 6361	4225	2077	SA-712.1	688112-688996 p	Similar to transcriptional regulator, LysR family
SEQ ID n° 6362	4226	2078	SA-713.1	687257-688076 p	Unknown
SEQ ID n° 6363	4227	2079	SA-714.1	686320-687093 p	putative transmembrane protein
SEQ ID n° 6364	4228	2080	SA-715.1	685667-686323 p	similar to ABC transporter (ATP-binding protein)

SEQ ID n° 6365	4229	2081	SA-716.1	684812-685450 m	similar to unknown proteins
SEQ ID n° 6366	4230	2082	SA-717.2	683949-684734 p	similar to competence associated membrane nuclease
SEQ ID n° 6367	4231	2083	SA-719.2	1023804-1025141 m	similar to plasmid proteins
SEQ ID n° 6368	4232	2084	SA-72.1	2166688-2167410 p	Similar to osmoprotectant ABC transporter (ATP-binding protein)
SEQ ID n° 6369	4233	2085	SA-720.1	1023205-1023790 m	Unknown
SEQ ID n° 6370	4234	2086	SA-721.2	1022249-1023087 m	similar to plasmid partition protein ParA
SEQ ID n° 6371	4235	2087	SA-722.2	1021974-1022252 m	Unknown
SEQ ID n° 6372	4236	2088	SA-723.2	1021578-1021981 m	similar to replication initiation protein from <i>Staphylococcus</i> plasmid
SEQ ID n° 6373	4237	2089	SA-725.2	1021282-1021573 m	Unknown
SEQ ID n° 6374	4238	2090	SA-726.2	1019800-1021128 m	Unknown
SEQ ID n° 6375	4239	2091	SA-727.1	1018711-1019387 m	similar to unknown protein
SEQ ID n° 6376	4240	2092	SA-728.1	1017948-1018721 m	similar to unknown protein
SEQ ID n° 6377	4241	2093	SA-729.1	1016320-1017915 p	similar to oligopeptide and pheromone binding protein
SEQ ID n° 6378	4242	2096	SA-731.2	1014797-1015687 p	similar to integrase/recombinase
SEQ ID n° 6379	4243	2097	SA-732.1	1013816-1014754 p	similar to two-component sensor histidine kinase
SEQ ID n° 6380	4244	2098	SA-733.1	1013151-1013819 p	similar to two-component response regulator
SEQ ID n° 6381	4245	2099	SA-734.1	1011086-1013041 p	1,2 transport/binding proteins and lipoproteins
SEQ ID n° 6382	4246	2100	SA-735.1	1010332-1011084 p	similar to ABC transporter (ATP-binding protein)
SEQ ID n° 6383	4247	2101	SA-736.1	1009866-1010306 p	similar to <i>Lactococcus lactis</i> nisin-resistance protein C-terminal part
SEQ ID n° 6384	4248	2102	SA-737.1	1009345-1009884 p	similar to <i>Lactococcus lactis</i> nisin-resistance protein N-terminal part
SEQ ID n° 6385	4249	2103	SA-738.1	1008691-1009179 m	similar to unknown protein
SEQ ID n° 6386	4250	2104	SA-739.1	1007811-1008659 p	similar to other lipoprotein
SEQ ID n° 6387	4251	2105	SA-74.1	2167413-2168927 p	similar to osmoprotectant ABC transporter permease and substrate binding protein
SEQ ID n° 6388	4252	2106	SA-740.1	1005935-1007678 p	similar to unknown protein
SEQ ID n° 6389	4253	2107	SA-741.1	1005523-1006857 p	similar to glucose-inhibited division protein
SEQ ID n° 6390	4254	2108	SA-742.1	1004711-1005409 p	similar to transcriptional regulator (GntR family)
SEQ ID n° 6391	4255	2109	SA-743.2	1002936-1004498 m	similar to GMP synthetase
SEQ ID n° 6392	4256	2110	SA-744.3	439342-440142 p	similar to unknown proteins
SEQ ID n° 6393	4257	2111	SA-745.1	440132-440767 p	similar to unknown protein
SEQ ID n° 6394	4258	2112	SA-746.1	441254-441733 p	similar to unknown proteins

SEQ ID n° 6395	4259	2113	SA-747.1	441709-442920 p	similar to transcription termination-antitermination factor nusA
SEQ ID n° 6396	4260	2114	SA-748.1	442942-443238 p	similar to unknown protein
SEQ ID n° 6397	4261	2115	SA-749.1	443231-443533 p	similar to putative ribosomal protein
SEQ ID n° 6398	4262	2116	SA-75.1	2169006-2171546 m	membrane protein similar to other proteins
SEQ ID n° 6399	4263	2117	SA-751.1	443553-446336 p	initiation factor 2
SEQ ID n° 6400	4264	2118	SA-752.1	446427-446795 p	ribosome binding factor A
SEQ ID n° 6401	4265	2119	SA-753.1	446879-447883 m	similar to esterase
SEQ ID n° 6402	4266	2120	SA-754.1	448047-448463 p	similar to negative transcriptional regulator (copper transport operon)
SEQ ID n° 6403	4267	2121	SA-756.1	448476-450710 p	similar to copper-transporting ATPase (Copa)
SEQ ID n° 6404	4268	2122	SA-757.1	450751-450957 p	similar to copper chaperone (copper transport operon)
SEQ ID n° 6405	4269	2123	SA-758.1	451087-451881 p	similar to unknown protein
SEQ ID n° 6406	4270	2124	SA-759.1	451696-452508 p	similar to unknown protein
SEQ ID n° 6407	4271	2125	SA-76.1	2171530-2172279 m	similar to other proteins
SEQ ID n° 6408	4272	2126	SA-760.1	452621-455263 p	DNA polymerase I
SEQ ID n° 6409	4273	2127	SA-761.1	455293-455733 p	similar to unknown protein
SEQ ID n° 6410	4274	2128	SA-762.1	455815-456294 p	similar to transcription regulator (Fur family)
SEQ ID n° 6411	4275	2129	SA-765.1	456447-458012 p	similar to fibrinogen binding protein, putative peptidoglycan linked protein (LPXTG motif)
SEQ ID n° 6412	4276	2130	SA-766.1	458125-458811 p	similar to two-component response regulator
SEQ ID n° 6413	4277	2131	SA-767.1	458813-459850 p	similar to two-component sensor histidine kinase
SEQ ID n° 6414	4278	2132	SA-768.2	459864-460604 m	similar to unknown protein
SEQ ID n° 6415	4279	2133	SA-769.2	460791-461933 p	similar to RNA-quanine transglycosylase
SEQ ID n° 6416	4280	2134	SA-77.1	2172407-2172783 m	similar to unknown proteins
SEQ ID n° 6417	4281	2135	SA-770.1	462043-462351 p	similar to unknown protein (putative zinc finger motif)
SEQ ID n° 6418	4282	2136	SA-772.1	462358-462897 p	similar to biotin synthase
SEQ ID n° 6419	4283	2137	SA-773.1	463036-463812 p	similar to unknown protein
SEQ ID n° 6420	4284	2138	SA-774.2	463812-464318 p	similar to unknown protein
SEQ ID n° 6421	4285	2143	SA-78.2	2172831-2175149 m	similar to unknown proteins
SEQ ID n° 6422	4286	2145	SA-782.2	633310-635034 p	similar to negative regulator of Flz ring formation protein EzrA
SEQ ID n° 6423	4287	2146	SA-783.1	635128-635769 p	similar to phosphoserine phosphatase
SEQ ID n° 6424	4288	2147	SA-784.1	635790-636275 m	similar to unknown proteins
SEQ ID n° 6425	4289	2148	SA-785.1	636288-636743 m	similar to unknown proteins
SEQ ID n° 6426	4290	2149	SA-786.1	636941-638248 p	endolase

SEQ ID n° 6427	4291	2150	SA-787.1	638356-639420 m	similar to unknown proteins
SEQ ID n° 6428	4292	2151	SA-788.1	638649-640332 p	similar to 5-enolpyruvylshikimate-3-phosphate synthase
SEQ ID n° 6429	4293	2152	SA-789.1	640925-641437 p	similar to shikimate kinase
SEQ ID n° 6430	4294	2154	SA-790.1	641494-642867 p	similar to membrane bound transcriptional regulator
SEQ ID n° 6431	4295	2155	SA-792.1	642968-644323 p	similar to putative RNA methyltransferase
SEQ ID n° 6432	4296	2156	SA-793.1	644431-644850 p	hypothetical CDS
SEQ ID n° 6433	4297	2157	SA-794.1	644770-645507 p	similar to diadenosine tetraphosphatase, acid phosphatase
SEQ ID n° 6434	4298	2158	SA-795.1	645828-646346 p	similar to unknown proteins
SEQ ID n° 6435	4299	2159	SA-796.1	645475-646711 m	similar to putative transcriptional regulator (TetR/AcrR family) C-terminal part
SEQ ID n° 6436	4300	2160	SA-797.1	646692-647000 m	similar to putative transcriptional regulator (TetR/AcrR family) N-terminal part
SEQ ID n° 6437	4301	2161	SA-798.1	647193-647515 p	similar to C protein alpha-antigen from <i>Streptococcus agalactiae</i> N-terminal part
SEQ ID n° 6438	4302	2162	SA-799.1	647636-648862 m	similar to transposase, truncated
SEQ ID n° 6439	4303	2163	SA-8.1	1028864-1031071 m	similar to unknown proteins
SEQ ID n° 6440	4304	2164	SA-80.1	2175298-2175927 p	similar to transcriptional regulator (TetR/AcrR family)
SEQ ID n° 6441	4305	2165	SA-800.1	648505-648780 m	similar to transposase N-terminal part
SEQ ID n° 6442	4306	2166	SA-801.1	648913-649050 p	similar to unknown protein
SEQ ID n° 6443	4307	2167	SA-803.1	649438-649785 m	similar to chaperonin (heat shock protein 33 homolog)
SEQ ID n° 6444	4308	2168	SA-804.1	649978-650398 m	similar to transcriptional regulator (C-terminal part)
SEQ ID n° 6445	4309	2169	SA-805.1	650399-651187 m	similar to transcriptional regulator (N-terminal part)
SEQ ID n° 6446	4310	2170	SA-806.1	651570-653234 p	Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 6447	4311	2171	SA-807.1	653323-654246 p	Putative peptidoglycan bound protein (LPXTG motif)
SEQ ID n° 6448	4312	2172	SA-808.1	654246-655165 p	similar to sortase protein
SEQ ID n° 6449	4313	2173	SA-809.3	655122-655973 p	similar to sortase protein
SEQ ID n° 6450	4314	2174	SA-81.1	2175913-2176209 m	similar to unknown proteins
SEQ ID n° 6451	4315	2176	SA-811.2	2144199-2144348 p	50S Ribosomal protein L33
SEQ ID n° 6452	4316	2177	SA-812.1	2144001-2144183 p	50S Ribosomal protein L32
SEQ ID n° 6453	4317	2178	SA-814.1	2142501-2143781 m	histidyl-RNA synthetase
SEQ ID n° 6454	4318	2179	SA-817.2	2140657-2142408 m	aspartyl-RNA synthetase
SEQ ID n° 6455	4319	2180	SA-819.2	2139723-2140667 m	similar to unknown proteins
SEQ ID n° 6456	4320	2181	SA-82.1	2178453-2177064 m	30S ribosomal protein S4
SEQ ID n° 6457	4321	2182	SA-820.1	2136743-2139615 m	similar to unknown proteins
SEQ ID n° 6458	4322	2183	SA-821.1	2138408-2138716 p	similar to unknown proteins
SEQ ID n° 6459	4323	2184	SA-822.1	2138629-2138320 p	arginyl-RNA synthetase

SEQ ID n° 6460	4324	2185	SA-823.1	2135970-2136416 m	similar to arginine repressor ArgR
SEQ ID n° 6461	4325	2186	SA-825.1	2133337-2135913 m	DNA mismatch repair protein MutS
SEQ ID n° 6462	4326	2187	SA-826.1	2133077-2133280 p	similar to cold shock protein E
SEQ ID n° 6463	4327	2188	SA-827.1	2130878-2132851 m	similar to DNA mismatch repair MutL
SEQ ID n° 6464	4328	2189	SA-828.1	2129614-2130846 m	putative membrane-spanning protein (efflux transporter ?)
SEQ ID n° 6465	4329	2190	SEQ ID n° 6465	2129022-2129612 m	similar to Holliday junction DNA helicase
SEQ ID n° 6466	4330	2191	SA-83.1	2177394-2177661 m	similar to unknown proteins
SEQ ID n° 6467	4331	2192	SA-831.1	2128448-2128998 m	similar to 3-methyl-adenine DNA glycosylase I
SEQ ID n° 6468	4332	2193	SA-832.1	2127100-2128399 m	similar to competence-damage inducible protein ClnA
SEQ ID n° 6469	4333	2194	SA-833.1	2125887-2127026 m	recombination protein RecA
SEQ ID n° 6470	4334	2195	SA-834.1	2125273-2126571 m	similar to unknown proteins
SEQ ID n° 6471	4335	2196	SA-835.1	2124805-2125071 m	similar to unknown proteins
SEQ ID n° 6472	4336	2197	SA-837.1	2124395-2124805 m	similar to unknown proteins
SEQ ID n° 6473	4337	2198	SA-838.1	2124043-2124360 m	similar to unknown proteins
SEQ ID n° 6474	4338	2199	SA-839.2	2122822-2123793 m	similar to unknown proteins
SEQ ID n° 6475	4339	2200	SA-84.1	2177693-2179048 m	replicative DNA helicase DnaC
SEQ ID n° 6476	4340	2201	SA-842.3	216500-216530 p	Similar to trehalose-specific PTS enzyme IIABC
SEQ ID n° 6477	4341	2202	SA-843.1	218762-220377 p	similar to trehalose-6-phosphate hydrolase
SEQ ID n° 6478	4342	2203	SA-844.1	220597-222633 p	similar to hypothetical transcriptional antiterminator (Bg/G family)
SEQ ID n° 6479	4343	2204	SA-845.1	222636-222920 p	similar to unknown proteins
SEQ ID n° 6480	4344	2205	SA-846.1	222933-224288 p	putative transmembrane protein similar to unknown proteins
SEQ ID n° 6481	4345	2207	SA-848.1	224291-225148 p	similar to other proteins (including putative transketolase)
SEQ ID n° 6482	4346	2208	SA-849.1	225145-226074 p	similar to other proteins (including putative transketolase)
SEQ ID n° 6483	4347	2209	SA-85.1	2179091-2179543 m	50S ribosomal protein L9
SEQ ID n° 6484	4348	2210	SA-850.1	228102-227442 p	similar to unknown proteins
SEQ ID n° 6485	4349	2211	SA-851.1	227530-227799 p	ribosomal protein S15
SEQ ID n° 6486	4350	2212	SA-852.1	228180-230309 p	polynucleotide phosphorylase, alpha chain
SEQ ID n° 6487	4351	2213	SA-853.1	230311-231063 p	similar to unknown protein
SEQ ID n° 6488	4352	2214	SA-854.1	231072-231656 p	similar to serine acetyltransferase
SEQ ID n° 6489	4353	2215	SA-855.1	231666-231848 p	Unknown
SEQ ID n° 6490	4354	2216	SA-856.1	231845-233188 p	cysteinyl-RNA synthetase
SEQ ID n° 6491	4355	2217	SA-857.1	233181-233567 p	similar to unknown proteins
SEQ ID n° 6492	4356	2218	SA-858.1	233676-234425 p	similar to tRNA/IRNA methyltransferase
SEQ ID n° 6493	4357	2219	SEQ ID n° 6493	234422-234940 p	similar to unknown protein
SEQ ID n° 6494	4358	2220	SA-86.1	2179549-2181531 m	similar to unknown proteins

SEQ ID n° 6495	4359	2221	SA-861.1	235033-235693 p	similar to unknown protein
SEQ ID n° 6496	4360	2222	SA-863.3	236878-236859 m	similar to transposase
SEQ ID n° 6497	4361	2223	SA-864.3	181438-182697 m	tyrosyl-RNA synthetase
SEQ ID n° 6498	4362	2224	SA-865.2	182088-185705 p	similar to penicillin-binding protein 1b
SEQ ID n° 6499	4363	2226	SA-868.1	185629-189204 p	RNA polymerase beta-subunit
SEQ ID n° 6500	4364	2227	SA-87.1	2181568-2183489 m	Similar to GdA protein
SEQ ID n° 6501	4365	2228	SA-872.1	189321-192371 p	RNA polymerase beta-subunit
SEQ ID n° 6502	4366	2229	SA-874.1	193085-193450 p	similar to unknown proteins
SEQ ID n° 6503	4367	2230	SA-875.1	193623-194594 p	similar to transporter (competence protein)
SEQ ID n° 6504	4368	2231	SA-876.1	194440-195531 p	probably part of the DNA transport machinery, ComGB protein
SEQ ID n° 6505	4369	2232	SA-877.1	195528-195657 p	similar to exogenous DNA-binding protein comGC
SEQ ID n° 6506	4370	2233	SA-878.1	195832-196245 p	similar to hypothetical competence proteins
SEQ ID n° 6507	4371	2234	SA-879.1	196217-196516 p	similar to unknown proteins
SEQ ID n° 6508	4372	2235	SA-880.1	196470-196831 p	similar to hypothetical competence proteins
SEQ ID n° 6509	4373	2236	SA-881.1	196909-197280 p	similar to unknown proteins
SEQ ID n° 6510	4374	2237	SA-882.1	197395-198369 p	similar to unknown proteins
SEQ ID n° 6511	4375	2238	SA-883.1	198401-199594 p	acetate kinase
SEQ ID n° 6512	4376	2239	SA-884.1	199745-199951 p	similar to transcriptional regulator
SEQ ID n° 6513	4377	2240	SA-885.2	200186-200643 p	similar to unknown proteins
SEQ ID n° 6514	4378	2241	SA-887.2	579476-579673 p	Unknown
SEQ ID n° 6515	4379	2242	SA-889.1	579717-580648 m	similar to dihydroxylate dehydrogenase A
SEQ ID n° 6516	4380	2243	SA-89.1	2183669-2184280 m	similar to unknown proteins
SEQ ID n° 6517	4381	2244	SA-890.1	580836-582071 m	similar to Cell Wall Mucopeptide Branching Enzyme
SEQ ID n° 6518	4382	2245	SA-891.1	582090-583301 m	similar to cell wall mucopeptide branching enzyme
SEQ ID n° 6519	4383	2246	SA-892.1	583314-584534 m	similar to cell wall mucopeptide branching enzyme
SEQ ID n° 6520	4384	2247	SA-893.1	584534-585346 m	similar to unknown proteins
SEQ ID n° 6521	4385	2248	SA-894.1	585417-586733 m	similar to unknown proteins
SEQ ID n° 6522	4386	2249	SA-895.1	586809-587195 p	similar to unknown proteins
SEQ ID n° 6523	4387	2250	SA-896.1	587539-590223 p	Similar to cation-transporting P-ATPase
SEQ ID n° 6524	4388	2251	SA-897.1	590268-591128 m	similar to unknown proteins
SEQ ID n° 6525	4389	2252	SA-898.1	591280-593211 p	similar to fructose-1,6-bisphosphatase
SEQ ID n° 6526	4390	2253	SA-899.1	593301-594425 p	Similar to other proteins
SEQ ID n° 6527	4391	2254	SA-9.1	1031191-1031673 m	Unknown
SEQ ID n° 6528	4392	2255	SA-90.1	2184312-2185433 m	similar to RNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase

SEQ ID n° 6529	4393	2256	SA-901.1	594579-595692 p	Similar to peptide chain release factor RF-2
SEQ ID n° 6530	4394	2257	SA-902.1	595611-595303 p	Similar to cell division ATP-binding protein FtsE
SEQ ID n° 6531	4395	2258	SA-904.1	596287-597216 p	Similar to cell-division protein FtsX
SEQ ID n° 6532	4396	2259	SA-905.1	597268-597979 m	Similar to unknown proteins
SEQ ID n° 6533	4397	2260	SA-906.2	597976-596611 m	Similar to unknown proteins
SEQ ID n° 6534	4398	2261	SA-903.4	909837-910037 p	H-transferring ATP synthase c chain
SEQ ID n° 6535	4399	2262	SA-908.2	910120-910536 p	H-transferring ATP synthase c chain
SEQ ID n° 6536	4400	2263	SA-909.1	910854-911351 p	H-transferring ATP synthase b chain
SEQ ID n° 6537	4401	2264	SA-91.1	2165679-2168347 p	similar to L-serine dehydratase beta subunit
SEQ ID n° 6538	4402	2265	SA-910.1	911351-911887 p	H-transferring ATP synthase delta chain
SEQ ID n° 6539	4403	2266	SA-912.1	911803-913408 p	H-transferring ATP synthase alpha chain
SEQ ID n° 6540	4404	2267	SA-912.1	913424-914305 p	H-transferring ATP synthase gamma chain
SEQ ID n° 6541	4405	2268	SA-913.1	914379-915785 p	H-transferring ATP synthase beta chain
SEQ ID n° 6542	4406	2269	SA-914.1	915788-916211 p	H-transferring ATP synthase epsilon chain
SEQ ID n° 6543	4407	2270	SA-916.1	916569-917840 p	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
SEQ ID n° 6544	4408	2271	SA-917.1	918108-918965 p	similar to competence associated membrane nuclease
SEQ ID n° 6545	4409	2272	SA-918.1	919256-920286 p	Phenylalanyl-RNA synthetase alpha chain
SEQ ID n° 6546	4410	2273	SA-919.1	920379-920900 p	similar to other proteins
SEQ ID n° 6547	4411	2274	SA-920.1	920954-923359 p	Phenylalanyl-RNA synthetase beta chain
SEQ ID n° 6548	4412	2275	SA-921.1	923428-924096 m	similar to unknown proteins (C-terminal part)
SEQ ID n° 6549	4413	2276	SA-923.1	924207-927440 p	similar to ATP-dependent exonuclease, subunit B
SEQ ID n° 6550	4414	2277	SA-925.1	927430-931053 p	similar to ATP-dependent exonuclease, subunit A
SEQ ID n° 6551	4415	2278	SA-926.1	931066-931992 p	similar to cation transporter
SEQ ID n° 6552	4416	2279	SA-928.2	931967-933343 m	similar to putative RNA modification GTPase TrmE
SEQ ID n° 6553	4417	2280	SA-93.1	2168362-2187234 p	similar to L-serine dehydratase alpha subunit
SEQ ID n° 6554	4418	2281	SA-930.2	866828-867787 m	Similar to ribonucleotide diphosphate reductase small subunit
SEQ ID n° 6555	4419	2282	SA-931.2	867890-870149 m	Similar to ribonucleotide reductase large subunit
SEQ ID n° 6556	4420	2283	SA-932.2	870227-870451 m	Similar to glutaredoxin
SEQ ID n° 6557	4421	2284	SA-934.1	870833-871096 p	Similar to histidine-containing phosphocarrier protein of the phosphotransferase system (PTS)
SEQ ID n° 6558	4422	2285	SA-936.1	871101-872834 p	phosphoenolpyruvate:sugar phosphotransferase system enzyme
SEQ ID n° 6559	4423	2286	SA-937.1	872984-874411 p	similar to glyceraldehyde-3-phosphate dehydrogenase
SEQ ID n° 6560	4424	2287	SA-939.1	874551-875804 p	similar to oligosaccharide deacetylase
SEQ ID n° 6561	4425	2288	SA-94.1	2187369-2188046 m	similar to other proteins

SEQ ID n° 6562	4426	2289	SA-941.1	875835-876917 m	similar to RNA helicase
SEQ ID n° 6563	4427	2290	SA-942.1	877062-877691 p	similar to uridine kinase
SEQ ID n° 6564	4428	2291	SA-943.1	877778-878275 p	similar to unknown proteins
SEQ ID n° 6565	4429	2292	SA-944.1	878275-879933 p	similar to DNA polymerase III gamma/tau subunit
SEQ ID n° 6566	4430	2293	SA-945.1	880028-880222 p	similar to unknown proteins
SEQ ID n° 6567	4431	2294	SA-946.1	880203-881138 m	similar to transcriptional repressor of the biotin operon
SEQ ID n° 6568	4432	2295	SA-947.1	881323-882519 m	S-adenosylmethionine synthetase
SEQ ID n° 6569	4433	2296	SA-948.1	883038-884945 p	similar to fibronectin-binding protein
SEQ ID n° 6570	4434	2297	SA-949.1	885012-885557 p	Unknown
SEQ ID n° 6571	4435	2298	SA-950.1	885717-885845 p	hypothetical protein
SEQ ID n° 6572	4436	2299	SA-951.1	885953-886519 p	similar to unknown proteins
SEQ ID n° 6573	4437	2300	SA-952.1	886516-887070 p	similar to unknown proteins
SEQ ID n° 6574	4438	2301	SA-953.2	887074-888360 p	similar to cation ABC transporter (ATP-binding protein)
SEQ ID n° 6575	4439	2302	SA-954.1	1170326-1171621 m	Unknown
SEQ ID n° 6576	4440	2303	SA-955.1	1171761-1172060 m	Similar to unknown protein
SEQ ID n° 6577	4441	2304	SA-956.1	1172071-1173318 m	Similar to DNA-methyltransferase
SEQ ID n° 6578	4442	2305	SA-957.1	1173315-1174946 m	Similar to plasmid relaxase and mobilisation protein A
SEQ ID n° 6579	4443	2306	SA-958.1	1174918-1175232 m	similar to unknown proteins
SEQ ID n° 6580	4444	2307	SA-959.1	1175295-1175858 m	Unknown
SEQ ID n° 6581	4445	2308	SA-96.1	2188179-2188718 m	similar to aggregation promoting protein (adhesin involved in high frequency of conjugation)
SEQ ID n° 6582	4446	2309	SA-960.1	1175861-1176157 m	hypothetical CDS
SEQ ID n° 6583	4447	2310	SA-961.1	1176201-1176500 m	Unknown
SEQ ID n° 6584	4448	2311	SA-964.1	1176582-1176758 m	similar to plasmid unknown proteins
SEQ ID n° 6585	4449	2312	SA-966.1	1179790-1180155 m	Unknown
SEQ ID n° 6586	4450	2313	SA-967.1	1180197-1182242 m	Similar to transfer complex protein TrsK - Lactococcus lactis plasmid pMRC01
SEQ ID n° 6587	4451	2314	SA-968.1	1182242-1182733 m	Unknown
SEQ ID n° 6588	4452	2315	SA-969.1	1182755-1183537 m	Similar to gram positive plasmid protein
SEQ ID n° 6589	4453	2316	SA-970.1	1183537-1183809 m	Unknown
SEQ ID n° 6590	4454	2317	SA-971.1	1183829-1184434 m	Unknown
SEQ ID n° 6591	4455	2318	SA-973.1	1184455-1187145 m	similar to plasmid unknown proteins
SEQ ID n° 6592	4456	2319	SA-974.1	1187178-1187708 p	Unknown
SEQ ID n° 6593	4457	2320	SA-975.2	1187902-1190292 m	Similar to plasmid transfer complex protein TrsE
SEQ ID n° 6594	4458	2321	SA-976.2	1899710-1900897 m	similar to two-component sensor histidine kinase
SEQ ID n° 6595	4459	2322	SA-977.1	1898029-1899564 m	Similar to D-alanine-D-alanyl carrier protein ligase

SEQ ID n° 6596	4460	2323	SA-978.1	1896767-1898032 m	similar to LTA D-alanylation protein DIB
SEQ ID n° 6597	4461	2324	SA-98.1	2188934-2188728 m	putative ABC transporter (permease)
SEQ ID n° 6598	4462	2325	SA-980.1	1895513-1896752 m	Similar to D-alanyl carrier protein
SEQ ID n° 6599	4463	2326	SA-981.1	1895258-1896520 m	similar to LTA D-alanine transfer protein DId
SEQ ID n° 6600	4464	2327	SA-982.1	1894691-1895083 m	Unknown
SEQ ID n° 6601	4465	2328	SA-983.1	1893399-1894691 m	Unknown
SEQ ID n° 6602	4466	2329	SA-984.1	1893076-1893408 m	Unknown
SEQ ID n° 6603	4467	2330	SA-985.1	1892725-1893006 m	Unknown
SEQ ID n° 6604	4468	2331	SA-986.4	1891761-1892543 m	similar to unknown proteins
SEQ ID n° 6605	4469	2332	SA-987.4	1891208-1891774 m	similar to unknown proteins
SEQ ID n° 6606	4470	2333	SA-988.4	1890755-1891204 m	histidine triad family protein
SEQ ID n° 6607	4471	2334	SA-989.1	1889856-1890728 m	Similar to 16 RNA (adenine-N6,)-dimethyltransferase
SEQ ID n° 6608	4472	2335	SA-99.1	2189721-2190563 m	1.2 Transport/binding proteins and lipoproteins
SEQ ID n° 6609	4473	2336	SA-990.1	1889001-1889852 m	Similar to 23S ribosomal RNA methyltransferase
SEQ ID n° 6610	4474	2337	SA-991.1	1887973-1888845 m	similar to unknown proteins
SEQ ID n° 6611	4475	2338	SA-993.1	1887304-1887956 m	similar to ribulose-5-phosphate 3-epimerase
SEQ ID n° 6612	4476	2339	SA-994.1	1886679-1887311 m	Similar to unknown proteins
SEQ ID n° 6613	4477	2340	SA-995.1	1885403-1886677 m	Similar to unknown proteins
SEQ ID n° 6614	4478	2341	SA-996.1	1884472-1885413 m	similar to unknown proteins
SEQ ID n° 6615	4479	2342	SA-997.2	1883563-1884375 m	similar to transcription repressor of purine operon PurR
SEQ ID n° 6616	4480	2343	SA-998.2	200712-201377 p	similar to unknown proteins
SEQ ID n° 6617	4481	2344	SA-999.1	201398-202168 m	similar to pyrroline-5-carboxylate reductase

TABLEAU 4. Localisation des 139 contigs de séquence SEQ ID No. 1 à SEQ ID No. 139 sur la séquence génomique complète (SEQ ID No. 2345).

SEQ ID	Contig	Position sur génome complet (= SEQ ID n°2345)		Sens (m=minus / p=plus)
		position Début	position Fin	
SEQ ID n°1	Contig1	1356648	1355991	m
SEQ ID n°2	Contig2	341651	341120	m
SEQ ID n°3	Contig3	476798	476418	m
SEQ ID n°4	Contig4	1475712	1475086	m
SEQ ID n°5	Contig5	784818	784243	m
SEQ ID n°6	Contig6	1756826	1757251	p
SEQ ID n°7	Contig7	1950108	1949648	m
SEQ ID n°8	Contig8	138225	138876	p
SEQ ID n°9	Contig9	2097891	2098283	p
SEQ ID n°10	Contig10	1238491	1237984	m
SEQ ID n°11	Contig11	1882130	1881745	m
SEQ ID n°12	Contig12	1089348	1088935	m
SEQ ID n°13	Contig13	555788	555189	m
SEQ ID n°14	Contig14	2017928	2017437	m
SEQ ID n°15	Contig15	1154094	1154701	p
SEQ ID n°16	Contig16	752647	753091	p
SEQ ID n°17	Contig17	1355561	1355078	m
SEQ ID n°18	Contig18	1255951	1256101	p
SEQ ID n°19	Contig19	792712	793148	p
SEQ ID n°20	Contig20	481787	482228	p
SEQ ID n°22	Contig22	1590263	1590842	p
SEQ ID n°23	Contig23	508269	508918	p
SEQ ID n°24	Contig24	1142198	1142488	p
SEQ ID n°25	Contig25	1982019	1981737	m
SEQ ID n°26	Contig26	119342	119919	p
SEQ ID n°28	Contig28	1124069	1123256	m
SEQ ID n°29	Contig29	266586	266900	p
SEQ ID n°30	Contig30	111013	111623	p
SEQ ID n°31	Contig31	1804173	1804706	p
SEQ ID n°32	Contig32	2170341	2169828	m
SEQ ID n°33	Contig33	1959867	1959394	m
SEQ ID n°34	Contig34	1295529	1294939	m
SEQ ID n°35	Contig35	178592	178071	m
SEQ ID n°36	Contig36	1857103	1856614	m
SEQ ID n°37	Contig37	1063484	1063911	p
SEQ ID n°38	Contig38	198025	197570	m
SEQ ID n°39	Contig39	1486076	1486553	p
SEQ ID n°40	Contig40	2033914	2034352	p
SEQ ID n°41	Contig41	737932	738486	p
SEQ ID n°42	Contig42	729008	728453	m
SEQ ID n°43	Contig43	1671733	1672151	p

SEQ ID n°44	Contig44	1103091	1103644	p
SEQ ID n°45	Contig45	700139	699583	m
SEQ ID n°46	Contig46	207521	206897	m
SEQ ID n°47	Contig47	1064808	1065099	p
SEQ ID n°48	Contig48	1091636	1092281	p
SEQ ID n°49	Contig49	1701764	1700906	m
SEQ ID n°50	Contig50	609072	609590	p
SEQ ID n°51	Contig51	1459271	1458780	m
SEQ ID n°52	Contig52	60603	60154	m
SEQ ID n°53	Contig53	289646	289284	m
SEQ ID n°54	Contig54	1536438	1536058	m
SEQ ID n°55	Contig55	509420	510430	p
SEQ ID n°56	Contig56	1559964	1558709	m
SEQ ID n°58	Contig58	2166712	2165923	m
SEQ ID n°59	Contig59	1919605	1920984	p
SEQ ID n°60	Contig60	962333	960438	m
SEQ ID n°61	Contig61	1363649	1365724	p
SEQ ID n°62	Contig62	1140306	1137284	m
SEQ ID n°63	Contig63	1702242	1706039	p
SEQ ID n°64	Contig64	1490271	1493283	p
SEQ ID n°65	Contig65	783206	785628	p
SEQ ID n°66	Contig66	852318	849615	m
SEQ ID n°67	Contig67	1882303	1880181	m
SEQ ID n°68	Contig68	1614050	1618058	p
SEQ ID n°69	Contig69	1484885	1490042	p
SEQ ID n°70	Contig70	510495	516449	p
SEQ ID n°71	Contig71	125082	121213	m
SEQ ID n°72	Contig72	1557644	1551892	m
SEQ ID n°73	Contig73	145707	143269	m
SEQ ID n°74	Contig74	859105	852465	m
SEQ ID n°75	Contig75	1219383	1215342	m
SEQ ID n°76	Contig76	1091627	1086724	m
SEQ ID n°77	Contig77	1245975	1251984	p
SEQ ID n°78	Contig78	115260	121688	p
SEQ ID n°79	Contig79	1100300	1092624	m
SEQ ID n°80	Contig80	1107948	1100525	m
SEQ ID n°81	Contig81	1245466	1237461	m
SEQ ID n°82	Contig82	2111296	2104033	m
SEQ ID n°83	Contig83	33479	27132	m
SEQ ID n°84	Contig84	1339614	1350526	p
SEQ ID n°85	Contig85	2070423	2058143	m
SEQ ID n°86	Contig86	1462530	1470059	p
SEQ ID n°87	Contig87	526582	517432	m
SEQ ID n°88	Contig88	1484487	1470171	m
SEQ ID n°89	Contig89	1124087	1136746	p
SEQ ID n°90	Contig90	1879890	1866931	m
SEQ ID n°91	Contig91	1721684	1706045	m
SEQ ID n°92	Contig92	1358184	1357897	m
SEQ ID n°93	Contig93	1577596	1560798	m
SEQ ID n°94	Contig94	115130	103188	m

SEQ ID n°95	Contig95	1921051	1933881	p
SEQ ID n°96	Contig96	1944905	1933782	m
SEQ ID n°97	Contig97	1919624	1906953	m
SEQ ID n°98	Contig98	2090559	2103658	p
SEQ ID n°99	Contig99	1237482	1219423	m
SEQ ID n°100	Contig100	1123110	1108191	m
SEQ ID n°101	Contig101	1551836	1529458	m
SEQ ID n°102	Contig102	1818811	1800978	m
SEQ ID n°103	Contig103	764781	783195	p
SEQ ID n°104	Contig104	1086606	1065938	m
SEQ ID n°105	Contig105	125425	143102	p
SEQ ID n°106	Contig106	962438	984387	p
SEQ ID n°107	Contig107	1169838	1190193	p
SEQ ID n°108	Contig108	2090426	2070667	m
SEQ ID n°109	Contig109	1140315	1169462	p
SEQ ID n°111	Contig111	238297	258413	p
SEQ ID n°112	Contig112	216686	237881	p
SEQ ID n°113	Contig113	2209521	16967	m
SEQ ID n°114	Contig114	1883537	1906918	p
SEQ ID n°115	Contig115	145772	172009	p
SEQ ID n°116	Contig116	508181	477405	m
SEQ ID n°117	Contig117	859233	888273	p
SEQ ID n°118	Contig118	1529046	1494213	m
SEQ ID n°119	Contig119	473132	438871	m
SEQ ID n°120	Contig120	1981657	1945366	m
SEQ ID n°121	Contig121	1613824	1577594	m
SEQ ID n°122	Contig122	1765846	1800817	p
SEQ ID n°123	Contig123	2111499	2153851	p
SEQ ID n°124	Contig124	1721668	1765765	p
SEQ ID n°125	Contig125	984406	1025178	p
SEQ ID n°126	Contig126	1293488	1339586	p
SEQ ID n°127	Contig127	216691	176332	m
SEQ ID n°128	Contig128	1818941	1866861	p
SEQ ID n°129	Contig129	849565	785796	m
SEQ ID n°130	Contig130	888292	960270	p
SEQ ID n°131	Contig131	2208563	2155215	m
SEQ ID n°132	Contig132	33590	88257	p
SEQ ID n°133	Contig133	1982609	2057812	p
SEQ ID n°134	Contig134	1700642	1618142	m
SEQ ID n°135	Contig135	1293063	1190375	m
SEQ ID n°136	Contig136	1366980	1462324	p
SEQ ID n°137	Contig137	390853	434186	p
SEQ ID n°138	Contig138	357393	259739	m
SEQ ID n°139	Contig139	527049	716899	p

TABLEAU 5. Propriété d'adhérence à des cellules épithéliales humaines en culture de la souche NEM316 de *S. agalactiae* et de souches mutantes dérivées.

Souche	Gène inactivé	% d'adhésion ^a	
		Cellules A549	Cellules Hela
NEM316	aucun	9	16
NEM1979	IPF N° 1268 (<i>srtA</i>)	1,5	2
NEM2056	IPF N° 678	2	n.t.
NEM2057	IPF N° 1503	4,5	n.t.

- 5 ^a, le pourcentage d'adhésion correspond au nombre de bactéries (Unité Formant des Colonies, UFC) restant adhérentes aux cellules après lavage avec du tampon PBS par rapport au nombre d'UFC ajoutées à la monocouche de cellules épithéliales.

TABLEAU 6. Gènes de la souche de *S. agalactiae* NEM316 codant pour des protéines de surface avec un motif d'ancrage LPXTG^a

Seq ID (ADN)	IPF N°	taille phases	Site de coupure	Protéines homologues	% d'acides aminés identiques (similaires) / longueur de la région similaire ^b	Fonction prédite ^c
6194	523	1126	LPXT/G	Alp2 (<i>S. agalactiae</i>) Alp3 (<i>S. agalactiae</i>) R28 (<i>S. pyogenes</i>)	74 (77) / 798 71 (76) / 877 69 (75) / 1103	inconnue
6236	571	1310	"	Hsa (<i>S. gordonii</i>) SrpA (<i>S. cristatus</i>)	50 (60) / 1314 43 (53) / 1248	Protéine liant l'acide sialique
5497	220	1634	"	Ssp-5 (<i>S. gordonii</i>), Paa (<i>S. intermedius</i>)	30 (43) / 1385 31 (45) / 1285	Protéine liant l'acide sialique
5491	2192	512	"	EaeH (<i>E. coli</i> O157:H7)	25 (38) / 358	Adhésine
5103	1716	643	"	M-like protein (<i>S. equi</i>) PspC (<i>S. pneumoniae</i>)	31 (46) / 302 23 (38) / 795	inconnue Adhésine
4705	1247	932	"	SpaA (<i>S. sobrinus</i>)	38(52) / 406	inconnue
5610	2337	308	"	No homology in public databases		inconnue
5234	1861	543	"	Cell surface protein (<i>S. mutans</i>) CbpD (<i>S. pneumoniae</i>)	50(62) / 183 30(60) / 220	inconnue Protéine liant la choline
4926	1503	1570	"	PrtS (<i>S. thermophilus</i>)	49 (65) / 1596	Serine protéinase
6331	678	800	"	CpdB (<i>S. dysgalactiae</i>) YRN (<i>Bacillus subtilis</i>)	57(70) / 694 47(66) / 630	Cyclo-nucléotide phosphodiesterase

6247	585	680			AmiC (<i>S. pyogenes</i>) YbgE (<i>L. lactis</i>)	36 (54) / 478 35 (54) / 492	Amidase
5842	280	1252	"	"	PuIA (<i>S. pyogenes</i>)	65 (79) / 1095 23(47) / 373	Amylopullulanase alkaline inconnue
5741	2495	410	"	"	CG15040 gene product <i>Drosophila melanogaster</i> Antigen p200 (<i>Babesia bigemina</i>)	26(50) / 273	inconnue
4921	15	933	"	"	SpaA (<i>S. sobrinus</i>) Pas (<i>S. intermedius</i>)	37(32) / 405 36(32) / 399	inconnue inconnue
5090	17	240	"	"	Plasmid-encoded protein (<i>E. faecalis</i>)	33 (49) / 225	inconnue
5180	18	753	"	"	Sec10 (<i>E. faecalis</i>)	24 (37) / 715	Surface exclusion protein
4706	1248	236	"	"	Plasmid-encoded protein (<i>E. faecalis</i>)	31 (47) / 263	inconnue
4708	1250	743	"	"	Sec10 (<i>E. faecalis</i>)	22 (40) / 784	Surface exclusion protein
5677	2414	253	"	"	Plasmid-encoded protein (<i>E. faecalis</i>)	33 (47) / 211	inconnue
6246	584*	192	"	"	No homology in public databases		inconnue
6411	765	521	"	"	No homology in public databases		inconnue
5578	2300	901	IPXT/G		PFBP (<i>S. pyogenes</i>)	32(46) / 176	Protéine liant la fibronectine
6446	806	554	"	"	Hypothetical protein 2 (<i>Lactobacillus leichnamii</i>) Fimbrial structural subunit (<i>Acetivomyces naeslundii</i>)	27(42) / 512 25(38) / 577	inconnue inconnue
6447	807	307	"	"	No homology in public databases		inconnue
5607	2334	674	"	"	No homology in public databases		inconnue

6209	538	1055	LPXT/S	SPy0843 (<i>S. pyogenes</i>) BspA (<i>Bacteroides forsythus</i>)	72 (81) / 1050 24 (41) / 566	inconnue inconnue
6215	547	1233	"	SepB (<i>S. agalactiae</i>)	38(55) / 1194	Protéase à sérine
5406	2082	1150	LPXT/N	SepB (<i>S. agalactiae</i>)	99(99) / 1150	C5a peptidase
5658	2390	690	"	SPy0872 (<i>S. pyogenes</i>)	60(74) / 688	5'-nucleotidase sécrétée
4965	1551	890	FPKT/G	No homology in public databases		inconnue

^a, Les protéines ancrées au peptidoglycane ont été identifiées par la recherche d'un motif LPXTG ou un motif voisin C-terminal suivi d'un domaine hydrophobe et d'acides aminés basiques. Les similarités par BLASTP avec des protéines à domaine LPXTG connues ont aussi été utilisées.

^b, Seulement les similarité avec une probabilité BLASTP <10⁻¹⁰ ont été considérées comme significatives. ^c, La fonction a été prédite par analogie avec celles des protéines homologues contenues dans la bases de séquences protéique nrprot du NCBI.

TABLEAU 7. Distribution des gènes codant pour des protéines de surface à motif LPXTG parmi des isolats cliniques indépendants de 5 sérotypes de *S. agalactiae*.

Seq ID (ADN)	N° d'IPF	Proportion des souches portant le gène						
		Type Ia 23 isolats	Type Ib 7 isolats	Type II 12 isolats	Type III 39 isolats	Type V 16 isolats	non groupé 2 isolats	Fréquence totale 99 isolats
4926	1503	100	100	100	100	100	100	100
6331	678	100	100	100	100	100	100	100
5491	2192	100	100	100	100	100	100	100
5234	1861	100	100	100	100	100	100	100
6246	584	100	100	100	100	100	100	100
5842	280	100	100	100	100	100	100	100
6247	585	86,9	85,7	91,7	92,3	81,3	100	88,9
4965	1551	34,8	85,7	100	94,8	93,8	100	80,8
6447	807	26,1	85,7	83,3	92,3	93,8	100	79,8
5610	2337	86,9	100	100	56,4	100	50	78,8
6236	571	82,6	100	83,3	46,1	100	50	71,7
5103	1716	91,0	100	83,3	38,5	81,3	50	67,7
5607	2334	56,5	100	83,3	46,1	100	50	65,6
6411	765	30,4	71,4	41,7	61,5	87,5	100	57,6
4921	15	65,2	0	41,7	59	12,5	50	46,5
5090	17	4,3	14,3	16,7	20,5	6,3	0	13,1
5180	18	4,3	14,3	0	20,5	6,3	0	11,1
4706	1248	0	0	0	12,8	6,3	0	6
5497	220	0	14,3	8,3	5,1	0	0	4,5
4708	1250	0	14,3	0	5,1	0	0	3
5677	2414	0	0	0	7,7	0	0	3

TABLEAU 8. Lipoprotéines

Seq ID (ADN)	N° d'IPF	Annotation
6527	9	unknown
6030	339	similar to unknown proteins
6035	344	Similar to ABC transporter (binding protein)
6137	460	Similar to ABC transporter (binding protein)
6178	504	similar to unknown proteins
6294	638	Similar to unknown proteins
6335	682	Similar to adhesion proteins
6377	729	similar to oligopeptide and pheromone binding protein
6386	739	similar to other lipoprotein
4495	1018	Similar to (oligopeptide) ABC transporter (binding protein)
4596	1119	similar to ribose ABC transporter (binding protein)
4636	1162	similar to (amino acid ?) ABC transporter (binding protein)
4730	1280	similar to ABC transporter (binding protein)
4816	1377	Similar to nickel ABC transporter (binding protein)
4836	1399	similar to phosphate ABC transporter (binding protein)
4906	1481	Similar to D,D-carboxypeptidase
4920	1499	similar to peptidyl-prolyl cis-trans isomerase
4925	1502	similar to metal ABC transporter (binding protein)
4963	1547	Unknown
5021	1617	Similar to unknown lipoprotein
5158	1775	similar to ferrichrome ABC transporter (binding protein)
5247	1879	similar to oligopeptide ABC transporter (binding protein)
5306	1955	similar to glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein)
5417	2099	similar to putative ABC transporter (binding protein)
5423	2103	Unknwon, similar to unknown protein and to B. subtilis SpoIIJ protein
5450	2133	laminin-binding surface protein
5486	2185	putative ABC transporter (binding protein)

5559	2278	putative ABC transporter (binding protein)
5591	2314	similar to protease maturation protein
5677	2414	Similar to plasmid related proteins, Putative peptidoglycan bound protein (LPXTG motif)
5718	2464	Similar to unknown proteins
5732	2482	similar to ferrichrome ABC transporter (binding protein)
5799	2597	similar to amino acid ABC transporter (binding protein)
5800	2598	similar to phosphate ABC transporter (binding protein)
5837	2789	Unknown
5861	2843	Similar to amino acid ABC transporter (binding protein)
5883	2875	Unknown
5923	2922	Similar to amino acid ABC transporter (binding protein)

- Les gènes codant pour des lipoprotéines ont été identifiés sur la base de la prédiction du motif de coupure / modification de type lipoprotéine [S. Hayashi, H. C. Wu, *J Bioenerg Biomembr* 22, 451 (1990)] et d'un peptide signal (identifié en utilisant
- 5 SignalP vs2.0 [H Nielsen, *Prot Engin* 12, 13-9. (1999)]) et par l'analyse des résultats de comparaison sur les banques de séquence protéiques en utilisant BLAST [S. F. Altschul et al., *Nucleic Acids Res* 25, 3389-402. (1997)].

Tableau 9. Autres protéines de surface

10

Seq ID (ADN)	N° d'IPF	Annotation
6037	347	group B streptococcal surface immunogenic protein
4972	1562	Putative cell wall protein, weakly similar to peptidase or esterase
6569	948	similar to fibronectin-binding protein
5234	1861	similar to cell wall proteins
5530	2238	possible surface protein
5223	1847	CAMP factor

Ces protéines ont été identifiées sur la base de similarité avec d'autres protéines de surface bactérienne et la prédiction d'un peptide signal et ne faisant pas partie des classes des protéines ancrées au peptidoglycane et lipoprotéines.

5 **TABLEAU 10.** Protéines impliquées dans la biosynthèse de composés polysaccharidiques de la paroi de *S. agalactiae*.

Seq ID (ADN)	N° d'IPF	Annotation	Commentaires
4861	1430	similar to Streptococcus mutans RgpG protein required for biosynthesis of rhamnose-glucose polysaccharide	
6214	544	similar to rhamnosyltransferase	
6061	381	Unknown, Similar to UDP-N-acetylmuramoylalanine--D-glutamate ligase	
6517	890	similar to Cell Wall Muropeptide Branching Enzyme	
6518	891	similar to cell wall muropeptide branching enzyme	
6519	892	similar to cell wall muropeptide branching enzyme	
4743	1295	similar to glycosyltransferases	
6343	692	similar to hexosyltransferase	
6342	691	similar to glucosyl transferase	
5326	1977	Similar to UDP-D-glucose:galactosyl glucosyltransferase	
4952	1532	similar to N-acetylneuraminic acid synthetase	
5619	2346	capsular polysaccharide biosynthesis protein	Biosynthèse de la capsule
5618	2345	similar to glycosyl transferase	
5617	2344	similar to glycosyl transferase	
5616	2343	capsular polysaccharide repeating-unit polymerase	
5615	2342	beta-1,4-galactosyltransferase	
5614	2341	beta-1,4-galactosyltransferase enhancer	
5613	2340	similar to glucose-1-phosphate transferase	
5611	2339	capsular polysaccharide chain length regulator/exporter	
5696	2437	putative chain length regulator CpsC	
5971	301	similar to dTDP-glucose-4,6-dehydratase	
5233	1860	similar to to Cell Wall Muropeptide Branching Enzyme	

5602	2329	similar to capsular polyglutamate biosynthesis	
5156	1773	Similar to UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase	
5574	2297	Similar to putative hexosyltransferase	
5573	2296	Similar to rhamnosyl transferase 1	
5654	2386	Similar to capsular polysaccharide synthesis protein	
5656	2388	Similar to putative rhamnosyltransferase	
5526	2233	Similar to putative rhamnosyltransferase	
5527	2235	Similar to nucleotide-sugar dehydratase	
5529	2237	Similar to Pneumococcal LicD2 protein involved in phosphorylcholine metabolism	
5534	2241	similar to rhamnosyltransferase	
5625	2354	similar to putative rhamnosyltransferase	
5626	2355	dTDP-L-rhamnose synthase	
6223	555	Similar to putative glucosyl transferase	
6229	562	Similar to hypothetical glycosyl transferase	
6230	563	Similar to putative glycosyltransferase	
6231	565	Similar to putative glycosyl transferase	
6232	566	Similar to putative glycosyl transferase	
6233	567	Similar to putative glycosyl transferase	
5764	2518	similar to putative sugar transferase	
6095	416	similar to UDP-N-acetylglucosamine pyrophosphorylase	
5089	1699	Similar to UDP-N-acetylmuramate-alanine ligase	
5466	2158	similar to glycosyl transferase	
5465	2157	similar to glycosyl transferase	

Ces gènes ont été identifiés par l'analyse des résultats de similarité avec les séquences protéiques connues en utilisant le logiciel BLASTP. Les produits de ces gènes pourraient intervenir dans la biosynthèse de polysaccharides qui pourraient être

5 des constituants de préparations vaccinales.

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REVENDICATIONS

1. Séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi les séquences SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345.
2. Séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi :
- a) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345 ;
 - 10 b) une séquence nucléotidique hybridant dans des conditions de forte stringence avec une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, et comprenant au moins 20 nucléotides ;
 - c) une séquence nucléotidique complémentaire d'une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, ou complémentaire d'une séquence
 - 15 nucléotidique telle que définie en a), ou b), ou une séquence nucléotidique de l'ARN correspondant à l'une des séquences a) ou b) ;
 - d) une séquence nucléotidique d'un fragment représentatif d'une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, ou d'un fragment représentatif d'une séquence nucléotidique telle que définie en a), b) ou c) et
 - 20 comprenant au moins 20 nucléotides ;
 - e) une séquence nucléotidique comprenant une séquence telle que définie en a), b), c) ou d) ; et
 - f) une séquence nucléotidique telle que définie en a), b), c), d) ou e) modifiée et comportant au plus 10 % de nucléotides modifiés par rapport à la séquence de
 - 25 référence.
3. Séquence nucléotidique selon la revendication 2, caractérisée en ce qu'il s'agit d'une séquence issue d'une séquence choisie parmi SEQ ID No. 1 à SEQ ID No. 139 et SEQ ID No. 2345, et en ce qu'elle code pour un polypeptide, choisi de préférence parmi les séquences SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No.
- 30 2346 à SEQ ID No. 4481.
4. Séquence nucléotidique caractérisée en ce qu'elle comprend une séquence nucléotidique choisie parmi :
- a) une séquence nucléotidique selon la revendication 3 ou choisie parmi les séquences SEQ ID No. 4482 à SEQ ID No. 6617 ;

- b) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence nucléotidique selon la revendication 3 ;
- c) une séquence nucléotidique s'hybridant dans des conditions de forte stringence avec une séquence nucléotidique selon la revendication 3 et comprenant au moins 20 nucléotides ;
- d) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a), b), c) ou d) et comprenant au moins 20 nucléotides ; et
- f) une séquence telle que définie en a), b), c), d) ou e) modifiée et comportant au plus 10 % de nucléotides modifiés par rapport à la séquence de référence.

5. Polypeptide codé par une séquence nucléotidique selon l'une des revendications 2 à 4.

6. Polypeptide selon la revendication 5, caractérisé en ce qu'il est choisi parmi les polypeptides choisis parmi SEQ ID No. 140 à SEQ ID No. 2344, et SEQ ID No. 2346 à SEQ ID No. 4481.

7. Polypeptide caractérisé en ce qu'il comprend un polypeptide choisi parmi :

- a) un polypeptide selon l'une des revendications 5 et 6 ;
- b) un polypeptide présentant au moins 80 % d'identité avec un polypeptide selon l'une des revendications 5 et 6 ;
- c) un fragment d'au moins 5 acides aminés d'un polypeptide selon l'une des revendications 5 et 6, ou tel que défini en b) ;
- d) un fragment biologiquement actif d'un polypeptide selon l'une des revendications 5 et 6, ou tel que défini en b) ou c) ; et
- e) un polypeptide selon l'une des revendications 5 et 6 ou tel que défini en b), c) ou d) modifié et comportant au plus 10 % d'acides aminés modifiés par rapport à la séquence de référence.

8. Séquence nucléotidique codant pour un polypeptide selon la revendication 7.

9. Séquence nucléotidique isolée codant pour un polypeptide spécifique de *Streptococcus agalactiae* choisi parmi les polypeptides de séquence SEQ ID No. 140 à SEQ ID No. 2344 et SEQ ID No. 2346 à SEQ ID No. 4481.

10. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans la biosynthèse des acides aminés ou l'un de ses fragments.
11. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9,
- 5 caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs ou l'un de ses fragments.
12. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide d'enveloppe cellulaire ou situé à la
- 10 surface de *Streptococcus agalactiae* ou l'un de ses fragments.
13. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans la machinerie cellulaire ou l'un de ses fragments.
14. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9,
- 15 caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme intermédiaire central ou l'un de ses fragments.
15. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme énergétique ou l'un de ses fragments.
- 20 16. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme des acides gras et des phospholipides ou l'un de ses fragments.
17. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9,
- 25 caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides ou l'un de ses fragments.
18. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae*
- 30 impliqué dans les fonctions de régulation ou l'un de ses fragments.
19. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de réplication ou l'un de ses fragments.

20. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de transcription ou l'un de ses fragments.
- 5 21. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de traduction ou l'un de ses fragments.
22. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de transport et de liaison des protéines ou l'un de ses fragments.
- 10 23. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans l'adaptation aux conditions atypiques ou l'un de ses fragments.
24. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans la sensibilité aux médicaments et analogues ou l'un de ses fragments.
- 15 25. Séquence nucléotidique selon l'une des revendications 2 à 4, 8 et 9, caractérisée en ce qu'elle code pour un polypeptide de *Streptococcus agalactiae* impliqué dans les fonctions relatives aux transposons ou l'un de ses fragments.
- 20 26. Séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi :
- a) une séquence choisie parmi les séquences SEQ ID N° 6194,6236,5497,5791,5103,4705,5610,5234,4926,6331,6247,5842,5741,4921,5090,518 0,4706,4708,5677,6246,6411,5578,6446,6447,5607,6209,6215,5406,5658,4965, de
- 25 préférence parmi les séquences SEQ ID N°4926,6331,5491,5234,6246,5842 ;
- b) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence nucléotidique du a) ;
- c) une séquence nucléotidique s'hybridant dans des conditions de forte stringence avec une séquence nucléotidique du a) ou b) et comprenant au moins 20
- 30 nucléotides ;
- d) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a), b) ou c) ;
- e) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a), b), c) ou d) et comprenant au moins 20 nucléotides ; et

f) une séquence telle que définie en a), b), c), d) ou e) modifiée et comportant au plus 10 % de nucléotides modifiés par rapport à la séquence de référence ;

et en ce qu'elle code pour une protéine de surface avec un motif d'ancrage LPXTG.

- 5 27. Séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi les séquences SEQ ID N°6035,6137,6335,6377,6386,4495,4596,4636,4730,4816,4836,4906,4920,4925,5158,5247, 5306,5417,5450,5486,5559,5591,5677,5732,5799,5800,5861,5923 et en ce qu'elle code pour une lipoprotéine.
- 10 28. Séquence nucléotidique isolée de *Streptococcus agalactiae*, caractérisée en ce qu'elle est choisie parmi les séquences SEQ ID N°4861,6214,6061,6517,6518,6519,4743,6343,6342,5326,4952,5619,5618,5617,5616,5615,5614,5613,5611,5696,5971,5233,5602,5156,5574,5573,5654,5656,5526,5527,5529,5534,5625,5626,6223,6229,6230,6231,6232,6233,5764,6095,5089,5466,5465 et en ce
- 15 qu'elle code pour une protéine impliquée dans la biosynthèse de composés polysaccharidiques de paroi.
29. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans la biosynthèse des acides aminés ou l'un de ses fragments.
- 20 30. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs ou l'un de ses fragments.
31. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide d'enveloppe cellulaire ou situé à la surface de *Streptococcus*
- 25 *agalactiae* ou l'un de ses fragments.
32. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans la machinerie cellulaire ou l'un de ses fragments.
33. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il
- 30 s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme intermédiaire central ou l'un de ses fragments.
34. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme énergétique ou l'un de ses fragments.

35. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme des acides gras et des phospholipides ou l'un de ses fragments.
- 5 36. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides ou l'un de ses fragments.
37. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans les fonctions de régulation ou l'un de ses fragments.
- 10 38. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de réplication ou l'un de ses fragments.
39. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de
- 15 transcription ou l'un de ses fragments.
40. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de traduction ou l'un de ses fragments.
41. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il
- 20 s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans le processus de transport et de liaison des protéines ou l'un de ses fragments.
42. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans l'adaptation aux conditions atypiques ou l'un de ses fragments.
- 25 43. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans la sensibilité aux médicaments et analogues ou l'un de ses fragments.
44. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il s'agit d'un polypeptide de *Streptococcus agalactiae* impliqué dans les fonctions
- 30 relatives aux transposons ou l'un de ses fragments.
45. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il est codé par une séquence selon la revendication 26 et est une protéine de surface avec un motif d'ancrage LPXTG.

46. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il est codé par une séquence selon la revendication 27 et est une lipoprotéine.
47. Polypeptide selon l'une des revendications 5 à 7, caractérisé en ce qu'il est codé par une séquence selon la revendication 28 et est une protéine impliquée dans la biosynthèse de composés polysaccharidiques de paroi.
48. Séquence nucléotidique utilisable comme amorce ou comme sonde, caractérisée en ce que ladite séquence est choisie parmi les séquences nucléotidiques selon l'une des revendications 2 à 4, 8 à 28.
49. Séquence nucléotidique selon la revendication 48, caractérisée en ce qu'elle est marquée par un composé radioactif ou par un composé non radioactif.
50. Séquence nucléotidique selon l'une des revendications 48 et 49, caractérisée en ce qu'elle est immobilisée sur un support, de manière covalente ou non-covalente.
51. Séquence nucléotidique selon la revendication 50, caractérisée en ce qu'elle est immobilisée sur un support tel qu'un filtre à haute densité ou une puce à ADN.
52. Séquence nucléotidique selon l'une des revendications 49 à 51 pour la détection et/ou l'amplification de séquences nucléiques.
53. Puce à ADN ou filtre, caractérisée en ce qu'elle contient au moins une séquence nucléotidique selon la revendication 51.
54. Puce à ADN ou filtre selon la revendication 53, caractérisée en ce qu'elle contient en outre au moins une séquence nucléotidique d'un micro-organisme autre que *Streptococcus agalactiae*, immobilisée sur le support de ladite puce.
55. Puce à ADN ou filtre selon la revendication 54, caractérisée en ce que le micro-organisme autre est choisi parmi un micro-organisme associé à *Streptococcus agalactiae*, une bactérie du genre *Streptococcus*, et un variant de *Streptococcus agalactiae*.
56. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé, caractérisé en ce qu'il comprend une puce à ADN ou un filtre selon la revendication 53.
57. Kit ou nécessaire pour la détection et/ou l'identification d'un micro-organisme, caractérisé en ce qu'il comprend une puce à ADN ou un filtre selon l'une des revendications 54 et 55.
58. Kit ou nécessaire pour la détection et/ou la quantification de l'expression d'au moins un gène de *Streptococcus agalactiae*, caractérisé en ce qu'il comprend une puce à ADN ou un filtre selon l'une des revendications 53 à 55.

59. Vecteur de clonage, et/ou d'expression, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 1 à 4, 8 à 28.
60. Cellule hôte, caractérisée en ce qu'elle est transformée par un vecteur selon la revendication 59.
- 5 61. Cellule hôte selon la revendication 60, caractérisée en ce qu'il s'agit d'une bactérie appartenant au genre *Streptococcus*.
62. Cellule hôte selon la revendication 61, caractérisée en ce qu'il s'agit d'une bactérie appartenant à l'espèce *Streptococcus agalactiae*.
63. Végétal ou animal, excepté l'Homme, comprenant une cellule transformée selon l'une des revendications 60 à 62.
- 10 64. Procédé de préparation d'un polypeptide, caractérisé en ce que l'on cultive une cellule transformée par un vecteur selon la revendication 59 dans des conditions permettant l'expression dudit polypeptide et que l'on récupère ledit polypeptide recombinant.
- 15 65. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 64.
66. Procédé de préparation d'un polypeptide synthétique selon l'une des revendications 5 à 7, 29 à 47, caractérisé en ce que l'on effectue une synthèse chimique dudit polypeptide.
- 20 67. Polypeptide hybride, caractérisé en ce qu'il comprend au moins la séquence d'un polypeptide selon l'une des revendications 5 à 7, 29 à 47 et 65, et une séquence d'un polypeptide susceptible d'induire une réponse immunitaire chez l'homme ou l'animal.
68. Séquence nucléotidique codant pour un polypeptide hybride selon la revendication 67.
- 25 69. Vecteur caractérisé en ce qu'il contient une séquence nucléotidique selon la revendication 68.
70. Anticorps monoclonal ou polyclonal, ses fragments, ou anticorps chimérique, caractérisé en ce qu'il est capable de reconnaître spécifiquement un polypeptide selon l'une des revendications 5 à 7, 29 à 47, 65 et 67.
- 30 71. Anticorps selon la revendication 70, caractérisé en ce qu'il s'agit d'un anticorps marqué.

72 Procédé pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes :

- 5 a) mise en contact de l'échantillon biologique avec un anticorps selon l'une des revendications 70 et 71 ;
b) mise en évidence du complexe antigène-anticorps éventuellement formé.

73. Procédé pour la détection de l'expression d'un gène de *Streptococcus agalactiae* caractérisé en ce que l'on met en contact une souche de *Streptococcus agalactiae*, avec un anticorps selon la revendication 70 ou 71 et que l'on détecte le
10 complexe antigène/anticorps éventuellement formé.

74. Kit ou nécessaire pour la mise en œuvre d'un procédé selon la revendication 72 ou 73, caractérisé en ce qu'il comprend les éléments suivants :

- a) un anticorps selon l'une des revendications 70 et 71 ;
b) éventuellement, les réactifs pour la constitution du milieu propice à la réaction
15 immunologique ;
c) éventuellement, les réactifs permettant la mise en évidence des complexes antigène-anticorps produits par la réaction immunologique.

75. Polypeptide selon l'une des revendications 5 à 7, 32 à 47, 65 et 67, ou anticorps selon l'une des revendications 64 et 65, caractérisé en ce qu'il est immobilisé
20 sur un support, notamment une puce à protéine.

76. Puce à protéine, caractérisée en ce qu'elle contient au moins un polypeptide selon l'une des revendications 5 à 7, 32 à 47, 65 et 67, ou au moins un anticorps selon l'une des revendications 70 et 71, immobilisé sur le support de ladite puce.

77. Puce à protéine selon la revendication 76, caractérisée en ce qu'elle contient
25 en outre au moins un polypeptide de micro-organisme autre que *Streptococcus agalactiae* ou au moins un anticorps dirigé contre un composé de micro-organisme autre que *Streptococcus agalactiae*, immobilisé sur le support de ladite puce.

78. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé,
30 caractérisé en ce qu'il comprend une puce à protéine selon l'une des revendications 76 et 77.

79. Kit ou nécessaire pour la détection et/ou l'identification d'un micro-organisme, caractérisé en ce qu'il comprend une puce à protéine selon la revendication 77.

80. Procédé de détection et/ou d'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé dans un échantillon biologique, caractérisé en ce qu'il met en œuvre une séquence nucléotidique selon l'une des revendications 2 à 4, 8, 9, 11 à 13, 17 à 25, 48 à 52 et 68.

5 81. Procédé selon la revendication 80, caractérisé en ce qu'il comporte les étapes suivantes :

- a) éventuellement, isolement de l'ADN à partir de l'échantillon biologique à analyser, ou obtention d'un ADNc à partir de l'ARN de l'échantillon biologique ;
- b) amplification spécifique de l'ADN de bactéries appartenant à l'espèce *Streptococcus*
10 *agalactiae* ou à un micro-organisme associé à l'aide d'au moins une amorce selon l'une des revendications 48 à 52 ;
- c) mise en évidence des produits d'amplification.

82. Procédé selon la revendication 80, caractérisé en ce qu'il comprend les étapes suivantes :

- 15 a) mise en contact d'une sonde nucléotidique selon l'une des revendications 48 à 52, avec un échantillon biologique, l'acide nucléique contenu dans l'échantillon biologique ayant, le cas échéant, préalablement été rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme
20 associé ;
- b) mise en évidence de l'hybride éventuellement formé entre la sonde nucléotidique et l'acide nucléique de l'échantillon biologique.

83. Procédé selon la revendication 80, caractérisé en ce qu'il comprend les étapes suivantes :

- 25 a) mise en contact d'une sonde nucléotidique immobilisée sur un support selon la revendication 50 avec un échantillon biologique, l'acide nucléique de l'échantillon ayant, le cas échéant, été préalablement rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé ;
- 30 b) mise en contact de l'hybride formé entre la sonde nucléotidique immobilisée sur un support et l'acide nucléique contenu dans l'échantillon biologique, le cas échéant après élimination de l'acide nucléique de l'échantillon biologique n'ayant pas hybridé avec la sonde, avec une sonde nucléotidique marquée selon la revendication 49 ;

c) mise en évidence du nouvel hybride formé à l'étape b).

84. Procédé selon la revendication 83, caractérisé en ce que, préalablement à l'étape a), l'ADN de l'échantillon biologique ou l'ADNc obtenu éventuellement par transcription inverse de l'ARN de l'échantillon, est amplifié à l'aide d'au moins une amorce selon l'une des revendications 48 à 52.

85. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique selon l'une des revendications 48 à 52;
- 10 b) éventuellement, les réactifs nécessaires à la mise en œuvre d'une réaction d'hybridation ;
- c) éventuellement, au moins une amorce selon l'une des revendications 48 à 52 ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

86. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique, dite sonde de capture, selon la revendication 50 ;
- b) une sonde oligonucléotidique, dite sonde de révélation, selon la revendication 49;
- c) éventuellement, au moins une amorce selon l'une des revendications 48 à 52 ainsi
- 20 que les réactifs nécessaires à une réaction d'amplification de l'ADN.

87. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae* ou à un micro-organisme associé, caractérisé en ce qu'il comprend les éléments suivants :

- a) au moins une amorce selon l'une des revendications 48 à 52;
- 25 b) éventuellement, les réactifs nécessaires pour effectuer une réaction d'amplification d'ADN ;
- c) éventuellement, un composant permettant de vérifier la séquence du fragment amplifié, plus particulièrement une sonde oligonucléotidique selon l'une des revendications 48 à 52.

- 30 88. Procédé selon les revendications 72, 73 et 80 à 84 ou kit ou nécessaire selon les revendications 74, 78, 79 et 85 à 87 pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Streptococcus agalactiae*, caractérisé en ce que ladite amorce et/ou ladite sonde sont choisies parmi les séquences nucléotidiques selon l'une des revendications 2 à 4, 8 à 28, 48 à 52, et 68 spécifiques de l'espèce *Streptococcus*

agalactiae, en ce que lesdits polypeptides sont choisis parmi les polypeptides selon l'une des revendications 5 à 7, 32 à 47, 65 et 67 spécifiques de l'espèce *Streptococcus agalactiae* et en ce que lesdits anticorps sont choisis parmi les anticorps selon l'une des revendications 70 et 71 dirigés contre les polypeptides choisis parmi les polypeptides selon l'une des revendications 5 à 7, 32 à 47, 65 et 67 spécifiques de l'espèce *Streptococcus agalactiae*.

89. Souche de *Streptococcus agalactiae*, caractérisée en ce qu'elle contient au moins une mutation dans au moins une séquence nucléotidique selon l'une des revendications 2 à 4, 8 à 28.

10 90. Souche de *Streptococcus agalactiae* selon la revendication 89, caractérisée en ce que la mutation mène à une inactivation du gène.

91. Souche de *Streptococcus agalactiae* selon la revendication 89, caractérisée en ce que la mutation mène à une surexpression du gène.

92. Utilisation d'une séquence nucléotidique selon l'une des revendications 2 à 4, 8 à 28, d'un polypeptide selon l'une des revendications 5 à 7, 32 à 47, 65 et 67 d'un anticorps selon l'une des revendications 70 et 71, d'une cellule selon l'une des revendications 60 à 62, et/ou d'un animal transformé selon la revendication 63 pour la sélection de composé organique ou inorganique capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la réplication cellulaire de cellules eucaryotes ou procaryotes ou capables d'induire, d'inhiber ou d'aggraver chez un organisme animal ou humain les pathologies liées à une infection par *Streptococcus agalactiae* ou par un micro-organisme associé.

93. Méthode de sélection de composé capable de se lier à un polypeptide selon l'une des revendications 5 à 7, 32 à 47, 65 et 67, capable de se lier à une séquence nucléotidique selon l'une des revendications 2 à 4, 8 à 28, ou capable de reconnaître un anticorps selon l'une des revendications 70 et 71, et/ou capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la réplication cellulaire de cellules eucaryotes ou procaryotes, ou capable d'induire, d'inhiber ou d'aggraver chez un organisme animal ou humain les pathologies liées à une infection par *Streptococcus agalactiae*, caractérisée en ce qu'elle comprend les étapes suivantes :

a) mise en contact dudit composé avec ledit polypeptide, ladite séquence nucléotidique, avec une cellule transformée selon l'une des revendications 60 à 62, et/ou administration dudit composé à un animal transformé selon la revendication 63 ;

- b) détermination de la capacité dudit composé à se lier avec ledit polypeptide ou ladite séquence nucléotidique, ou de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, ou de moduler la croissance ou la réplication cellulaire, ou d'induire, d'inhiber ou d'aggraver chez ledit organisme animal ou humain les pathologies liées à une infection par *Streptococcus agalactiae* ou par un micro-organisme associé.

94. Composition pharmaceutique comprenant un composé choisi parmi les composés suivants :

- a) une séquence nucléotidique selon l'une des revendications 2 à 4, 8 à 28 ;
b) un polypeptide selon l'une des revendications 5 à 7, 32 à 47, 65 et 67;
c) un vecteur selon la revendication 59 ou 69 ; et
d) un anticorps selon la revendication 70 ou 71.

95. Composition selon la revendication 94, éventuellement en association avec un véhicule pharmaceutiquement acceptable.

96. Composition pharmaceutique selon l'une des revendications 94 et 95 pour la prévention et le traitement d'une infection par une bactérie appartenant à l'espèce *Streptococcus agalactiae*.

97. Composition immunogène, caractérisée en ce qu'elle comprend un ou plusieurs polypeptides selon l'une des revendications 5 à 7, 32 à 47, 65, et/ou un ou plusieurs polypeptides hybrides selon la revendication 67.

98. Utilisation d'une cellule selon l'une des revendications 60 à 62, ou d'un vecteur selon l'une des revendications 59 ou 69 pour la préparation d'une composition vaccinale.

99. Composition vaccinale, caractérisée en ce qu'elle contient un polynucléotide selon l'une des revendications 1 à 4, 8 à 28, un vecteur selon l'une des revendications 59 ou 69, et/ou une cellule selon l'une des revendications 60 à 62.

100. Composition vaccinale, caractérisée en ce qu'elle contient au moins un polypeptide codé par un polynucléotide de séquence choisie parmi SEQ ID N°1503,678,2192,1861,584,280.

101. Composition vaccinale selon la revendication 100, caractérisée en ce qu'il s'agit d'une composition vétérinaire

102. Composition immunogène capable d'induire une réponse immunitaire cellulaire ou humorale pour la prévention ou le traitement d'une infection par une bactérie appartenant à l'espèce *Streptococcus agalactiae*, caractérisée en ce qu'elle

comprend une composition immunogène selon la revendication 97, ou une composition vaccinale selon la revendication 99 ou 100, en association avec un véhicule pharmaceutiquement acceptable et éventuellement un ou plusieurs adjuvants de l'immunité appropriés.

- 5 103. Banque génomique de *Streptococcus agalactiae* CIP 82.45 (ATCC 12403).
104. Banque d'ADN génomique selon la revendication 101, caractérisée en ce que ladite banque d'ADN est clonée dans un plasmide.
105. Banque selon la revendication 101 ou 102, caractérisée en ce qu'il s'agit
10 de la banque déposée à la CNCM le 28 décembre 2000 sous le N° I-2610.
106. Utilisation des banques génomiques selon l'une des revendications 101 à 103 pour isoler des séquences nucléotidiques spécifiques de *Streptococcus agalactiae*, caractérisée en ce que les séquences nucléotidiques de *Streptococcus* autres que *Streptococcus agalactiae* CIP 82.45 (ATCC 12403) sont alignées et en ce que les
15 données obtenues par cet alignement sont traitées pour isoler lesdites séquences spécifiques.
107. Procédé d'identification de séquence spécifique de *Streptococcus agalactiae*, caractérisé par l'alignement de séquences nucléotidiques de *Streptococcus agalactiae* selon les revendications 1 à 4, 8 à 9 et le traitement des données obtenues par
20 cet alignement pour isoler les séquences spécifiques.
108. Souche mutante NEM 1979 de *Streptococcus agalactiae* selon la revendication 89 déposée à la CNCM le 24 avril 2002 sous le N° I-2861.
109. Souche mutante NEM 2056 de *Streptococcus agalactiae* selon la revendication 89 déposée à la CNCM le 24 avril 2002 sous le N° I-2862.
- 25 110. Souche mutante NEM 2057 de *Streptococcus agalactiae* selon la revendication 89 déposée à la CNCM le 24 avril 2002 sous le N° I-2863.